SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	1.0.		17.27 4.462e-11 47-70
	ļ	1	PR00449D 10.79 7.120e-
		1	11 109-123
235	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 7.300e-
		SIGNATURE	10 251-265 PR00019B
	1		11.36 5.320e-09 119-
			133 PR00019B 11.36
225	200000		1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300c- 10 245-259 PR00019B
		DIGHT ON B	11.36 5.320e-09 113-
	<b>!</b>	1	127 PR00019B 11.36
			1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN	PD00289 9.97 8.448e-09
	L	REPEAT PRESYNA.	67-81
240	PR00011	TYPE III EGF-LIKE	PR00011D 14.03 3.492e-
		SIGNATURE	10 616-635
241	PR00011	TYPE III EGF-LIKE	PRODOLID 14.03 3.492e-
244	BL00903	SIGNATURE Cytidine and	10 616-635 BL00903 12.93 8.941e-
~31	500000	deoxycytidylate	12 54-64
	ļ	deaminases zinc-binding	
		region s.	
245	DM00179	w KINASE ALPHA ADHESION	DM00179 13.97 8.043e-
		T-CELL.	09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e-
			40 186-239 BL00246B 20.32 1.000e-40 305-
		ľ	351 BL00246B 13.69
	Į		4.176e-36 105-140
	ł		BL00246A 15.75 2.286e-
			24 70-90 BL00246C
		1	15.56 4.857e-22 150-
250	222222	NEW YORK OF THE PROPERTY OF TH	175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e-
254	BL00674	AAA-protein family	BL00674B 4.46 1.000e-
•		proteins.	09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE	PD01796 15.01 6.045e-
		COBALT ZINC CADMIU.	09 61-88
255	BL50002	Src homology 3 (SH3)	BL50002B 15.18 2.800e-
258	PR00094	domain proteins profile. ADENYLATE KINASE	10 421-435 PR00094C 12.94 2.200e-
258	PR00094 .	SIGNATURE	18 87-104 PR00094D
	1	- ZOMA ONE	12.52 2.731e-14 161-
	1	1	177 PR00094A 10.31
	1	1	5.500e-14 11-25
	1	İ	PR00094B 11.01 4.115e-
	1		13 39-54 PR00094E
	[		11.25 7.333e-13 178-
250	BT 00902	UTT family past-i	193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e-
262	BL00388 ·	Proteasome A-type	BL00388A 23.14 1.000e-
		subunits proteins.	40 8-54 BL00388B
	i		31.38 3.864e-33 66-108
	1	1	BL00388D 20.71 1.000e-
	1		21 153-184 BL00388C
	1	1	18.79 8.147e-16 126-
-524	Dragge	- A. C. V.	148
264	BI-00903	Cytidine and	BL00903 12.93 5.821e- 09 91-101
	Į.	deoxycyticylate deaminases zinc-binding	03 31-101
	1	region s.	1
267	BL00107	Protein kinases ATP-	BL00107B 13.31 1.529e-
		binding region proteins.	09 241-257
270	BL00226	Intermediate filaments	BL00226D 19.10 1.000e-
		proteins.	37 352-409 BL00226B
		<del></del>	

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	·	·	23.86 8.043e-35 196- 244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e- 15 96-111
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	PD02952C 15.76 9.731e- 16 235-265 PD02952B 15.57 5.625e-09 215- 229
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e- 40 106-160 PD02929B 18.36 8.800e-17 179- 199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e- 09 213-250
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR03424D 14.32 6.45le- 11 39-59
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e- 13 137-184 BL00052B 15.17 5.143e-12 208- 235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e- 13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e- 21 51-68 PR00319B 11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e- 21 38-55 PR00319B 11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366c- 09 149-163
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e- 12 203-216
295	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e- 15 322-339 BL00028 16.07 9.471e-14 433- 450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e- 13 760-77 BL00028 16.07 9.550e-13 788- 805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e- 12 461-478 BL00028 16.07 8.435e-12 844- 861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e- 11 211-228 BL00028 16.07 5.154e-11 732- 749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e- 11 816-833 BL00028 16.07 7.231e-11 676- 693 BL00028 16.07

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,		·	BL00028 16.07 4.086e- 09 517-534 BL00028 16.07 7.429e-09 489- 506
296	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.333e- 16 111-136 BL00215A 15.82 2.723e-11 10-35 BL00215B 10.44 9.526e- 11 152-165 BL00215B 10.44 7.375e-10 59-72 BL00215A 15.82 9.824e- 10 205-230
302	PF00953	Glycosyl transferase.	PF00953C 19.70 8.773e- 34 236-269 PF00953A 19.68 5.000e-25 102- 129. PF00953B 6.17 1.000e-13 182-194
304	PF00152	tRNA synthetases class	PF00152D 21.30 8.364e- 28 422-461 PF00152C 28.03 9.250e-21 220- 257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e- 11 44-67
305	PD01066	PROTEIN ZINC FINGER ZINC-PINGER METAL- BINDING NU.	PD01066 19.43 8.250e- 35 37-76
305	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 5.840e- 09 92-135
307	PR00454	ETS DOMAIN SIGNATURE	PRO0454C 11.24 7.808e- 09 1167-1186
30B	PR00237	RHODDPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237B 13.03 5.091e- 13 188-212 PR00237G 19.63 7.207e-13 268- 295 PR00237A 11.48 4.375e-11 24-49 PR00237C 15.69 3.057e- 10 101-124 PR00237D 8.94 4.750e-10 137-159 PR00237P 13.57 5.364e- 10 230-255 PR00237B 13.50 9.438e-10 57-79
309	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 7.577e- 24 315-339 BL00522F 14.90 1.310e-15 470- 494 BL00522A 25.52 1.265e-14 179-226 BL00522E-19.63 8.615e- 14 430-460 BL00522B 27.30 9.625e-12 267- 313
310	BL00326	Tropomyosins proteins.	BL00326D 8.76 5.235e- 10 856-897
312	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.706e- 14 151-174 BL00290B 13.17 9.000e-12 211- 229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20
315	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 5.091e- 15 63-76
317	BL01020	SAR1 family proteins.	BL01020C 15.35 3.198e- 17 79-130
318	BL00216	Sugar transport proteins.	BL00216B 27.64 4.696e- 11 164-214
320	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109B 12.27 4.814e- 10 216-235

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
JULY ID HU.	NO.	Zanata IIVII	
<b></b>	1	SIGNATURE	
321	BL00027	'Homeobox' domain	BL00027 26.43 5.688e-
	<u> </u>	proteins.	10 329-372
322	PR00109	TYROSINE KINASE	PR00109B 12.27 8.765e-
		CATALYTIC DOMAIN	12 558-577
224	Dr. 02 242	SIGNATURE	DV 01242 25 01 0 272
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e- 30 183-236 BL01241
			35.81 3.222c-13 282-
	1		335
326	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 4.000e-
		proteins.	12 515-566 BL00412D
			16.54 5.705e-11 516-
			567 BL00412D 16.54
	1		7.848e-10 518-569 BL00412D 16.54 1.827e-
	1		09 514-565 BL00412D
	1	*	16.54 1.918e-09 513-
			564 BL00412D 16.54
(1)	L		2.102e-09 520-571
328	BL00232	Cadherins extracellular	BL00232B 32.79 9.557e-
		repeat proteins domain	20 151-199 BL00232B 32.79 2.246e-18 41-89
		proteins.	BL00232B 32.79 5.985e-
			18 370-418 BL00232B
		1	32.79 5.500e-16 258-
			306 BL00232B 32.79
			9.384e-15 475-523
			BL00232C 10.65 2.537e- 12 256-274 BL00232C
1		i	10.65 4.326e-11 368-
			386 BL00232C 10.65
{	·		7.261e-11 473-491
	1		BL00232C 10.65 7.457e-
			11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e- 09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e-
		Caracina Communica Particularia	18 27-49
333	BL01016	Glycoprotease family	BL01016C 22.84 3.925e-
		proteins.	32 70-115 BL01016E
,		•	14.88 5.286e-19 149-
		1	177 BL01016H 13.71   7.577e-13 291-301
ļ	1	ĺ	BL01016D 8.86 3.298e-
			11 127-140 BL01016G
	ł	İ	7.14 5.622e-10 261-271
ļ		l	BL01016A 5.65 7.167e-
	i	1	10 4-19 BL01016P 13.34 1.563e-09 200-
	!		212 BL01016B 8.93
		1	8.855e-09 38-50
339	BL01115	GTP-binding nuclear	BL01115A 10.22 5.500e-
		protein ran proteins.	11 17-61
340	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 1.231e-
	1	ZINC-FINGER METAL-	33 10-49
341	BL01160	BINDING NU. Kinesin light chain	BL01160B 19.54 5.042e-
J-1	2001100	repeat proteins.	09 55-109
342	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.400e-
		ZINC-FINGER METAL-	30 16-55
		BINDING NU.	
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-
			40 20-68
346	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-
		CATALYTIC DOMAIN	11 135-154
247	DD00100	SIGNATURE	DD00100D 12 22 4 264
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

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		CATALYTIC DOMAIN SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins	BL01187B 12.04 1.783e- 13 100-116 BL01187B 12.04 8.435e-13 276- 292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e- 10 54-70 BL01187B 12.04 5.725e-09 231- 247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e- 11 542-553
355	PF00628	PHD-finger.	PF00628 15.84 1.000e- 11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e- 09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e- 15 261-274 PD00066 13.92 6.500e-13 233- 246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e- 13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e- 09 71-126 PF00791B 28.49 7.440e-09 184- 239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e- 11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e- 10 73-95 PR00450C 12.22 3.278e-09 109- 131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF002420 13.51 2.328e- 09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 1038-1092
367	PR.00019	LZUCINE-RICH REPERT SIGNATURE	PR00019B 11.36 1.360e- 09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e- 09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 9.000e- 15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e- 14 30-49 PR00011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e- 09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e- 12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.757e- 34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170R 6.48 2.739e-

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380	BL00107	Protein kinases ATP- binding region proteins.	10 88-118 BL00107A 18.39 1.000e- 23 276-307 BL00107B 13.31 1.692e-12 342-
381	BC00455	Putative AMP-binding	358 BL00455 13.31 5.714e- 12 50-66
382	PR00624	domain proteins. HISTONE H5 SIGNATURE	PR00624G 4.08 4.900e- 09 524-544
384	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
385	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e- 09 67-80
386	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 6.000e- 10 97-130
388	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e- 13 516-529
389	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.667e- 09 151-174
390	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.200e- 15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e- 11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e- 09 272-285 BL00215B 10.44 8.500e-09 165- 178
394	BL00674	AAA-protein family proteins.	BL00674B 4.46 2.723e- 16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.579e- 11 141-155
398	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761B 9.93 6.764e- 09 55-74
399	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.907e- 10 118-142
401	PF00676	Dehydrogenase E1 component.	PF00676B 24.71 8.071e- 18 331-369 PF00676D 14.40 3.854e-15 486- 506 PF00676C 16.88 9.182e-14 454-478
402	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 4.673e- 28 4432-4469 BL00514G 15.98 6.092e-14 4555- 4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e- 10 4519-4534 BL00514H 14.95 4.955e-10 4584- 4609
403	PP00992	Troponin.	FF00992A 16.67 5.974e- 09 105-140
404	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.450e- 10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e- 09 50-64 PR00019B 11.36 1.000e-09 96-110
405	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e- 20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e- 18 358-406 BL00232B 32.79 5.500e-16 246-

			DROW MC+
SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		294 BL00232B 32.79
			9.384e-15 463-511
	İ	ľ	BL00232C 10.65 2.537e-
			12 244-262 BL00232C
			10.65 4.326e-11 356-
	ì		374 BL00232C 10.65
d*	ļ	ļ	7.261e-11 461-479
**		į	BL00232C 10.65 7.457e-
			11 27-45
407	PF00426	Outer Capsid protein VP4	PF00426S 15.67 5.634e-
		(Hemagglutinin).	09 902-940 BL01160B 19.54 9.695e-
409	BL01160	Kinesin light chain	09 126-180
	77.00.713	repeat proteins.	BL00741B 14.27 2.731e-
410	BL00741	dissociation stimulators	09 252-275
		CDC24 family sign.	0, 232 2,3
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e-
7.1.	1200040	i box domain produin.	09 86-100
412	BL00603	Thymidine kinase	BL00603B 11.39 8.500e-
		cellular-type proteins.	09 542-557
415	BL00866	Carbamoyl-phosphate	BL00866B 36.29 3.571e-
	1	synthase subdomain	31 245-291 BL00866C
		proteins.	23.26 9.000e-25 331-
			366
418	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 6.114e-
		TERMINAL TAIL SIGNATURE	09 590-602 PF00791B 28.49 7.955e-
421	PF00791	Domain present in ZO-1	14 23-78 PF00791B
		and Unc5-like netrin	28.49 3.653e-12 273-
		receptors.	328 PF00791B 28.49
			4.273e-11 156-211
ļ			PF00791B 28.49 7.818e-
			11 89-144 PF00791B
		1	28.49 1.524e-10 56-111
į·		ļ	PF00791C 20.98 3.559e-
	• *		09 37-76 PF00791C
ļ		!	20.98 5.235e-09 170-
		1	209 PF00791C 20.98 5.235e-09 381-420
			PF00791B 28.49 6.202e-
			09 189-244 PF00791B
ļ			28.49 7.028e-09 435-
i i	l .	į .	490 PF00791B 28.49
			8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e-
			28 1645-1679
425	PR00109	TYROSINE KINASE	PR00109D 17.04 5.881e-
		CATALYTIC DOMAIN	10 228-251
100		SIGNATURE	BL00518 12.23 4.600e-
429	BL00518	Zinc finger, C3HC4 type	11 31-40
431	77.00030	(RING finger), proteins.  DEAD-box subfamily ATP-	BL00039D 21.67 1.844e-
431	BL00039	dependent helicases	34 490-536 BL00039A
l		proteins.	18.44 5.615e-19 205-
			244 BL00039B 19.19
			8.920e-16 251-277
	1		BL00039C 15.63 5.781e-
l	1		15 333-357
432	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 7.652e-
			12 169-185
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e-
L			10 382-405
436	BL00415	Synapsins proteins.	BL00415N 4.29 B.643e-
			11 195-239 BL00415N
			4.29 3.036e-09 809-853
443	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE	PR00834F 10.91 6.040e-
		I MAMILLY SHANATHUK	1 11 441-454
446	PF01140	Matrix protein (MA),	PF01140D 15.54 9.663e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		p15.	10 183-218 PF01140D 15.54 3.093e-09 246-
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PRC0568G 13.95 5.551e- 09 39-53
451	PP00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e- 10 47-59
452	BL00790	Receptor tyrosine kinase class V proteins.	BL007901 20.01 2.821e- 09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e- 25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e- 17 230-249 PR00380B 12.64 4.724e-16 194- 212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e- 24 246-267 PR00253B 13.47 2.000e-23 272- 294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e- 21 452-473
467	PR00849 BL00678	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e- 09 910-937 BL00678 9.67 8.200e-12
		Trp-Asp (WD) repeat proteins proteins.	33-44
472	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.721e- 09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e- 12 814-852
474	BL00481	Thiol-activated cytolysins proteins.	BL00481E 13.07 8.909e- 09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e- 09 393-408
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.900e- 38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B 11.83 4.333e-18 430- 448 PR00405A 17.71 4.971e-18 411-431
482	PRG0049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e- 10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e- 09 937-952 PR00049D 0.00 8.322e-09 939-954
486	PR00007	COMPLEMENT CIQ DOMAIN SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A 19.33 6.192e-22 626- 653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e- 13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e- 09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e-
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.882e- 27 30-69 PD01066 19.43 3.430e-10 71-110
490	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.864e- 09 663-678
492	BL01128	Shikimate kinase proteins.	BL01128A 18.84 6.464e- 17 58-92
497	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	<del></del>	polyprotein).	15 21-71
498	BL00120	Lipases, serine proteins.	BL00120B 11.37 7.923e- 09 185-200
500	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.353e- 11 299-318
501	BL01159	ww/rsp5/wwp domain proteins.	BL01159 13.85 8.579e- 12 131-146
505	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e- 17 492-510
508	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 5.800e- 19 705-722
509	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417B 20.62 2.938e- 16 362-395 DM01417D 11.08 3.800e-13 322- 338
510	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e- 09 346-370
511	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
		group 1.	09 293-317
512	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e- 09 366-390
513	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 110-160 PD01841B 14.35 1.000e-40 181- 222 PD01841D 17.87 1.000e-40 243-295 PD01841F 13.36 1.000e-
	·		40 333-382 PD01841G 24.26 1.000e-40 386- 440 PD01841L 18.42 1.000e-40 968-1010 PD01841I 23.00 4.545e- 37 762-804 PD01841E 18.60 3.750e-36 295- 333 PD01841J 14.94
			6.023e-35 851-888 PD01841H 21.30 2.909e- 33 490-527 PD01841K 14.81 7.088e-33 924- 954 PD01841C 13.78 9.386e-23 222-243 PD01841M 10.82 8.594e- 21 1054-1073 PD01841I 23.00 2.667e-13 549- 591
514	PR00153	CYCLOPHILIN PEPTIDYL- PROLYL CIS-TRANS	PR00153C 11.01 7.188e- 13 95-111 PR00153E
515	BL00740	ISOMERASE SIGNATURE MAM domain proteins.	9:10 4.150e-12 122-138 BL00740A 13.87 7.188e- 12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-
517	BL00242	Integrins alpha chain proteins.	BL00242C 16.86 8.320e- 09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e- 39 20-68 DM00031B 15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 8.375e- 10 61-95
526	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 3.308e- 12 322-343 PF00789C 20.98 5.269e-09 367- 392
526	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 1.500e- 16 120-164

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529	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 3.893e- 09 60-73
532	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e- 17 11-36 BL00215A
533	DY AAO : 6	Mitochondrial energy	15.82 8.660e-11 123- 148 BL00215A 15.82 4.000e-
533	BL00215	transfer proteins.	17 11-36 BL00215A 15.82 8.660e-11 97-122
534	BL00098	Thiolases acyl-enzyme intermediate proteins.	BL00098C 21.65 2.800e- 38 181-227 BL00098B 32.59 5.345e-38 86-141 BL00098D 26.30 8.364e- 35 245-288 BL00098E 22.12 1.000e-34 314- 352 BL00098F 10.18 4.971e-22 365-386
	<u> </u>		BL00098A 10.60 6.455e- 11 38-50
535	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370E 11.96 7.429e- 22 321-340 PR00370D 16.33 6.143e-21 185- 204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e- 21 27-46 PR00370C 12.72 3.500e-20 140- 157 PR00370A 3.35 6.442e-17 4-20
536	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.429e- 16 285-302 BL00028 16.07 6.294e-14 341- 358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e- 11 397-414 BL00028 16.07 4.462e-11 453- 470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e-
537	BL00762	WHEP-TRS domain	10 313-330 BL00762A 23.43 9.419e- 15 844-881
538	BL00762	proteins. WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 819-856
539	BL00762	WHEP-TRS domain . proteins.	BL00762A 23.43 9.419e- 15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE SIGNATURE	PR00985A 12.10 9.000e- 10 357-375
541	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 1.000e- 40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e- 30 179-218 PD02102C 26.34 8.929e-26 100- 146
543	BF00058	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e- 10 48-65 BL00028 16.07 6.400e-10 193- 210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95
545	BL00250	TGF-beta family proteins.	BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354- 390
547	PR00319	BETA G-PROTEIN	PR00319B 11.47 2.714e-

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		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210- 227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins	8501204A 17.74 1.000e- 40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B 15.41 4.333e-16 102- 116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN PAMILY SIGNATURE	PR00326A 8.75 8.364e- 15 255-276
551	PF00632	HECT-domain (ubiquitin- transferase).	PF00632C 20.66 3.302e- 23 1569-1601 PF00632B 18.45 3.700e-21 1515- 1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e- 14 187-205 BL00290A 20.89 2.059e-14 130- 153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e- 09 846-879
559	DM01111	1 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e- 09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e- 32 118-155
564	BL00141	Bukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e- 10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e- 15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.977e- 13 229-268
569	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
570	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508-
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	9800193D 14.36 1.857e- 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 524- 553
575	BL00752 BL00030	XPA protein.  Eukaryotic RNA-binding	BL00752B 19.17 9.703e- 10 885-929 BL00030A 14.39 7.000e-
		region RNP-1 proteins.	09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

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		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952- 965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e- 09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 9.000e- 11 217-231 PRO0019B 11.36 1.360e-09 386- 400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e- 09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e- 20 335-357
583	PR00343	SELECTIN SUPERPAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14 3.186e-11 784-804
586	PF00013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASK.	DM00892C 23.55 4.409e- 13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321- 336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e- 12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.308e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e- 10 336-354
596	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.789e- 18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e- 10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

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SEQ ID NO:	ACCESSION NO.	DESCRIPTION	KESUBIS.
			5.000e-11 61-73
		1	BL00242D 13.57 4.986e-
	į		10 291-316
601	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 5.610e-
		REPEAT SIGNATURE	09 198-213
602	PR00278	PANCREATIC HORMONE	PR00278A 12.43 4.569e-
		SIGNATURE	10 331-348
603	BL00479	Phorbol esters /	BL00479C 12.01 3.250e-
		diacylglycerol binding	12 170-183
	γ.	domain proteins.	
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e-
			09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e-
·			10 295-339
606	PR00926	MITOCHONDRIAL CARRIER	PR00926F 17.75 1.000e-
		PROTEIN SIGNATURE	13 335-358
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
			15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
<u> </u>	Discourse	GODONALIZATIO SECURIO POGRATORA	15 211-228
612	DM01206	CORONAVIRUS NUCLEOCAPSID . PROTEIN.	DM01206B 10.69 7.411e- 10 877-897 DM01206B
		PROTEIN.	10.69 8.027e-10 861-
			881 DM01206B 10.69
		<b>\$</b>	9.137e-10 873-893
			DM01206B 10:69 1.456e-
			09 859-879 DM01206B
		İ	10.69 1.797e-09 879-
			899 DM01206B 10.69
ı	Ī	'	4.076e-09 865-885
	į		DM01206B 10.69 7.038e-
	1		09 898-91B DM01206B
			10.69 7.949e-09 871-
			891 DM01206B 10.69
		anamata was namana	8.291e-09 767-787 PD02699A B.91 2.023e-
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	28 129-158 PD02699C
	J	BINDING DNA.	24.84 1.000e-27 317-
	Ì		364 PD02699B 18.28
			1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 4.086e-
		SIGNATURE	22 288-310 PR00380D
	•		9.93 3.721e-17 486-508
			PR00380B 12.64 2.241e-
			16 410-428 PR00380C
	1		13.18 2.976e-13 436-
			455
617	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 4.086e-
		SIGNATURE	22 288-310 PR00380D
	1	<b>\</b>	9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-
	t	1	f -
	ı		16 410-428 PR00380C
1			13.18 2.976e-13 436- 455
618	DM01206	CORONAVIRUS NUCLEOCAPSID	DM012C6B 10.69 5.143e-
010	MINTERO	PROTEIN.	12 531-551 DM01206B
- X		TAVABLE.	10.69 2.603e-10 535-
-			555
621	PR00700	PROTEIN TYROSINE	PR00700B 16.80 3.160e-
		PHOSPHATASE SIGNATURE	21 561-582
622	BL00239	Receptor tyrosine kinase	BL00239F 28.15 3.222e-
		class II proteins.	10 647-692 BL00239C
	1		18.75 8.304e-10 543-
			566
623	PR00407	EUKARYOTIC MOLYBDOPTERIN	PR00407K 9.94 8.448e-
	9	DOMAIN SIGNATURE	09 326-339
624	BL00641	Respiratory-chain NADH	BL00641C 21.10 1.000e-
		dehydrogenase 75 Kd	40 157-202 BL00641E

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,		subunit proteins.	24.37 1.000e-40 255- 308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e- 37 48-80 BL00641B 12.62 5.846e-34 113- 139 BL00641D 13.23 9.308e-29 216-240
627	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	PR00103E 17.80 2.500e- 18 367-380 PR00103B 13.39 2.080e-14 297- 312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e- 12 346-358 PR00103C 15.68 1.000e-11 334- 344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e- 10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PRODUBLA 10.53 6.211e- 16 4-22
631	PP00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 8.500e- 14 37-50
632	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e- 10 1324-1344 DM01206B 10.69 4.822e-10 1276- 1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e- 10 1280-1300 DM01206B 10.69 4.532e-09 1320- 1340 DM01206B 10.69 7.266e-09 1326-1346
635	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.600e- 23 145-176 BL00107B 13.31 2.636e-13 211- 227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e- 30 101-143 BL00657B 22.27 7.750e-26 149- 192
637	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 10 607-623
643	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
647	PF00628	PHD-finger.	PF00628 15.84 2.350e- 13 385-400 PF00628 15.84 3.455e-12 464- 479
648	B1,01129	Hypothetical yabO/yceC/afhB family proteins.	BL01129E 13.25 4.000e- 25 332-357 BL01129C 25.56 8.200e-23 236- 279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 3.908e- 10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e- 13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e- 12 1026-1045
653	PR00253	GAMMA-ĀMINOBŪTYRĪC ACID (GABA) RECEPTOR SIGNATURB	PR00253A 9.15 4.000e- 24 253-274 PR00253C 13.85 8.800e-24 313- 335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

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	NO.		20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RB.	PD01719A 12.89 4.452e- 11 969-997 PD01719A 12.89 3.961e-10 128- 156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e- 09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 563-578
658	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e- 13 539-572 DM00215 19.43 4.750e-12 549- 582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e- 10 548-581 DM00215 19.43 4.054e-1C 550- 583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e- 10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e- 09 224-236
661	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e- 23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
666	PR00819	CHXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.988e- 10 704-720
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e- 16 135-178
568	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e- 09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 1.000e- 34 356-410 PD00131C 19.59 1.346e-26 504- 542
673	PR00667	RETINAL PIGMENT BPITHELIUM-RETINAL GPCR SIGNATURE	PR00667G 15.33 7.557e- 10 106-123
674	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 593-608 PR00320B 12.19 4.115e-12 635- 650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e- 10 635-650 PR00320C 13.01 6.400e-10 593- 608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 572-587 PR00320B 12.19 4.115e-12 614-

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			629 PR00320C 13.01 8.435e-11 696-711
0			PR00320C 13.01 2.800e- 10 614-629 PR00320C
		·	13.01 6.400e-10 572-
			587 PR00320B 12.19 3.250e-09 572-587
676	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.667e- 09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 3.700e-
	Ti di di di di di di di di di di di di di	x3-H type (and similar).	16 225-236 PP00642 11.59 7.900e-12 187-
680	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.754e-
681	BL00019	Actinin-type actin-	BL00019D 15.33 4.200e-
682	PR00700	binding domain proteins.  PROTEIN TYROSINE	19 227-257 PR00700D 12.47 4.000e-
687	PR00049	PHOSPHATASE SIGNATURE WILM'S TUMOUR PROTEIN	09 99-118 PR00049D 0.00 8.500e-
689		SIGNATURE	10 538-553
689	BL01024	Protein phosphatase 2A regulatory subunit PR55	BL01024A 10.26 1.000e- 40 22-69 BL01024B
		proteins.	8.91 1.000e-40 86-127
			BL01024C 7.80 1.000e-
	İ		40 146-185 BL01024D 13.22 1.000e-40 185-
			222 BL01024K 11.96
			1.000e-40 222-266 BL01024F 9.42 1.000e-
	3		40 266-317 BL01024G
			11.09 1.000e-40 317-
	1		349 BL01024H 13.88 1.000e-40 389-442
691	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.071e- 31 152-195
692	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e-
693	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
694	BL00211	proteins. ABC transporters family	09 45-57 BL00211A 12.23 5.050e-
696	BL00680	proteins. Methionine	09 58-70 BL00680 14.37 5.304e-
		aminopeptidase subfamily 1 proteins.	17 173-195
697	BL00741	Guanine-nucleotide	BL00741B 14,27 3.418e-
		dissociation stimulators CDC24 family sign.	11 242-265
698	DM01930	2 kw FINGER SMCX SMCY	DM01930B 15.41 1.367e-
		YDR096W.	37 170-215 DM01930F
			14.16 B.232e-28 267- 303 DM01930B 19.86
			9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X SIGNATURE	PR00869A 12.80 1.281e- 16 245-263
701	PR00048	C2H2-TYPE ZINC PINGER	PR00048A 10.52 2.174e-
		SIGNATURE	10 77-91 PR00048A 10.52 6.870e-10 133-
			147 PRO0048A 10.52
			8.826e-10 105-119
		~	PR00048A 10.52 5.320e- 09 161-175
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e-
			25 326-356 BL00523A 13.36 5.050e-16 38-55
			BL00523B 8.64 5.909e-
			15 86-98 BL00523C 12.64 5.500e-13 137-
<b>~</b>	L	I	12.04 5.5UUE-13 13/-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
/			148 BL00523D 9.89 1.844e-11 290-302 BL00523G 9.46 5.500e- 10 513-523 BL00523F 10.85 6.351e-09 413- 424
703	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e- 12 376-390 PR00048B 6.02 1.000e-10 334-344 PR00048B 6.02 1.474e- 09 364-374
707	PD00787	SYNTHASE BIOSYNTHESIS TRANSFERASE.	PD00787A 14.84 8.941e- 14 66-82
708	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 8.500e- 10 B22-841
712	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Y 10.69 4.977e- 38 425-465 DM01354X 13.86 7.300e-34 376- 415 DM01354V 12.97 4.923e-17 311-358 DM01354W 12.64 5.596e- 10 356-376
713	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 7.545e- 27 450-496 BL00039A 18.44 2.537e-18 147- 186 BL00039C 15.63 2.216e-14 280-304 BL00039B 19.19 1.947e- 13 194-220
715	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383R 10.35 4.981e- 10 150-161
717	PF00777	Sialyltransferase family.	PF00777C 18.60 4.035e- 21 106-161
718	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e- 39 20-68 DM00031B 15.41 2.688e-28 84-118 DM00031C 12.79 1.300e- 12 131-142
71.9	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243B 17.54 1.000e- 40 131-172 BL00243C 16.42 1.000e-40 172- 208 BL00243D 24.07 1.000e-40 222-274 BL00243F 22.63 1.000e- 40 314-358 BL00243I 31.77 6.571e-39 607- 650 BL00243E 16.70 3.077e-35 274-304. BL00243G 21.38 3.625e- 34 358-400 BL00243H 17.53 5.235e-29 567- 593 BL00243A 17.61 3.250e-21 63-84 BL00243H 17.53 7.167e- 16 477-503 BL00243H 17.53 2.304e-11 524- 550 BL00243H 17.53 5.304e-11 606-632 BL00243I 31.77 1.380e- 09 610-653
720	PR00217	43 KD POSTSYNAPTIC	PR00217C 10.91 B.022e-
722	PR00704	PROTEIN SIGNATURE CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	09 20-36 PR00704D 11.05 5.909e- 34 135-161 PR00704P 13.61 7.000e-26 190- 218 PR00704E 12.55 8.071e-26 165-189

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			PR00704B 17.94 2.241e- 23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e- 18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
727	PR00320	G-PROTEIN BETA WD-40 REPRAT SIGNATURE	PR00320C 13.01 2.125e- 13 277-292 PR00320A 16.74 1.310e-11 277- 292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e- 11 323-338 PR00320B
			12.19 4.343e-10 323- 338 PR00320B 12.19 6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e- 16 288-307 PR00195E 9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C- x3-H type (and similar).	PF00642 11.59 9.082e- 10 787-798
738	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039A 18.44 2.565e- 28 26-65 BL00039D 21.67 2.105e-20 338- 384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e- 11 73-99
739	BL01289	TSC-22 / dip / bun family proteins.	BL01289A 12.18 8.909e- 31 326-353 BL01289B 10.45 9.571e-17 353- 383
742	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 7.078e- 12 41-81
743	BL00965	Phosphomannose isomerase type I proteins.	BL00965C 23.78 1.000e- 40 256-305 BL00965B 17.77 1.600e-25 126- 153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL0002ID 24.56 4.563e- 25 231-273 BL0002IB 13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain proteins.	BL00612B 11.35 2.034e- 11 93-126
749	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.880e- 10 135~157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e- 11 384-429 BL00795C 17.06 9.444e-11 370- 415
754	BL00051	Ribosomal protein L39e proteins.	BL00051 20.92 1.935e- 16 4-50
755	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e- 09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e- 12 99-150
762	3L00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 33-88
763	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 9.137e- 10 206-240
764	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.800e- 29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e- 10 309-324 BL01208B 15.83 8.031e-10 165-

SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
			180 BL01208B 15.83 4.162e-09 85-100
770	BF00031	Nuclear hormones receptors DNA-binding region proteins.	BL00031A 19.55 9.571e- 32.208-241 BL00031B 22.25 5.500e-27 242- 274
772	PRO0449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.450e- 18 4-26 PR00449E 13.50 3.520e-14 142- 165 PR00449C 17.27 3.032e-13 44-67 PR00449D 10.79 8.579e- 13 107-121 PR00449B 14.34 3.455e-11 27-44
773	BL00523	Sulfatases proteins.	BL00523E 19.27 9.333e- 23 299-329 BL00523A 13.36 2.200e-13 47-64 BL00523B 8.64 2.607e- 13 91-103 BL00523D 9.89 7.923e-12 224-236 BL00523C 12.64 4.512e- 10 141-152 BL00523F 10.85 5.821e-10 373- 384
775	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e- 09 568-585
776	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e- 09 621-638
777	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e- 09 595-612
778	BF00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 8.412e- 11 322-341 BL00030A 14.39 7.000e-10 220- 239
779	PR00079	GLUCOSE-6-PHOSPHATE DEHYDROGENASE SIGNATURE	PR00079B 12.98 2.929e- 26 193-222 PR00079E 16.65 4.150e-23 348- 375 PR00079C 8.68 6.351e-16 246-264 PR00079D 13.51 7.070e- 16 264-281 PR00079A 16.12 6.769e-13 169- 183
781	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.250e- 17 10-35 BL00215A 15.82 6.000e-16 221- 246 BL00215A 15.82 7.857e-12 108-133 BL00215B 10.44 9.526e- 11 168-181
783	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 6.276e-09 159-173
785	BL00690	DRAH-box subfamily ATP- dependent helicases proteins.	BL00690B 13.38 1.000e- 12 147-165 BL00690A 6.87 5.320e-10 114-124 BL00690C 7.51 3.189e- 09 218-228
786	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 8.500e- 16 50-73 PR00449A 13.20 5.235e-14 8-30
	,		PR00449E 13.50 2.853e- 11 150-173 PR00449D 10.79 1.545e-09 111- 125
788	DM01206	CORONAVÍRUS NUCLEOCAPSID PROTEIN.	11 150-173 PR00449D 10.79 1.545e-09 111-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			22.78 5.050e-33 633-
			671 BL00915D 27.02 1.529e-21 795-831
			BL00915A 10.09 1.000e-
			13 395-407
791	PR00208	GLIADIN AND LMW GLUTENIN	PR00208A 12.59 6.294e-
	}	SUPERFAMILY SIGNATURE	10 120-138 PR0020BA
			12.59 6.294e-10 121-
		ļ	139 PR00208A 12.59 6.294e-10 122-140
		•	PR00208A 12.59 6.294e-
		·	10 123-141 PR00208A
			12.59 6.294e-10 124-
			142 PR00208A 12.59
	ł	Į	6.294e-10 125-143
			PR00208A 12.59 6.294e- 10 126-144 PR00208A
			12.59 6.294e-10 127-
	1		145 PR00208A 12.59
	į.		6.294e-10 128-146
	1		PR00208A 12.59 6.294e-
	-		10 129-147 PR00208A 12.59 7.411e-09 130-
	,		148 PR00208A 12.59
	}	<b>,</b>	7.658e-09 131-149
	1	1	PR00208A 12.59 7.904e-
			09 132-150 PR00208A
			12.59 8.274e-09 118-
	į.		136 PR00208A 12.59 B.274c-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e-
753	120203	CADIBLE STORYLORD	16 302-320 PR00205A
		·	14.73 1.257e-11 284-
	1	[	300 PR00205C 13.65
796	25.00450	1000000	1.333e-11 337-352 BL00412D 16.54 4.000c-
/96	BL00412	Neuromodulin (GAP-43) proteins.	12 196-247 BL00412D
	1	Process	16.54 5.705e-11 197-
			248 BL00412D 16.54
	ļ		7.848e-10 199-250
	l	<b>[</b>	BL00412D 16.54 1.827e-
			16.54 1.918e-09 194-
			245 BL00412D 16.54
	L	[	2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.339e-
708	DV 07 053		13 40-58
799	BL01052	Calponin family repeat proteins.	BL01052C 18.51 1.000e- 40 87-127 BL01052A
	1	Process.	16.12 1.529e-32 3-35
}	1		BL01052B 15.31 1.257e-
	1		25 52-78 BL01052D
	1		10.26 5.737e-25 174-
L	DV 00745		194
800	BL00348	p53 tumor antigen proteins.	BL00348F 23.19 3.714e- 09 197-240
801	Br00309	Vertebrate galactoside	BL00309C 18.65 1.621e-
		binding lectin proteins.	09 62-87
802	PR00245	OLFACTORY RECEPTOR	PR00245D 10.47 5.224e-
		SIGNATURE	09 187-199
804	PF00774	Dihydropyridine	PF00774A 16.47 8.457e-
}		sensitive L-type calcium	10 110-156
909	Proocca	channel (Beta subuni.	PR00667C 11.71 9.875e-
808	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR	PROUBETC 11.71 9.875e-
ļ		SIGNATURE	av
B10	PD02346	PHOTOSYSTEM II PROTEIN	PD02346F 12.89 4.340e-
		PRECURSOR	09 317-354
	<del>*</del>	<del></del>	

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit	BL00685B 14.41 6.779e-
		proteins.	14 54-95 BL00685A
			11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE	PR00080A 9.32 9.419e-
813	BL00357	SUPERFAMILY SIGNATURE Histone H2B proteins.	10 93-105 BL00357 7.74 1.988e-17
	220033.	mistone has proteins.	22-65
815	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 7.923e-
		METAL-BINDI.	15 158-171 PD00066
			13.92 5.200e-14 46-59 PD00066 13.92 7.000e-
			14 18-31 PD00066
			13.92 7.000e-13 130-
	ľ		143 PD00066 13.92
	ļ	·	7.500e-13 214-227 PD00066 13.92 9.000e-
			13 102-115 PD00066
			13.92 4.429e-12 186-
		·	199 PD00066 13.92
816	BL01195	Peptidyl-tRNA hydrolase	1.783e-11 74-87
	5504155	proteins.	BL01195C 20.12 3.348e- 20 100-139
820	BLC0520	Interleukin-10 family	BL00520A 6.21 6.471e-
		proteins.	09 1-14
822	BL00972	Ubiquitin carboxyl-	BL00972A 11.93 8.113e-
		terminal hydrolases family 2 proteins.	09 224-242
825	PR00876	NEMATODE METALLOTHIONEIN	PR00876B 7.66 2.268e-
		SIGNATURE	10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN	PD02855A 18.37 4.732c-
		DNA/PANTOTHEN.	28 88-124 PD02855B 8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING	PR00405B 11.83 7.000e-
		PROTEIN SIGNATURE	21 44-62 PR00405C
	•		19.41 1.000e-13 65-87
			PR00405A 17.71 7.283e-
831	2R00019	LEUCINE-RICH REPEAT	PR00019A 11.19 1.000e-
		SIGNATURE	09 47-61 PR00019B
			11.36 1.720e-09 136-
			150 PR00019B 11.36 3.880e-09 44-58
832	PR00011	TYPE III EGF-LIKE	PR00011B 13.08 3.438e-
		SIGNATURE	16 164-183 PR00011D
00			14.03 6.850e-16 164-
			183 PR00011A 14.06 8.364e-14 164-183
		, ,	PR00011C 24.25 5.415e~
			12 231-260 PR00011D
			14.03 9.852e-11 212-
934	PD00306	PROTEIN GLYCOPROTEIN	PD003067 10 76 7 0000
	1200303	PRECURSOR RE.	PD00306A 10.26 7.000e- 12 232-246
835	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 4.000e-
224		PRECURSOR RE.	10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
837	DM00215	PRECURSOR RE. PROLINE-RICH PROTEIN 3.	12 216-230 DM00215 19 42 2 8980
		THE PROPERTY.	DM00215 19.43 3.898e- 09 78-111
839	PD02784	PROTEIN NUCLEAR	PD02784B 26.46 8.302e-
		RIBONUCLEOPROTRIN.	09 73-116
840	PR00700	PROTEIN TYROSINE	PR00700B 16.80 5.091e-
j		PHOSPHATASE SIGNATURE	22 369-390 PR00700D
j			12.47 5.765e-21 491- 510 PR00700C 13.17
.			4.750e-14 449-467
			PR00700F 11.18 8.500e-

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			11 538-549 PR00700E 17.57 3.100e-10 522- 538
841	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.404e- 13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.	PD02785B 14.43 1.000e- 40 58-112 PD02785A 15.23 1.915e-28 8-57
845	BLC0826	MARCKS family proteins.	BL00826C 7.63 6.738e- 09 203-230
846	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e 10 15-24
849	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e- 08 340-349
850	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 6.506e- 09 12-27
851	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 7.000e- 16 246-280
852	BL00420	Speract receptor repeat proteins domain	BL00420B 22.67 1.000e- 40 723-778 BL00420B
		proteins.	22.67 1.321e-38 933- 988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e-
	Ð	, -	27 587-642 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67
	٠.		4.205e-26 163-218 BL00420B 22.67 5.731e-
0)		,	23 55-110 BL004208 22.67 6.464e-20 377- 432 BL004208 22.67
			2.800e-15 830-885 BL00420C 11.90 1.900e- 13 355-366 BL00420C
	-		11.90 1.900e-12 808- 819 BL00420C 11,90
•			3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C
			11.90 5.119e-11 1018- 1029 BL00420C 11.90 7.955e-10 567-578
853	BL00420	Speract receptor repeat	BL00420B 22.67 1.000e-
		proteins domain proteins.	40 756-811 BL00420B 22.67 1.321e-38 966- 1021 BL00420B 22.67 8.457e-28 482-537
			BL00420B 22.67 4.500e- 27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67
			4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B
`			22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918
			BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841-
- -	ļ		852 BL00420C 11.90 3.550e-12 248-259
			BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1051-
Ĺ,	L	<u> </u>	1062 BL00420C 11.90

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			7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDB CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 2.778e- 09 64-83
859	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 2.929e- 13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e- 10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e- 17 23-41 PR00988C 13.64 8.714e-16 107- 123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e- 12 176-188 PR00988D 5.95 8.250e-11 163-174 PR00988B 11.60 4.512e- 10 60-72
863	BL00215	Mitochondrial energy transfer proteins.	BL00215B 10.44 8.071e- 12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775E 8.06 1.000e- 24 198-221 PR00775B 3.52 1.837e-23 107-130 PR00775D 8.91 4.484e- 17 171-189 PR00775A 9.90 8.342e-17 86-107 PR00775C 10.68 9.379e- 17 153-171 PR00775G 10.64 6.850e-15 267- 286 PR00775F 12.76 6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e- 09 89-121
867	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 5.596e- 29 14-53
868	BL01287	RNA 3'-terminal phosphate cyclase proteins.	BL01287A 17.95 2.688e- 26 16-48
869	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e- 10 304-337
872	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 30-85
874	BL00188	Biotin-requiring enzymes attachment site proteins.	BL00188 30.29 9.036e- 32 665-711
876	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e- 09 298-315
877	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	FD02102A 16.74 4.176e- 10 97-141
879	BL01189	Ribosomal protein S12e proteins.	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125
882	BL00284	Serpins proteins.	BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56
896	BL00216	Sugar transport proteins.	BL00216B 27.64 4.375e- 21 35-85
897	PR00391	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE . ICE NUCLEATION PROTEIN	PR00391E 12.50 7.785e- 15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e- 13 191-207 PR00391A 7.83 5.390e-11 16-36
		TOUR HOCHEMITON PROTEIN	PR00327C 6.37 5.247e-

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		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 7.800e- 26 386-432 BL00039A 18.44 6.674e-16 113- 152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e- 11 236-260
901	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 16 254-267 PD00066 13.92 8.200e-16 282- 295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e- 16 366-379 PD00066 13.92 8.200e-16 394- 407 PD00066 13.92 8.200e-14 338-351
902	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 9.321e- 11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e-
904	PR00381	KINESIN LIGHT CHAIN SIGNATURE	PR00381E 8.75 6.586e- 25 335-356 PR00381B 18.17 2.667e-24 204- 224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e- 24 226-245 PR00381D 13.94 1.084e-22 291- 309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e- 13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e- 11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e- 09 333-351 PR00381C 12.48 7.120e-09 310- 329
906	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e~
907	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 513-537
908	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.308e-11 144-155
910	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01056 19.43 2.800e- 30 48-87
912	BL01104	Ribosomal protein L13e proteins.	BL01104C 15.14 6.000e- 09 364-392
922	3L00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.842e-09 500-511
923	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.500e- 09 323-338 PR00320C 13.01 5.500e-09 187- 202
924	PD02161 BL00019	PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT. Actinin-type actin- binding domain proteins.	PD02181D 12.85 8.609e- 09 36-54 BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510c-11 61-84 BL00019D 15.33 9.338e-
928	BL00678	Trp-Asp (WD) repeat	11 205-235 BL00019A 12.56 2.373e-10 34-45 BL00678 9.67 9.308e-11

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
		proteins proteins.	273-284 BL00678 9.67
}	}	,	1.600e-10 314-325 BL00678 9.67 7.600e-10
į		1	360-371 BL00678 9.67
			8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.857e-
		(RING finger), proteins.	10 137-146
930	BL01085	Ribulose-phosphate 3-	BL01085D 16.55 4.600e-
		epimerase family proteins.	24 134-165 BL01085B 10.15 5.680e-22 30-52
		process.	BL01085E 18.87 8.676e-
			20 172-202 BL01085C
•			21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3-	BLC1085D 16.55 4.600e-
		epimerase family	24 152-183 BL01085B
1		proteins.	10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-
			20 190-220 BL01085C
			21.81 2.038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE	PD00301A 10.24 6.400e-
03.6	D7003.63	CALCIUM-BI.	09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e- 12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-
		Example 1	10 5-49
940	PR00862	PROLYL OLIGOPEPTIDASE	PR00862D 16.17 4.086e-
		SERINE PROTEASE (S9A)	09 63-84
945	BL01230	SIGNATURE	
745	BD01530	RNA methyltransferase trmA family proteins.	BL01230B 11.62 2.373e- 09 407-420
948	BL00479	Phorbol esters /	BL00479B 12.57 7.429e-
<u> </u>	ļ	diacylglycerol binding	18 52-68 BL00479A
		domain proteins.	19.86 2.200e-13 26-49
949	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.474e-09
954	PD01311	PROTEIN OXIDOREDUCTASE	PD01311A 30.23 5.909e-
		NAD INTERGENIC RE.	10 66-111
955	PF00651	BTB (also known as BR-	PF00651 15.00 3.250e-
956	PF00651	C/Ttk) domain proteins. BTB (also known as BR-	12 47-60
556	PF00651	C/Ttk) domain proteins.	PF00651 15.00 3.250e-
957	BL00379	CDP-alcohol	BL00379 24.64 1.610e-
		phosphatidyltransferases	15 111-148
		proteins.	
959	BL01115	GTP-binding nuclear	BL01115A 10.22 1.884e-
960	BL01115	grotein ran proteins. GTP-binding nuclear	10 31-75 BL01115A 10.22 3.438e-
		protein ran proteins.	14 110-154
962	BL00061	Short-chain	BL00061B 25.79 6.586e-
		dehydrogenases/reductase	13 198-236
0.63	Duggers	s family proteins.	
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e-
966	PR00308	TYPE I ANTIFREEZE	11 210-225 PR00308A 5.90 7.035e-
		PROTEIN SIGNATURE	09 55-70
967	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 1.286e-
		PROTEIN.	12 104-124 DM01206B
			10.69 5.299e-11 23-43
		-0.	DM01206B 10.69 8.274e- 10 73-93 DM01206B
	1		10.69 3.962e-09 108-
			128 DM01206B 10.69
	1		5.671e-09 38-58
969	PP01008	Initiation factor 2	PF01008B 25.59 4.724e-
	1	subunit.	31 417-460 PP01008C
		j.	12.25 5.333e-18 506- 526 PF01008A 20.14
	1	1	5.875e-15 369-390
	<del></del>		

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
970	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e- 10 112-143 BL01277A 17.39 9.806e-10 40-78
975	BL01159	ww/rsp5/wwP domain proteins.	BL01159 13.85 3.605e- 12 130-145 BL01159 13.85 4.122e-10 171- 186
977	PF00791	Domain present in 20-1 and Unc5-like netrin receptors.	PF00791C 20.98 2.235e- 09 55-94
978	BL01167	Ribosomal protein L17 proteins.	BL01167B 20.66 8.258e- 19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e- 13 33-48 BL00478B 14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e- 36 169-199 PR00312I 15.78 5.286e-35 332- 361 PR00312F 15.06 5.865e-35 199-229 PR00312H 13.31 8.313e- 35 263-291 PR00312J 13.73 5.688e-34 363- 392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e- 33 92-122 PR00312B 15.08 8.941e-33 62-92
981	PF00992	Troponin.	PR00312G 11.11 6.657e- 32 230-258 PR00312A 11.70 6.914e-27 35-59 PF00992A 16.67 8.816e-
982	PR00299	ALPHA CRYSTALLIN	09 414-449 PR00299F 13.20 2.367e-
		SIGNATURE	09 127-149
983	BL01150	Reapiratory-chain NADH dehydrogenase 20 Kd subunit proteins.	BL01150B 17.16 1.000e- 40 156-202 BL01150A 14.10 8.200e-39 100- 138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e- 14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e- 10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e- 10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e- 09 3-48
987	BL00939	Ribosomal protein Lle proteins.	BL00939F 17.27 5.393e- 09 B10-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 525-541
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 497-513
994	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e- 25 146-189
997	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.893e- 11 65-79
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e- 09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926C 16.07 1.750e- 24 73-94 PR00926D 10.53 3.250e-23 126- 145 PR00926F 17.75 6.211e-23 217-240 PR00926R 11.70 6.625e-

DESCRIPTION   RESULTS*	-18 24-39 41 1.000e- 00926F -09 120- 7 1.000e- L00406C 40 147-202 58 3.700e- BL00406E 38 327-377 5 3.348e- 7 1.000e- L00406C 40 147-202 41 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 00304A 16 46-63
16.07 2.125e   PR00926A 10.   15 11-25   PR   17.75 5.565e   143   143   143   143   143   140	-18 24-39 41 1.000e- 00926F -09 120- 7 1.000e- L00406C 40 147-202 58 3.700e- BL00406E 38 327-377 5 3.348e- 7 1.000e- L00406C 40 147-202 41 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 00304A 16 46-63
PR00926A 10. 15 11-25 PR 17.75 5.565e 143  1005  BL00406  Actins proteins.  BL00406B 5.4 40 88-143 B 6.75 1.000e- BL00406D 12. 40 270-325 1 8.44 7.375e- BL00406A 9.9 29 11-46  1006  BL00406  Actins proteins.  BL00406B 5.4 40 88-143 B 6.75 1.000e- BL00406E 8.4 40 88-143 B 6.75 1.000e- BL00406E 8.4 35 240-298 1 9.95 3.348e- BL00406E 8.4 35 240-298 1 9.95 3.348e- PR00304D 11.6 POLYPEPTIDE 1 22 384-407 (CHAPERONE) SIGNATURE  BL00406E 8.4 19 68-87 PR0 9.20 3.382e- PR00304B 11.6 19 68-87 PR0 9.20 3.382e- PR00304B 7.75 13 418-431 1009  PD01066 PROTRIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL- 32 9-48	41 1.000e- 00926F -09 120- 7 1.000e- L00406C 40 147-202 58 3.700e- BL00406E 38 327-377 5 3.348e- 7 1.000e- L00406C 40 147-202 41 1.000e- L00406C 40 147-202 41 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 00304A 16 46-63
15 11-25 PR   17.75 5.565e   143   143   140	00926F -09 120- 7 1.000e- L00406C 40 147-202 58 3.700e- BL00406E 38 327-377 5 3.348e- 7 1.000e- L00406C 40 147-202 41.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 98-118 60 46-63
17.75 5.565e 143  1005  BL00406  Actins proteins.  BL00406B 5.4 40 88-143 B 6.75 1,000e- BL00406D 12. 40 270-325 8.44 7.375e- BL00406A 9.9 29 11-46  BL00406  Actins proteins.  BL00406B 5.4 40 88-143 B 6.75 1,000e- BL00406B 8.44 40 88-143 B 6.75 1,000e- BL00406B 8.44 35 248-298 9.95 3.348e-  POLYPEPTIDE 1 22 384-407 1 (CHAPERONE) SIGNATURE  BL00304B 11.6 19 68-87 PR 9.20 3.382e- PR00304B 7.75 13 418-431  1009  PD01066  PROTEIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL- 32 9-48	7 1.000e- L00406C 40 147-202 58 3.700e- BL00406B 38 327-377 5 3.348e- 7 1.000e- L00406C 40 147-202 4 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 00304A
1005  BL00406  Actins proteins.  BL00406B 5.4 40 88-143 B 6.75 1.000e- BL00406A 9.99 29 11-46  BL00406A 9.99 29 11-46  Actins proteins.  BL00406B 5.4 40 88-143 B 6.75 1.000e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406E 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 9.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e- BL00406B 9.4 35 248-298 B 9.95 3.348e- BL00406B 9.4 35 248-298 B 9.95 3.348e- BL00406B 8.4 35 248-298 B 9.95 3.348e-	7 1.000e- L00406C 40 147-202 58 3.700e- BL00406B 38 327-377 5 3.348e- 7 1.000e- L00406C 40 147-202 4 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 6 7.577e- 00304A
Document   BL00406   Actins proteins.   BL00406B 5.4   40 88-143 B 6.75 1.000e-BL00406D 12.1   40 270-325   8.44 7.375e-BL00406A 9.9   29 11-46   BL00406B 5.4   40 88-143 B 6.75 1.000e-BL00406E 8.4   35 248-298   9.95 3.348e-3   9.95 3.348e-3   9.95 3.348e-3   9.95 3.348e-3   9.95 3.348e-3   9.95 3.348e-3   9.95 3.348e-3   9.95 3.348e-3   9.95 3.348e-3   9.95 3.348e-3   9.95 3.382e-3   9.95 3.	L00406C 40 147-202 58 3.700e- 83 327-377 5 3.348e- 7 1.000e- 600406C 40 147-202 4 1.000e- 8500406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 00304A 16 46-63
A0 88-143 B   6.75 1.000e-  BL00406D 12.1   40 270-325   8.44 7.375e-  BL00406A 9.9 29 11-46   BL00406B 5.4 40 88-143 B 6.75 1.000e-  BL00406E 8.44 40 88-143 B 6.75 1.000e-  BL00406E 8.44 35 248-298 9.95 3.348e-  PD0106E 8.44 40 88-145 B 9.95 3.348e-  POLYPEPTIDE 1 22 384-407 (CHAPERONE) SIGNATURE   8.69 4.667e-  PR00304B 11.6 19 68-87 PR 9.20 3.382e-  PR00304E 7.75 13 418-431   1009   PD0106E   PROTRIN ZINC FINGER   PD0106E 19.43 2 9-48   22 32 9-48   23 9-48   23 9-48   23 9-48   24 0 27 0 28 0 28 0 29 0 28 0 28 0 29 0 20 3 28 0 29 0 20 20 20 20 20 20 20 20 20 20 20 20 2	L00406C 40 147-202 58 3.700e- BL00406E 38 327-377 5 3.348e- 7 1.000e- L00406C 40 147-202 4 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 10304A 16 46-63
6.75 1.000e-    BL00406D 12.9     40 270-325     8.44 7.375e-    BL00406A 9.9     29 11-46     BL00406   Actins proteins.   BL00406B 5.4     40 88-143 B    6.75 1.000e-    BL00406B 5.4     40 88-143 B    6.75 1.000e-    BL00406B 5.4     40 88-143 B    6.75 1.000e-    BL00406B 5.4     40 88-143 B    6.75 1.000e-    BL00406B 5.4     40 88-143 B    6.75 1.000e-    BL00406B 9.9     BL00406B 5.4     40 88-143 B    6.75 1.000e-    BL00406A 9.9     29 11-46     PRO0304B 1.1     19 68-87 PRO     9.20 3.382e-    PRO0304B 7.79     13 418-431     1009   PD01066   PROTRIN ZINC FINGER     PD01066 19.43     ZINC-FINGER METAL   32 9-48	40 147-202 58 3.700e- BL00406E 38 327-377 5 3.348e- 7 1.000e- L00406C 40 147-202 41.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 10304A 16 46-63
BL00406D 12.1 40 270-325 8.44 7.375e- BL00406A 9.99 29 11-46  1006 BL00406 Actins proteins. BL00406B 5.4 40 88-143 B1 6.75 1.000e-4 BL00406E 8.44 35 248-298 9.95 3.348e-1 1007 PR00304 TAILLESS COMPLEX PR00304D 11.6 POLYPEPTIDE 1 22 384-407 (CHAPERONE) SIGNATURB 8.69 4.667e-2 PR00304B 11.6 19 68-87 PR0 9.20 3.382e-1 PR00304E 7.75 13 418-431 1009 PD01066 PROTRIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL- 32 9-48	58 3.700e- BL00406E 38 327-377 5 3.348e- 7 1.000e- L00406C 40 147-202 4 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 00304A 16 46-63
40 270-325   8.44 7.375e-BL00406A 9.99   29 11-46	BL00406E 38 327-377 5 3.348e- 7 1.000e- 600406C 40 147-202 4 1.000e- 8 1.000e- 8 1.000e- 9 11-46 04 8.714e- PR00304C 20 98-118 7.577e- 00304A 16 46-63
8.44 7.375e-    BL00406A 9.99     29 11-46     1006   BL00406   Actins proteins.   BL00406B 5.4     40 88-143   B      6.75 1.000e-    BL00406E 8.4     35 248-298       9.95 3.348e-    9.95 3.348e-    PR00304   TAILLESS COMPLEX   PR00304D 11.0     POLYPEPTIDE 1   22 384-407     (CHAPERONE) SIGNATURB   8.69 4.667e-    PR00304B 11.6     19 68-87   PR0     9.20 3.382e-    PR00304E 7.75     13 418-431     1009   PD01066   PROTRIN ZINC FINGER   PD01066 19.42     ZINC-FINGER METAL   32 9-48	38 327-377 5 3.348e- 7 1.000e- 600406C 10 147-202 3 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 98-118 60 7.577e- 10304A 16 46-63
BL00406A 9.99   29 11-46	5 3.348e- 7 1.000e- 600406C 40 147-202 4 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 60 7.577e- 10304A 16 46-63
29 11-46     1006     BL00406   Actins proteins.     BL00406B 5.4     40 88-143 Bi   6.75 1.000e-    BL00406E 8.4     35 248-298     9.95 3.348e-	7 1.000e- 00406C 40 147-202 4 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 00304A 16 46-63
1006 BL00406 Actins proteins. BL00406B 5.4 40 88-143 Bl 6.75 1.000e-1000 BL00406E 8.44 35 248-298 19.95 3.348e-1007 PR00304 TAILLESS COMPLEX PR00304D 11.0 22 384-407 (CHAPERONE) SIGNATURB 8.69 4.667e-2 PR00304B 11.0 19 68-87 PR0 9.20 3.382e-3 PR00304E 7.75 13 418-431 1009 PD01066 PR07FIN ZINC FINGER PD01066 19.43 21NC-FINGER METAL 32 9-48	G00406C 40 147-202 4 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 07.577e- 00304A 16 46-63
A0 88-143 B  6.75 1.000e-6	G00406C 40 147-202 4 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 07.577e- 00304A 16 46-63
6.75 1.000e-4	10 147-202 4 1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 50 7.577e- 0304A 16 46-63
BL00406E 8.44 35 248-298 1 9.95 3.348e-1 1007 PR00304 TAILLESS COMPLEX PR00304D 11.6 POLYPEPTIDE 1 22 384-407 1 (CHAPERONE) SIGNATURE 8.69 4.667e-2 PR00304B 11.6 19 68-87 PR0 9.20 3.382e-1 PR00304E 7.72 13 418-431 1009 PD01066 PROTRIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL 32 9-48	1.000e- BL00406A 29 11-46 04 8.714e- PR00304C 20 98-118 60 7.577e- 00304A 16 46-63
35 248-298   9.95 3.348e-298   1007   PR00304   TAILLESS COMPLEX   PR00304D 11.0   POLYPEPTIDE 1   22 384-407   1009   PD01066   PROTRIN ZINC FINGER   PD01066   PR010   PR0	3L00406A 29 11-46 24 8.714e- 20 98-118 50 7.577e- 20 98-16 46-63
9.95 3.348e-2 1007 PR00304 TAILLESS COMPLEX PR00304D 11.0 POLYPEPTIDE 1 22 384-407 1 (CHAPERONE) SIGNATURE 8.69 4.667e-2 PR00304B 11.0 19 68-87 PR0 9.20 3.382e-3 PR00304B 7.75 13 418-431 1009 PD01066 PROTRIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL 32 9-48	29 11-46 04 8.714e- PR00304C 20 98-118 50 7.577e- 00304A 16 46-63
1007 PR00304 TAILLESS COMPLEX PR00304D 11.0 POLYPEPTIDE 1 22 384-407 11.0 (CHAPERONE) SIGNATURE 8.69 4.667e-2 PR00304B 11.0 19 68-87 PR0 9.20 3.382e-2 PR00304E 7.79 13 418-431 1009 PD01066 PROTRIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL 32 9-48	74 8.714e- PR00304C 20 98-118 50 7.577e- 00304A 16 46-63
POLYPEPTIDE 1 22 384-407 1 (CHAPERONE) SIGNATURE 8.69 4.667e-2 PR00304B 11.6 19 68-87 PR0 9.20 3.382e-2 PR00304E 7.72 13 418-431 1009 PD01066 PROTRIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL 32 9-48	PR00304C 20 98-118 50 7.577e- 00304A 16 46-63
(CHAPERONE) SIGNATURE 8.69 4.667e-2 PR00304B 11.6 19 68-87 PR0 9.20 3.382e-2 PR00304B 7.72 13 418-431 1009 PD01066 PROTRIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL 32 9-48	20 98-118 50 7.577e- 00304A 16 46-63
PR00304B 11.6 19 68-87 PR0 9.20 3.382e-1 PR00304B 7.75 13 418-431 1009 PD01066 PROTRIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL 32 9-48	50 7.577e- 00304A 16 46-63
19 68-87 PR( 9.20 3.382e-1 PR00304B 7.75 13 418-431  1009 PD01066 PROTRIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL 32 9-48	00304A L6 46-63
9.20 3.382e-1 PR00304E 7.79 13 418-431 1009 PD01066 PROTEIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL 32 9-48	16 46-63
PR00304E 7.79 13 418-431 1009 PD01066 PROTEIN ZINC FINGER PD01066 19.42 ZINC-FINGER METAL 32 9-48	
13 418-431 1009 PD01066 PROTEIN ZINC FINGER PD01066 19.42 ZINC-FINGER METAL 32 9-48	
1009   PD01066   PROTEIN ZINC FINGER   PD01066 19.43	6.8/UE~
ZINC-FINGER METAL 32 9-48	2 0200
	2.9296-
BINDING NU.	
1011 PD01066 PROTBIN ZINC FINGER PD01066 19.43	2 92900
ZINC-FINGER METAL- 32 68-107	4.5250
BINDING NU.	
1012 BL00518 Zinc finger, C3HC4 type BL00518 12.23	6.143e-
(RING finger), proteins. 10 64-73	
1016 PD01168 SYNTHETASE LIGASE PD01168H 12.0	8 1.000e-
PROTEIN ALANYL. 11 174-194	
1018 PD00930 PROTEIN GTPASE DOMAIN PD00930B 33.7	2 1.391e-
ACTIVATION. 32 261-302 F	D00930A
25.62 9.550e-	22 157-
183	
1022 BL00175 Phosphoglycerate mutase BL00175A 15.4	
family phosphohistidine 12 6-26 BL00	
proteins. 23.75 8.062e-	
TI 3 3 THOUSEN ASIA PROUSUSD 16.3	4 1.439e-
SIGNATURE   10 158-185	
MACI/2 processes. BL00353B 11.4	
18 238-288 B	
14.83 8.844e-	TT 588-
1028   BL00183   Ubiquitin-conjugating   BL00183 28 97	
	1.310e-
enzymes proteins. 33 43-91 1033 PF00580 UvrD/REP helicase. PF00580A 13.3	
Troused 15:3	/ 4.720e-
1034 PR00413 HALOACID PR00413E 15.7	0.5.
FROUGLSE 15.7	в 3.429e-
DEHALOGENASE/EPOXIDE 09 154-171 HYDROLASE FAMILY	
SIGNATURE	
1000	
PD01066 PROTEIN ZINC FINGER PD01066 19.43 ZINC-FINGER METAL- 09 5-44	7.05/e^
BINDING NU.	
	4 050
	4.259e-
1000	
DEGUZZE COMMIN BEOUZE 28.84	9.036e-
proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17 7	
INCOSTOR 17.7	
RIBOSYLTRANSFERASE 20 56-78 PRO	0970D

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e-
			16 224-241 PR00970G 9.97 9.229e-15 242-258
			PR00970B 16.37 1.290e- 13 86-105 PR00970C
			11.05 1.643e-11 115- 130 PR00970E 11.23
1042	BL00678	Trp-Asp (WD) repeat	9.820e-11 202-218 BL00678 9.67 2.200e-10
1043	PR00048	proteins proteins. C2H2-TYPE ZINC FINGER	243-254
	1.00040	SIGNATURE	PR00048A 10.52 6.786e- 13 114-128 PR00048A 10.52 1.000e-09 172- 186
1045	BL00615	C-type lectin domain proteins.	BL00615A 16.68 1.720e- 11 218-236 BL00615B 12.25 1.857e-10 317- 331
1046	BL01092	Adenylate cyclases class-I proteins.	BL01092N 13.54 8.924e- 10 3-40
1047	BL01216	ATP-citrate lyase / succinyl-CoA ligases	BL01216D 21.75 4.316e- 28 314-344 BL01216A
1049	DM00031	family proteins.  IMMUNOGLOBULIN V REGION.	13.91 1.000e-10 97-112 - DM00031B 15.41 7.618e- 12 102-136
1050	BL01073	Ribosomal protein L24e proteins.	BD01073 24.30 1.000e- 40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e- 31 160-212
1055	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 5.235e- 11 98-117 BL00030B 7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins domain proteins.	BL00223C 24.79 8.754e- 23 262-317 BL00223A 15.59 9.478e-14 46-80 BL00223A 15.59 5.557e-
1060	BL00027	'Homeobox' domain proteins.	11 118-152 BL00027 26.43 3.455e- 35 158-201
1064	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.211e- 13 280-296
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101
	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236
1071	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 8.518e- 11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e- 09 350-387
1075	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e- 11 159-175
1077	PR00724	CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00724A 10.91 1.000e- 08 366-379
1078	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 1.000e- 12 170-195 BL00215A 15.82 7.529e-10 79-104
1079	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS+
		proteins proteins.	298-309
1081 .	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e- 10 23-57
1094	BI:00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e- 18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e- 12 162-182 BL00460C 14.35 5.500e-09 133- 156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 67-105 PD02811B 17.07 2.263e-21 118- 151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 60-98 PD02811B 17.07 2.263e-21 11- 144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e- 09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e-
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e- 10 15-37 PR00449E 13.50 1.857e-09 185- 208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e- 20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e- 10 63-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1117	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 4.857e- 10 290-306
1123	PR00412	BPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e- 12 301-324
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e- 09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis- trans isomerase signatur.	BL00170C 18.49 3.077e- 33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e-
1131	BL00636	Nt-dnaJ domain proteins.	15 10-37 BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e- 34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			32 159-188 PR00314A
1139	BL01115	GTP-binding nuclear	14.53 1.281e-22 13-34 BL01115A 10.22 6.364e-
		protein ran proteins.	13 13-57
1141	BL00107	Protein kinases ATP-	BL00107A 18.39 4.00Ge-
	]	binding region proteins.	19 451-482 BL00107B 13.31 3.377e-12 519-
			535
1148	PR00685	TRANSCRIPTION INITIATION	PR00685A 13.62 4.676e-
1155	PD01652	FACTOR IIB SIGNATURE RECEPTOR CELL NK	09 21-42 PD01652B 8.50 9.396e-
	1501032	GLYCOPROTEIN IMMUNOGLOB.	10 522-574 PD01652B
			8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894A 21.96 7.873e-
	ł	PROTEIN SIGNAL BE.	28 81-127 PD02894B 13.93 1.188e-27 178-
			211
1159	BL00623	GMC oxidoreductases	BL00623E 15.00 3.531e-
	İ	proteins.	20 391-414 BL00623C 10.86 4.240e-20 155-
			176
1161	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA	PD01937A 6.68 3.475e-
1162	PD01937	DNA PROTEIN POLYMERASE	09 330-341 PD01937A 6.68 3.475e-
		RNDONUCLEASE DNA	09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-
			10 214-239 PR00624D 11.94 1.961e-09 312-
			337
1167	BL00226	Intermediate filaments	BL00226B 23.86 7.384e-
1177	BL01032	Proteins.  Protein phosphatase 2C	09 302-350 BL01032G 8.33 1.422e-
		proteins.	10 34-48
1178	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 1.794e-
		REPEAT SIGNATURE	10 205-220 PR00320C
		•	220 PR00320B 12.19 .
			B.457e-10 35-50
			PR00320A 16.74 7.146e- 09 35-50 PR00320B
			12.19 9.100e-09 79-94
1180	PR00454	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-
1181	BL00291	Prion protein.	19 765-784 BL00291A 4.49 8.962e-
			11 152-187
1184	BL00720	Guanine-nucleotide dissociation stimulators	BL00720B 16.57 4.103e-
		CDC25 family sign.	18 1089-1113
1185	BL00215	Mitochondrial energy	BL00215A 15.82 4.553e-
		transfer proteins.	13 204-229 BL00215A
			15.82 1.429e-12 11-36 BL00215A 15.82 9.809e-
			11 104-129
1187	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 2.761e-
1188	BL00878	Orn/DAP/Arg	10 77-93 BL00878B 10.95 6.000e-
		decarboxylases family 2	16 189-204 BL00878C
		pyridoxal-P attachment	17.74 8.435e-15 225-
		si.	245 BL00878F 19.67 3.625e-13 379-402
			BL00878D 16.56 1.621e-
			09 270-289
1191	PD02939	PROTEIN GLUTATHIONE SYNTHETASE SY.	PD02939B 10.10 2.723e-
1		OTMINETASE SI,	12 203-220 PD02939C 20.01 1.000e-11 224-
		<u> </u>	252
1193	PR00345	STATHMIN FAMILY	PR00345B 7.12 2.800e-
		SIGNATURE	28 72-101 PR00345B

NO.	SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
PR00345C 4.54 9.100e- 28 101-125 PR00345N 13.46   1.97 1.964e-24 125- 149 PR00345N 13.46		NO.	·	
1194   PR00345   STATHMIN FAMILY   PR00345A 13.46   5.645e-16 43-62   10.97   PR00345A 13.46   10.97   PR00345E 7.12 2.800c-28   108-137   PR00345E 7.12 2.800c-28   108-137   PR00345E 7.12 2.800c-28   108-137   PR00345E 7.12 2.800c-28   108-137   PR00345E   1.52 2.800c-28   137-161   PR00345E   1.52 4.161-185   PR00345A 13.46   5.645e-16 79-98   10.97   1.954e-24   161-185   PR00345A 13.46   5.645e-16 79-98   10.97   1.954e-24   161-185   PR00345A 13.46   5.645e-16 79-98   1324-264   1324				8.54 7.652e-28 149-174
10.97   1.964e-24   125-149   PR00345h   13.46   5.645e-16   43-62   199   PR00345h   13.46   5.645e-16   43-62   28   108-137   PR00345F   7.12   2.800e-120   28   137-161   PR00345E   8.54   7.652e-28   185-21   10.97   1.964e-24   161-185   PR00345A   13.46   5.645e-16   79-98   10.97   1.964e-24   161-185   PR00345A   13.46   5.645e-16   79-98   124-264   125-47			1	
149 PR00345 13.46   5.645e-16 43-62   1194   PR00345 17.12 2.800e-28   10e-137   PR00345				
PRO0345   STATHMIN PAMILY   PRO0345B 7.12 2.800c-28 108-137 PRO0345E 8.54 7.652e-28 185-21c-28 185-28 185-21c-28 185-21c-28 185-21c-28 185-21c-28 185-21c-28 185-28				149 PR00345A 13.46
SIGNATURE   28 108-137 FR00345E   8.54 7.652e-28 185-29 10.97 1.964e-24 16.1-185   PR00345C 4.54 9.100e-28 137-161   PR00345D 10.97 1.964e-24 16.1-185   PR00345A 13.46   5.645e-16 79-98   10.97 1.964e-24 16.1-185   PR00345A 13.46   5.645e-16 79-98   11.95   PR00995B 17.37 1.120e-13 224-264   BL00982   Bacterial-type phytoene dehydrogenase proteins.   115-47   BL01298   Dihydrodipicolinate reductase proteins.   BL00982				
1.95	1194	PR00345		
PRO0345C 4.54 9.100e- 28 137-161 PRO0345D 10.97 1.964e-24 161- 185 PRO0345A 13.46			SIGNATURE	
195   PF00995   Sec1 family.   Sec1 family.   Sec2 family.   Sec2 fam				
185 PR00345A 13.46   5.645e-16 79-98   1195   PF00995   Sec1 family.   PF00995B 17.37 1.120e-13 224-264   1196   BL00982   Bacterial-type phytoene dehydxogenase proteins.   115-47   1197   BL01298   Dihydrodipicolinate reductase proteins.   115-47   1197   BL00061   Short-chain dehydrogenases/reductase proteins.   BL00061B 25.79 1.000e-14   152-190   14 152-190   14 152-190   14 152-190   15 152-190   1				28 137-161 PR00345D
1.195   FF00995   Sec1 family.   FF00995B 17.37 1.120e.   13 224-264   1196   BL00982   Bacterial-type phytoene   dehydrogenase proteins.   11 15-47   1197   BL01298   Dihydrodipicolinate   BL01298   13.90 5.959c.   1197   BL00061   Short-chain   BL01298   Stort-chain   Gehydrogenases/reductase   Stamily proteins.   BL00061B 25.79 1.000e.   14 152-190   14 152-190   14 152-190   15 16 16 16 16 16 16 16 16 16 16 16 16 16				
1195			,	D .
13 224-264   13 224-264   11 247-264   1196   1197   1197   1197   1198   1199   119	1195	PP00995	Sec1 family.	
Description	•			
Dibydrodipicolinate reductase proteins.   BL01298	1196	BL00982	Bacterial-type phytoene	BL00982A 18.41 6.738e-
Teductase proteins.   09 51-73   1203   BL00061   Short-chain   dehydrogenases/reductase   s family proteins.   BL00061B 25.79 1.000e-14 152-190   1204   PR00118   BETA-LACTAMASE CLASS A   SIGNATURE   09 213-229   BL01183   DubiE/CQ5   methyltransferase family   proteins.   BL01183   27.71 8.535e-27 264-307   BL01183D 21.31 1.429e-307   BL01183C 10.77 5.295e-309 246-258   BL01183C 10.77 5.295e-309 246-258   BL01183C 10.77 5.295e-309 246-258   BL01283C 10.77 5.295e-309 246-258   BL01283C 10.77 5.295e-309 246-258   BL01283C 10.77 5.295e-309 246-258   BL01283C 10.77 5.295e-309 246-258   BL01283C 10.77 5.295e-309 246-258   BL01283C 10.77 5.295e-309 246-258   BL01283C 10.77 5.295e-309 246-258   BL01283C 10.77 5.295e-309 246-258   BL01283C 10.77 5.295e-309 246-258   BL00379L 20.63 2.485e-309 246-258   BL00379L 20.6			dehydrogenase proteins.	
BL00061   Short-chain   dehydrogenases/reductase   s family proteins.	1197	BL01298		
dehydrogenases/reductase	1203	BL00061		
B family proteins   BETA-LACTAMASE CLASS A   PR00118F 16.42 9.386e-				
SIGNATURE   09 213-229			s family proteins.	
December   December	1204	PR00118		PR00118F 16.42 9.386e-
methyltransferase family proteins.    Methyltransferase family proteins.   37 184-229 BL01183D   27.71 8.535e-27 264-307 BL01183L 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e-09 246-258   BL00193C 10.77 5.295e-09 246-258   BL00979L 20.63 2.485e-10 246-258   BL00979L 20.63 2.485e-10 246-258   BL00979L 20.63 2.485e-10 246-258   BL00979L 20.63 2.485e-11 49-65 PF00023A 16.03 4.857e-11 49-65 PF00023B 14.20 1.818e-09 45-55   1212   PR00048   C2H2-TYPE ZINC FINGER PR00048A 10.52 7.750e-14 227-241 PR00048A 10.52 4.316e-11 199-213   PR00450   RECOVERIN FAMILY PR000450C 12.22 1.720e-10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e-09 44-64   PRO0450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e-09 44-64   PR00450C 12.22 3.506 PR00450C 12.22 3.506e-09 56-78 PR00450	1206	BY.01193		_l
Proteins   27.71 8.535e-27 264-307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e-09 246-258	2200	DEULLOS		
3.250e-23 51-73     BL01183C 10.77 5.295e-09 246-258     1208   BL00979   G-protein coupled receptors family 3     1209   PFC0023   Ank repeat proteins.   PF00023A 16.03 4.857e-11 49-65 PF00023B 14.20 1.818e-09 45-55     1212   PR00048   C2H2-TYPE ZINC FINGER   PR00048A 10.52 7.750e-14     SIGNATURE   SIGNATURE   PR00048A 10.52 7.750e-14     1213   PR00450   RECOVERIN FAMILY   PR00450C 12.22 1.720e-10 20-42   PR00450C     12.22 3.506e-09 56-78   PR00450D 16.58 6.769e-09 44-64     1216   BL00412   Neuromodulin (GAP-43)   BL00412D 16.54 5.598e-10 179-230     1219   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 5.348e-1222   PD00066     1220   PROTEIN ZINC-FINSER   PD00066 13.92 7.231e-15 406-13.92 7.231e-15 406-11 199     1220   PROTEIN ZINC-FINSER   PD00066 13.92 7.231e-15 406-11     1221   PROMESTAL-BINDI   PROTEIN 52   PROMESTAL-BINDI   PROME				1
BL01183C 10.77 5.295e- 09 246-258			•	
1208   BL00979   G-protein coupled receptors family 3   09 105-146   1209   PFC0023   Ank repeat proteins.   PF00023A 16.03 4.857e-11 49-65 PF00023B   14.20 1.818e-09 45-55   1212   PR00048   C2H2-TYPE ZINC FINGER   PR00048A 10.52 7.750e-14 227-241 PR00048A   10.52 4.316e-11 199-213   PR00450   RECOVERIN FAMILY   PR00450C 12.22 1.720e-10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e-09 44-64   PR00450   PR00450E   10 179-230   PR00450E   PR00450E   PR00450E   PR00450E   PR0450E   PR0450E   PR0450E   PR0450E   PR04			+	
1208   BL00979   G-protein coupled receptors family 3 proteins.   PF00023A 16.03 2.485e-1209   PFC0023   Ank repeat proteins.   PF00023A 16.03 4.857e-11 49-65 PF00023B 14.20 1.818e-09 45-55		*		
PFC0023	1208	BL00979	G-protein coupled	BL00979L 20.63 2.485e-
PFC0023				
11 49-65 PF00023B 14.20 1.818e-09 45-55 1212 PR00048 C2H2-TYPE ZINC FINGER PR00048A 10.52 7.750e- SIGNATURE 14 227-241 PR00048A 10.52 4.316e-11 199- 213 1213 PR00450 RECOVERIN FAMILY PR00450C 12.22 1.720e- SIGNATURE 10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e- 09 44-64 1216 BL00412 Neuromodulin (GAP-43) BL00412D 16.54 5.598e- proteins. 10 179-230 1219 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 5.348e- 1222 PD00066 PROTEIN ZINC-FINGER PD00066 13.92 7.231e- MBTAL-BINDI. 15 295-308 PD00066	1200	DECONS		
14.20 1.818e-09 45-55	1209	PEC0023	Ank repeat proteins.	
PR00048   C2H2-TYPE ZINC FINGER   PR00048A 10.52 7.750e-   SIGNATURE   14 227-241 PR00048A     10.52 4.316e-11 199-   213				
10.52 4.316e-11 199- 213  1213  PRO0450  RECOVERIN FAMILY SIGNATURE  10 20-42 PRO0450C 12.22 3.506e-09 56-78 PRO0450D 16.58 6.769e- 09 44-64  1216  BL00412  Neuromodulin (GAP-43) BL00412D 16.54 5.598e- 10 179-230  PRO0456  RIBOSOMAL PROTEIN P2 SIGNATURE  11 249-264  PROTEIN ZINC-FINGER METAL-BINDI.  15 295-308 PD00066 13.92 7.231e-15 406-	1212	PR00048		PR00048A 10.52 7.750e-
213			SIGNATURE	
PR00450   RECOVERIN FAMILY   PR00450C 12.22 1.720e-   SIGNATURE   10 20-42 PR00450C 12.22 3.506e-09 56-78     PR00450D 16.58 6.769e-09 44-64     PR00450D				
SIGNATURE   10 20-42 PR00450C   12.22 3.506e-09 56-78   PR00450D 16.58 6.769e-09 44-64	1213	PR00450	RECOVERIN FAMILY	
PR00450D.16.58 6.769e-   09 44-64     1216			SIGNATURE	10 20-42 PR00450C
1216   BL00412   Neuromodulin (GAP-43)   BL00412D 16.54 5.598e-proteins.   10 179-230     1219   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 5.348e-SIGNATURE   11 249-264     1222   PD00066   PROTEIN ZINC-FINGER   PD00066 13.92 7.231e-MBTAL-BINDI.   15 295-308 PD00066     13.92 7.231e-15 406-		•		
DEDOUGLE   DEUTOMODULIN (GAP-43)   BL00412D 16.54 5.598e-   DEUTOMODULIN   DEUT				
PRO0456   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 5.348e-   SIGNATURE   11 249-264     PD00066   PROTEIN ZINC-FINGER   PD00066 13.92 7.231e-   MRTAL-BINDI.   15 295-308 PD00066     13.92 7.231e-15 406-	1216	BL00412	Neuromodulin (GAP-43)	
SIGNATURE			proteins.	
PD00066 PROTEIN ZINC-FINGER PD00066 13.92 7.231e-MBTAL-BINDI. 15 295-308 PD00066 13.92 7.231e-15 406-	1219	PR00456		
MBTAL-BINDI. 15 295-308 PD00066 13.92 7.231e-15 406-	1222	PDOOGE		
13.92 7.231e-15 406-	1000	E710000		
1 27 100000 13.32				419 PD00066 13.92
2.286e-12 378-391				
PD00066 13.92 7.857e-	1			
12 434-447 PD00066 13.92 3.348e-11 350-				
363				
1223 BL50058 G-protein gamma subunit BL50058 27.23 1.000e-	1223	BL50058		
profile. 40 13-61	1336	DE 00412		
1226 BL00412 Neuromodulin (GAP-43) BL00412D 16.54 8.439e-	1440	BL00412		
proteins. 09 279-330 1227 BL00437 Catalase proximal heme- BL00437A 18.82 1.000e-	1227	BL00437		
ligand proteins. 40 49-101 BL00437B				
16.28 1.000e-40 114-				1
168 BL00437C 21.86			ı i	768 DT.00477C 21 06

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	,	,	1.000e-40 190-239 BL00437D 25.72 1.000e- 40 248-301 BL00437E 23.95 1.000e-40 327- 379
1230	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 8.297e- 10 6-60
1231	PR00735	GLYCOSYL HYDROLASE FAMILY 8 SIGNATURE	PR00735A 11.19 6.857e- 09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e- 10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e- 10 158-176
1235	BL00866	Carbamoyl-phosphate synthase subdomain proteins.	BL00866B 36.29 2.776e- 09 75-121
1237	BL00027	'Homeobox' domain proteins.	BL00027 26.43 1.818e- 21 36-79
1243	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e- 11 10-25
1246	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168L 9.47 2.837e- 10 31-46 PD01168L 9.47 4.490e-10 174-189 PD01168L 9.47 7.612e- 10 183-198
1249	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.800e-10 183-196
1254	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 2.440e- 36 96-144
1255	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e-
1256	BL00373	Phosphoribosylglycinamid e formyltransferase proteins.	BL00373C 10.35 3.348e- 12 143-156
1258	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.217e- 10 174-193
1259	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 8.286e- 10 31-40
1261	PR00070	DIHYDROFOLATE REDUCTASE SIGNATURE	PR00070D 11.63 1.000e- 15 112-127 PR00070C 13.09 9.500e-15 51-63 PR00070A 12.92 5.500e- 12 16-27
1262	BI.00462	Gamma- glutamyltranspeptidase proteins.	BL00452A 20.89 6.438e- 24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347
1263	BF00038	Myc-type, 'helix-loop- helix' dimerization domain proteins.	BL00038B 16.97 9.455e- 11 62-83
1264	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e- 11 17-61
1266	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 9.308e- 22 40-63 PR00449B 13.50 1.000e-16 137- 160 PR00449D 10.79 3.520e-11 102-116
1270	BL00276	Channel forming colicins proteins.	BL00276A 8.87 1.500e- 09 17-29
1275	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327C 15.47 9.769e- 09 228-243
1276	PR00412	EPOXIDE HYDROLASE	PR00412B 12.59 7.894e-

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	NO.	SIGNATURE	12 119-135 PR00412C
			11.30 1.857e-11 165- 179 PR00412A 13.23 3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.538e- 10 127-157
1279	BL00134	Serine proteases, trypsin family,	BL00134A 11.96 9.325e- 13 128-145
1280	BL01220	histidine proteins.  Phosphatidylethanolamine -binding protein family proteins.	BL01220C 14.75 9.348e- 15 248-276
1285	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.286e- 10 33-42
1287	PF00791	Domain passent in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.182e- 11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY SIGNATURE	PR008028 16.51 1.610e-
1297	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE	PR00716C 17.65 5.696e- 09 23-44
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e- 14 268-283
1301	BL00127	Pancreatic ribonuclease family proteins.	BL00127C 31.49 3.571e- 28 82-126 BL00127B 26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR SIGNATURE	PR00637B 11.27 4.250e- 09 290-306
1307	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.500e- 17 13-38 BL00215A 15.82 1.000e-16 226- 251 BL00215A 15.82
1308	PR00898	VASOPRESSIN V2 RECEPTOR	2.658e-13 107-132 PR00898H 11.34 4.682e-
1309	PD00301	SIGNATURE PROTEIN REPEAT MUSCLE	09 552-572 PD00301B 5.49 2.731e-
1310	BL00983	CALCIUM-BI. Ly-6 / u-PAR domain proteins.	09 390-401 BL00983C 12.69 9.654e- 13 73-89 BL00983B 8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family proteins.	BL00194 12.16 1.900e- 11 15-28
1314	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 8.969e-
1316	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e- 13 128-145
1320	BL00783	Ribosomal protein L13 proteins.	BL00783C 22.43 6.559e- 24 87-117 BL00783A 14.55 1.600e-19 8-33 BL00783B 12.76 3.500e- 12 74-86
1327	PF00514	Armadillo/beta-catenin- like repeat proteins.	PF00514A 31.30 7.268e- 11 82-120
1329	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.294e- 11 129-148 BL00030B 7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 7.239e- 09 25-43
1332	PR00161	NICKEL-DEPENDENT HYDROGENASE/B-TYPE CYTOCHROME SIGNATURE	PR00161C 9.51 4.930e- 09 317-337
1333	PD01066	PROTRIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.769e- 33 10-49
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e- 09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

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	МО.	PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e- 13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e- 16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e- 21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e- 09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e- 10 135-146
1348	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PP00651 15.00 7.231e- 13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e- 32 416-445 PR00193C 12.60 6.318e-31 179- 207 PR00193B 11.69 3.571e-24 133-159 PR00193B 19.47 9.069e- 22 470-499 PR00193A 15.41 1.783e-20 77-97
1352	PR00447	NATURAL RESISTANCE- ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	PR00447E 9.73 1.554e- 15 299-319 PR00447D 13.54 3.408e-15 200- 224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e- 10 353-373
1353	BF00303	S-100/ICaBP type calcium binding protein.	BL00303A 21.77 6.667e- 26 45-82 BL00303B 26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 5.950e- 29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e- 18 225-249 BL00039B 19.19 3.182e-14 141- 167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e- 12 84-101 PF00615C 10.06 8.412e-12 162- 176
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.234e- 29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e- 18 14-29 PR00925B 3.73 5.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87
1362	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117
1363	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	w Kinase Alpha Adhesion T-Cell.	DM00179 13.97 5.304e- 09 167-177
1368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e- 09 76-96
1370	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 1.794e-

SEQ ID NO		DESCRIPTION	RESULTS*
	NO.		10 1-19
1371	BL00242	Integrins alpha chain	BL00242B 8.13 8.615e-
	5550212	proteins.	09 469-479
1372	PR00625	DNAJ PROTBIN PAMILY	PR00625B 13.48 7.353e-
		SIGNATURE	19 46-67 PR00625A
1000			12.84 1.39le-16 14-34
1373	BL00434	HSY-type DNA-binding	BL00434C 23.85 3.778e-
1374	PR00962	domain proteins.  LETHAL(2) GIANT LARVAE	09 90-130 PR00952C 8.00 6.337e-
	1100302	PROTEIN SIGNATURE	09 505-526
1375	PD02475	MUCIN EPITHELIAL TUMOR-	PD02475A 23.18 8.552e-
•		ASSOCIATE.	10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.571e-
		ZINC-FINGER METAL-	32 24-63
1380	BL00194	BINDING NU. Thioredoxin family	DY 00104 12 16 0 222
1300	BLOOTS4	proteins.	BLC0194 12.16 8.333e- 12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 1.458e-
		ENDOSOMAL III.	15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 7.600e-10
1204		proteins proteins.	243-254
1384	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 7.600e-10
1385	BL00303	proteins proteins. S-100/ICaBP type calcium	271-282 BL00303B 26.15 6.203e-
2303	550000	binding protein.	10 95-132
1386	BL01160	Kinesin light chain	BL01160B 19.54 5.042e-
		repeat proteins.	09 1574-1628
1387	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.000e-
1200	7777.055	(RING finger), proteins.	11 52-61
1389	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 3.600e-
		BINDING NU.	30 10-49
1390	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 3.512e-
		ZINC-FINGER METAL-	31 32-71
		BINDING NU.	
1392	PR00308	TYPE I ANTIPREEZE PROTEIN SIGNATURE	PR00308C 3.83 9.723e-
1393	PR00380	KINESIN HEAVY CHAIN	10 127-137 PR00380A 14.18 9.625e-
		SIGNATURE	25 88-110 PR00380D
			9.93 2.406e-20 304-326
		j	PR00380B 12.64 4.414e-
			16 208-226 PR00380C
	,	1	13:18 6.538e-16 243-
1394	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 3.400e-
		METAL-BINDI.	14 462-475 PD00066
	1		13.92 8.800e-14 348-
	1		361 PD00066 13.92
	1		9.571e-12 405-418 · PD00066 13.92 6.087e-
			11 490-503 PD00066
			13.92 B.043e-11 320-
		4	333
1398	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.786c-
		ZINC-FINGER METAL- BINDING NU.	32 10-49
1400	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 7.038e-
		PROTEIN.	09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN	PD00930A 25.62 7.324e-
		ACTIVATION.	15 363-389
1407	BP00030	Eukaryotic RNA-binding	BL00030A 14.39 7.500e-
1400	PRO00==	region RNP-1 proteins.	10 457-476
1408	PR00019	LEUCINE-RICH REPEAT	PRO0019A 11.19 9.550e-
		SIGNATURE	11 179-193 PR00019A 11.19 8.826e-10 228-
			242 PRO0019B 11.36
			1.360e-09 199-213
			PR00019B 11.36 4.960e-

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1409	PR00510	NEBULIN SIGNATURE	09 176-190 PR00510A 9.09 4.150e-
	PR00510	NEHULIN SIGNATURE	12 182-202 PR00510B 12.96 8.767e-12 210- 230 PR00510F 9.88 8.172e-10 58-75 PR00510D 9.21 2.367e- 09 251-267
1410	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.696e- 09 31-44
1412	BL00358	Ribosomal protein L5 proteins.	BL00358B 22.76 1.00Ce- 40 57-103 BL00358C 13.75 6.087e-14 122- 136 BL00358D 14.26 5.500e-13 143-158 BL00358A 13.06 1.931e- 11 33-44
1414	BL00282	Kazal serine protease inhibitors family proteins.	BL00282 16.88 7.338e- 10 511-534
1415	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 4.300e- 29 40-77
1417	PR00681	RIBOSOMAL PROTEIN S1 SIGNATURE	PR00681G 12.54 2.149e- 09 38-60
1418	DM00973	3 kw resistance benomyl. YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.462e- 09 171-208
1419	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 1.571e- 09 428-443
1420	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941A 14.81 1.000e- 40 142-196 PD01941B 15.02 7.049e-30 400- 447 PD01941E 15.92 2.475e-20 817-864 PD01941C 19.96 3.118e- 19 488-543 PD01941D 27.18 9.614e-18 641- 690 PD01941F 28.52 5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e- 12 199-217
1423	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 6.318e- 11 1009-1028
1424	Bi:50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258
1425	PF00628	PHD-finger.	PF0062B 15.84 3.045e- 12 330-345
1426	PP00628	PHD-finger.	PF00628 15.84 3.045e- 12 377-392
1427	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PRO0405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282
1428	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 5.219e- 34 147-193
1429	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.920e- 10 577-592
1430	PRO0378	INOSITOL PHOSPHATASE SIGNATURE	PRO0378D 16.86 7.563e- 12 295-314 PRO0378B 13.80 8.650e-10 166- 186
1431	PR00928	GRAVES DISEASE CARRIER	PR00928B 13.53 3.769e-

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		PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e- 15 14-50 BL01113C 13.18 7.000e-12 82-102
1434	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 7.983e- 10 135-150
1436	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 1.000e- 12 84-103
1438	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.500e- 09 250-268 BL00290A 20.89 4.000e-09 188- 211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e- 09 38-52
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e- 09 88-102
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e- 08 114-138
1445	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL	PD01841A 21.71 1.000e- 40 73-123 PD01841B 14.35 1.000e-40 144- 185 PD01841D 17.87 1.000e-40 206-258 PD01841F 13.36 1.000e- 40 296-345 PD01841G
			24.26 1.000e-40 349- 403 PD01841I 23.00 1.000e-40 494-536 PD01841J 14.94 1.000e- 40 895-932 PD01841L 18.42 1.000e-40 1083- 1125 PD01841E 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e- 35 1041-1071 PD01841H 21.30 3.189e-31 435-
		•	472
1446	PF00816	H-NS histone family.	PF00816B 13.84 8.875e- 09 190-220
1447	PR00048	C2H2-TYPB ZINC FINGER SIGNATURE	PR00048A 10.52 2.080e- 09 402-416
1448	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315D 18.40 7.393e- 09 23-67
1451	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 2.800e- 10 94-104
1454	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 7.146e- 09 382-405
1455	PF00777	Sialyltransferase family.	PF00777C 18.60 2.929e- 22 4-59
1457	ВЬ00927	Trehalase proteins.	BL00927C 10.83 8.085e-
1460	BL00545	Aldose 1-epimerase proteins.	BL00545C 11.28 7.353e- 17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e- 09 140-153
1466	PR00097	ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE	PR00097C 9.42 9.069e- 09 233-245
1472	BL01129	Hypothetical yab0/yceC/sfhB family proteins.	BL01129E 13.25 5.250e- 22 170-195 BL01129C 25.56 9.526e-18 63-106
1473	BL00790	Receptor tyrosine kinase class V proteins.	BL007901 20.01 2.821e- 09 2114-2145
1475	PF00686	Starch binding domain proteins.	PF00686A 13.45 9.100e- 09 267-277

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1477	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e- 10 466-476
1478	вгооозо	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 9.400e- 10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10
1480	BL00290	Townson and and	292-305
1480	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.385c- 15 69-87 BL00290A 20.89 5.091e-11 12-35
1481	PR00150	PHOSPHOENOLPYRUVATE	PR00150F 10.45 9.039e-
		CARBOXYLASE SIGNATURE	09 21-51
1482	PF00780	Domain found in NIK1- like kinases, mouse citron and yeast ROM.	PF00780I 14.69 4.825e- 09 107-137
1483	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e- 09 108-162
1485	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 5.909e-
		ZINC-FINGER METAL- BINDING NU.	25 17-56
1486	BL00107	Protein kinases ATP-	BL00107B 13.31 1.529e-
		binding region proteins.	09 34-50
1488	BL00039	DEAD-box subfamily ATP- dependent helicases	BL00039D 21.67 9.586e- 10 116-162
1490	BL00166	proteins. Rnoyl-CoA	BL00166D 22.87 2,607e-
1430	PROOFEE	hydratase/isomerase	24 190-226 BL00166C
		proteins.	18.93 5.500e-14 140-
			167 BL00166B 16.92 9.357e-11 93-115
1491	BL00452	Guanylate cyclases	BL00452D 28.59 3.700e-
		proteins.	31 63-106 BL00452E 11.92 3.045e-13 115- 131
1492	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 3.667e-
		SIGNATURE	09 532-546
1497	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 11 384-400 BL00107A
		bunding region protecting.	18.39 5.345e-11 322- 353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e-
1502	BL00027	'Homeobox' domain	10 107-117 BL00027 26,43 4.789e-
2302	1 2200027	proteins.	24 112-155
1503	BL00027	'Homeobox' domain	BL00027 26.43 4.789e-
		proteins.	24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177R 20.64 5.800e-/ 24 448-475 BL01177C
	Į		17.39 5.333e-19 402-
			421 BL01177B 13.61 7.840e-16 155-171
			7.840e-16 155-171 BL01177D 17.50 1.900e- 15 427-445
1506	BC00972	Ubiquitin carboxyl-	BL00972D 22.55 5.500e-
		terminal hydrolases	14 311-336 BL00972A
	<u> </u>	family 2 proteins.	11.93 7.429e-14 48-66
		1	BL00972R 20.72 B.759e-
	ļ	1	10 341-363
1512	BL00523	Sulfatases proteins.	10 341-363 BL00523R 19.27 4.536e-
1512	BL00523	Sulfatases proteins.	BL00523R 19.27 4.536e- 22 76-106 BL00523D
1512	BL00523	Sulfatases proteins.	BL00523B 19.27 4.536e-
1512	BL00523	Sulfatases proteins.	BL00523R 19.27 4.536e- 22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e- 09 159-170 BL00523G
1512	BL00523		BL00523R 19.27 4.536e- 22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e- 09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00523R 19.27 4.536e- 22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e- 09 159-170 BL00523G 9.46 5.333e-09 256-266 BL00914 24.91 7.045e- 14 168-218
		Syntaxin / epimorphin	BL00523R 19.27 4.536e- 22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e- 09 159-170 BL00523G 9.46 5.333e-09 256-266 BL00914 24.91 7.045e-

NO.		I a conservation	DESCRIPTION	RESULTS*
1528   PRO0320   PROTEIN GREAT SIGNATURE   PRO0320 12.19 4.774e-11 19.207 PRO03208 12.19 4.774e-11 19.207 PRO03208 12.19 4.774e-11 19.207 PRO03208 12.19 4.774e-11 19.207 PRO03208 12.19 4.774e-11 19.207 PRO03208 12.19 9.743e-10 10.6-121 PRO03208 12.19 9.743e-10 10.8-121 PRO03208 12.19 9.743e-10 10.8-121 PRO03208 12.19 9.743e-10 10.8-121 PRO03208 12.19 9.743e-10 10.8-121 PRO03208 12.19 9.743e-10 10.19 11.11 7.593e-10	SEQ ID NO:	ACCESSION NO.	DESCRIPTION	in the state of th
BL00600B 19.60 5.091e-15 16-186 H00600C 16.18 6.040c-12 190-206 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 8.77 1.000c-11 343-356 BL00600P 9.70 1.00c-12 1			<del> </del>	
15.160-186 BLOOGOOC   1.8 6.1006COC   1.8 6.004c-12 190-206 BLOOGOOC 8.77   1.000e-11 33-356   BLOOGOOD 8.71   1.000e-11 33-356   BLOOGOOD 8.71   1.000e-10 281-295		1		
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DM01970   0 kw ZK632.12 YDR313C   DM01970B 0.60 4.508e   ENDOSOMAL III.   DM01970B 0.60 4.508e   I5 171-184   I5 171-184   I5 171-184   IT 171-184   IT 184   IT 184   IT 1853e   IT 1855e   IT 1855		J	}	
ENDOSOMAL III.   15 171-184   1539   PF00781   Diacylglycerol kinase catalytic domain proteins (presumed).				
ENDOSOMAL III.   15 171-184	1538	DM01970		
Catalytic domain   10 103-127				
PRO0965   PRO0965   OCULAR ALBINISM TYPE 1   PRO0965H 10.73 1.231e-   PRO1965   OCULAR ALBINISM TYPE 1   29 312-334 PR00965E   12.93 5.846e-29 172-   195 PR00965F 5.98	1539	PF00781		I .
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PROTEIN SIGNATURE  29 312-334 PR00965R 12:33 5.846e-29 172-195 PR00965F 5.98 1.123e-28 209-231 PR00965C 15.04 1.000e-27 131-151 PR00965D 5.84 1.000e-27 150-170 PR00965G 8.52 2.440e-27 258-279 PR00965B 4.80 8.650e-26 88-109 PR00965A 12:53 75-55 PR00965I 3.91 6.442e-25 385-406 PRO0965D 3.91 6.442e-25 385-406 PR00965D 3.91 6.442e-25 385-406 PR00965D 3.91 6.442e-25 385-406 PR0013D DNA-BINDING BINDING DNA-BI	15/0	DROOSE		PR00965H 10.73 1.231e-
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3.91 6.442e-25 385-406				1
DECIDITATION   DECODE   DECIDITATION   DECODE   DECIDITATION   DECODE   DECODE   DECIDITATION   DECODE   DECODE   DECODE   DECIDITATION   DECODE   DECODE   DECODE   DECODE   DECODE   DECODE   DECIDITATION   DECODE   DECO				
Protein family proteins.   17 163-207	1541	BL01013	Oxysterol-binding	BL01013D 26.81 9.719e-
BINDING DNA.  BINDING DNA.  40 599-646 PD02699A 8.91 2.286e-34 219-248 PD02699B 18.28 6.143e- 21 485-509 PR00049D 0.00 7.857e- 10 182-197 PR00049D 0.00 7.102e-09 67-82  BL00951  BR lumen protein retaining receptor proteins.  BL00951C 19.35 1.000e- 40 93-142 BL00951D 13.94 8.714e-40 142- 177 BL00951A 15.10 1.000e-38 2-38 . BL00951B 14.23 6.250e- 33 38-69  BL00536  Ubiquitin-activating enzyme proteins.  BL00536F 13.65 8.920e- 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 248-279  PR00139  ASPARAGINASE/GLUTAMINASE PR00139C 11.72 9.679e- 09 550-569  PR00049D WILM'S TUMOUR PROTEIN PR00049D 0.00 5.119e-			protein family proteins.	
S.91 2.286e-34 219-248	1543	PD02699		
PD02699B 18.28 6.143e-21 485-509		1	BINDING DNA.	
1544   PR00049   WILM'S TUMOUR PROTEIN   PR00049D 0.00 7.857e-	ŀ			
SIGNATURB   10 182-197 PR00049D   0.00 7.102e-09 67-82	·	1.		
SIGNATURB   10 182-197 PR00049D   0.00 7.102e-09 67-82	1544	PR00049	WILM'S TUMOUR PROTEIN	
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retaining receptor 40 93-142 BL00951D 13.94 8.714e-40 142-177 BL00951A 15.10 1.000e-38 2-38 . BL00951B 14.23 6.250e-33 38-69  1548 BL00536 Ubiquitin-activating BL00536F 13.65 8.920e-33 38-69 enzyme proteins. 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e-18 248-279 FAMILY SIGNATURE PRO0139C 11.72 9.679e-09 550-569 PR00049 WILM'S TUMOUR PROTEIN PR00049D 0.00 5.119e-		<u> </u>		
proteins.  13.94 8.714e-40 142- 177 BL00951A 15.10 1.00e-38 2-38 . BL00951B 14.23 6.250e- 33 38-69  1548  BL00536  Ubiquitin-activating enzyme proteins.  20.79-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 248-279  PR00139  ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE  PR00139C 11.72 9.679e- 09 550-569  PR00049D WILM'S TUMOUR PROTEIN  PR00049D 0.00 5.119e-	1547	BL00951		
177 BL00951A 15.10 1.000e-38 2-38 . BL00951B 14.23 6.250e- 33 38-69  1548  BL00536  Ubiquitin-activating enzyme proteins.  30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 248-279  1549  PR00139  ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE  PR00139C 11.72 9.679e- 09 550-569  PR00049D WILM'S TUMOUR PROTEIN  PR00049D 0.00 5.119e-	1			1
1.000e-38 2-38 . BL00951B 14.23 6.250e- 33 38-69  1548  BL00536  Ubiquitin-activating enzyme proteins.  30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 248-279  1549  PR00139  ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE  PR00139C 11.72 9.679e- 09 550-569  PR00049D WILM'S TUMOUR PROTEIN  PR00049D 0.00 5.119e-			process.	·
33 38-69     1548   BL00536   Ubiquitin-activating   BL00536F 13.65 8.920e-   30 279-318 BL00536D   22.91 5.737e-24 21-65   BL00536E 16.94 4.696e-   18 24B-279     1549   PR00139   ASPARAGINASE/GLUTAMINASE   PR00139C 11.72 9.679e-   FAMILY SIGNATURE   09 550-569   1553   PR00049   WILM'S TUMOUR PROTEIN   PR00049D 0.00 5.119e-   1553   PR00049   WILM'S TUMOUR PROTEIN   PR00049D 0.00 5.119e-   1548   PR00049D 0.00 5.119e-   1553			ľ	
1548 BL00536 Ubiquitin-activating BL00536F 13.65 8.920e- enzyme proteins. 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 248-279 1549 PR00139 ASPARAGINASE/GLUTAMINASE PR00139C 11.72 9.679e- FAMILY SIGNATURE 09 550-569 1553 PR00049 WILM'S TUMOUR PROTEIN PR00049D 0.00 5.119e-	1			1
enzyme proteins. 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e-18 248-279  PR00139 ASPARAGINASE/GLUTAMINASE PR00139C 11.72 9.679e-09 550-569  PR00049 WILM'S TUMOUR PROTEIN PR00049D 0.00 5.119e-				
22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 24B-279  1549 PR00139 ASPARAGINASE/GLUTAMINASE PR00139C 11.72 9.679e- FAMILY SIGNATURE 09 550-569  1553 PR00049 WILM'S TUMOUR PROTEIN PR00049D 0.00 5.119e-	1548	BL00536	-	
BL00536E 16.94 4.696e- 18 248-279   R00139   ASPARAGINASE/GLUTAMINASE   PR00139C 11.72 9.679e- FAMILY SIGNATURE   O9 550-569   PR00049D 0.00 5.119e-	1		enzyme proteins.	
18 248-279     1549     PR00139     ASPARAGINASE/GLUTAMINASE   PR00139C 11.72 9.679e-				
1549 PR00139 ASPARAGINASE/GLUTAMINASE PR00139C 11.72 9.679e- FAMILY SIGNATURE 09 550-569 1553 PR00049 WILM'S TUMOUR PROTEIN PR00049D 0.00 5.119e-			i	•
FAMILY SIGNATURE 09 550-569 1553 PR00049 WILM'S TUMOUR PROTEIN PR00049D 0.00 5.119e-	1549	PR00139	ASPARAGINASE/GLUTAMINASE	
1553 PR00049 WILM'S TUMOUR PROTEIN PR00049D 0.00 5.119e-				
SIGNATURE 09 58-73	1553	PR00049		
			SIGNATURE	09 58-73

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1556	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.276e- 13 67-105
1557	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1558	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1559	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1562	ВЬ00522	DNA polymerase family X proteins.	BL00522C 11.90 6.600e- 18 412-436 BL00522B 27.30 1.738e-16 364- 410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e-
		*	14 502-532 BL00522F 14.90 2.385e-13 551- 575
1563	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 1.947c- 11 46-59
1564	BL00299	Ubiquitin domain proteins.	BL00299 28.84 2.823e- 10 324-376
1566	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 8.594e- 17 184-228 BL01013C 9.97 4.906e-12 14-24
	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10 295-306
1570	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 5.235e- 17 297-313 BL00479A 19.86 6.625e-15 271- 294 BL00479A 19.86
			2.667e-14 147-170 BL00479B 12.57 6.294e- 12 173-189
1576	PROOGES	OXYTOCIN RECEPTOR SIGNATURE	PR00665G 12.36 4.673e- 24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e- 22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e- 19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e- 15 11-25
1577	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 9.308e- 10 127-137
1579	BL00524	Somatomedin B domain proteins.	BL00524A 9.65 6.776e- 14 52-73
1580	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894B 13.93 6.959e- 16 182-215 PD02894A 21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain proteins.	BL00411C 15.04 5.292e- 12 32-54 BL00411H 15.66 4.441e-11 245- 276
1582	PR00604	CLASS IA AND IB CYTOCHROME C SIGNATURE	PR00604A 11.13 2.440e- 09 79-87
1584	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 1.000e- 10 225-236
1585	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551C 14.62 9.455e- 11 125-145
1586	DM01354	kw Transcriptase Reverse II ORF2.	DM01354S 11.61 7.750e- 09 474-495

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1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e- 33 180-210 PR00072A 12.75 6.040e-25 120- 145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e- 22 276-295 PR00072E 10.54 1.360e-19 301- 318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e- 15 332-349
1589	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191H 15.64 1.537e- 22 61-113 BL00191K 17.38 9.027e-12 398- 442
1590	DM01970	O kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e- 13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUPL CHROMOSOMB.	DM00517B 10.96 6.625e- 16 1175-1193 DM00517A 8.21 1.000e-11 1015- 1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e- 27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e- 12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e- 10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e- 11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e- 09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e- 10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e- 10 136-187
1605	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.571e- 10 44-57
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e- 23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e- 08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.9B 7.353e- 10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e- 09 365-391
1613	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e- 09 932-983 BL00412D 16.54 7.153e-09 933- 984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL005591 13.63 3.531e- 25 54-83 BL00559K 13.17 2.957e-18 197- 224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e- 16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e- 22 500-541 PD01427A 19.94 8.773e-18 439-

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			472
1616	BL00115	Eukaryotic RNA	BL00115Z 3.12 7.485e-
	•	polymerase II	09 152-201 BL00115Z
		heptapeptide repeat	3.12 9.603e-09 145-194
1		proteins.	3.12 3.0036-03 143-134
1617	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 7.750e-
İ	ļ	binding protein.	32 51~88 BL00303A
			21.77 1.947e-31 4-41
1618	BL01254	Fetuin family proteins.	BL01254F 10.02 8.754e-
		1	09 137-147
1619	PD01888	PEPTIDE REDUCTASE	PD01888B 25.10 1.000e-
		PROTEIN METHI.	40 47-97 PD01888C
ļ		PROTECTION PROTECTION	21.56 7.000e-30 125-
	1	}	
	,	i	155 PD01888A 12.84
			8.800e-15 7-23
1621	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 3.455e-
		TERMINAL TAIL SIGNATURE	09 692-704 PR00239E
,			1.58 4.580e-09 697-709
	1		PR00239E 1.58 4.580e-
1			09 702-714 PR00239E
	1	1	1.58 5.193e-09 703-715
1622	PR00860	VERTEBRATE	PRO0860B 7.04 1.900e-
1022	FROUGE		
	1	METALLOTHIONEIN	18 27-41 PR00860C
		SIGNATURE	9.61 1.474e-14 41-51
ĺ	i		PR00860A 5.46 1.720e-
			14 5-18
1624	PR00784	MITOCHONDRIAL BROWN FAT	PR00784D 15.86 8.027e-
	İ	UNCOUPLING PROTEIN	11 77-95
	1	SIGNATURE	
1626	BL00325	Actin-depolymerizing	BL00325B 21.66 1.000e-
	ľ	proteins.	40 93-139 BL00325A
1		-	24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase	BL00064B 23.57 1.000e-
-051	1 220000	proteins.	40 82-130 BL00064C
	Ì	processis.	17.28 1.000e-40 137-
	i		
			182 BL00064E 27.20
	i .		1.000e-40 223-275
	J		BL00064F 25.14 7.882e-
	1		36 286-331 BL00064A
			21.16 1.000e-33 22-60
			BL00064D 14.19 6.500e-
	1		31 182-212
1632	PR00063	RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
		SIGNATURE	11 59-84 PR00063A
			11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239D 0.00 1.105e-
		TERMINAL TAIL SIGNATURE	11 36-49 PR00239C
			3.51 2.538e-09 37-45
1636	BL01210	Caveolins proteins.	BL01210B 13.92 9.531e-
_050		DIVECTING PROCERTIES.	
1637	BL00982	Land to the state of the state	10 133-183
1031	D000302	Bacterial-type phytoene	BL00982A 18.41 5.388e-
		dehydrogenase proteins.	11 11-43
1639	BL01183	ubiE/COQ5	BL01183B 21.31 8.144e-
	1	methyltransferase family	12 132-177
		proteins.	•
1640	PR00015	GRAM-POSITIVE COCCUS	PR00015B 9.84 8.468e-
	1	SURFACE PROTEIN ANCHOR	10 128-149
		SIGNATURE	
1641	PR00320	G-PROTEIN BETA WD-40	PR00320B 12.19 5.935e-
	1	REPEAT SIGNATURE	11 364-379 PR00320A
	1		16.74 7.828e-11 364-
	I	1	379 PR00320C 13.01
			2.800e-10 279-294
	,		PR00320C 13.01 2.800e-
	1		10 364-379 PR00320B
		I	
	İ		12.19 5 1146-10 279-
			12.19 5.114e-10 279-
			12.19 5.114e-10 279- 294 PR00320A 16.74 1.659e-09 279-294

SBQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00320A 16.74 2.098e- 09 229-244
1642	PF00023	Ank repeat proteins.	PF00023A 16.03 6.464e; 09 114-130
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e-
1644	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e- 17 56-89
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.270e- 21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e- 16 332-351 PR00380B 12.64 6.657e-15 292- 310
1647	DM01242	3 THREONINETRNA LIGASE.	DM01242C 17.15 9.791e- 37 340-381 DM01242E 23.00 5.071e-31 463- 505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e- 18 265-314 DM01242F 10.61 7.618e-14 526- 540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e- 10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e- 11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e- 12 11-35 BL00933E 13.80 9.217e-09 456- 472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e- 10 70-115
1654	BL00982	Bacterial-type:phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e- 16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e- 11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e- 10 442-455
1659	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e- 12 376-401 BL00972B 20.72 5.629e-09 446- 468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e- 15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PRO0105A 10.36 4.900e- 13 1140-1157 PR00105B 12.32 2.800e-12 1259- 1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e- 33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e- 19 51-68 PR00319B 11.47 8.200e-19 70-85

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
1664	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.050e-10 489-502
1667	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 8.500e-
		ZINC-FINGER METAL- BINDING NU.	38 7-46
1669	BL01153	NOL1/NOP2/sun family	BL01153D 19.69 1.188e-
		proteins.	17 115-141 BL01153C 13.67 B.977e-15 66-80
			BL01153B 20.52 1.885e-
			10 13-37
1671	PR00678	PI3 KINASE P85	PR00678H 9.13 3.100e-
		REGULATORY SUBUNIT	10 1146-1169
1672	BL00598	Chromo domain proteins.	BL00598 14.45 8.500e-
			20 27-49
1673	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.329e-
1674	PR00049	WILM'S TUMOUR PROTEIN	PR00049D D.00 7.580e-
	3	SIGNATURE	11 343-358 PR30049D
		*	0.00 1.286e-10 342-357
1676	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PRO0747H 12.76 8.636e-
`		FAMILI 47 SIGNATURE	14.50 2.286e-18 368-
			393 PR00747C 12.06
	!		7.500e-18 112-131
			PR00747A 14.05 4.600e-
			15,23 B.759e-17 163-
			183 PR00747E 15.13
		į.	8.244e-15 254-272
			PR00747B 7.65 5.355e-
		Į.	13.56 8.714e-10 311-
			328
1677	PR00747	GLYCOSYL HYDROLASE	PR00747H 12.76 8.636e-
		FAMILY 47 SIGNATURE	19 309-330 PR00747G
		i	275 PR00747C 12.06
		1	7.500e-18 112-131
			PR00747A 14.05 4.600e-
			7.65 5.355e-13 75-90
	1		PR00747F 13.56 8.714e-
1500	Drag cres		10 193-210
1680	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 406-417 BL00678 9.67
		L-coame bronden.	6.684e-09 320-331
1681	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.6C0e-10
		proteins proteins.	329-340 BL00678 9.67
1683	PR00326	GTP1/OBG GTP-BINDING	6.684e-09 243-254 PR00326A 8.75 1.346e-
		PROTEIN FAMILY SIGNATURE	13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR	PR00646H 6.32 4.188e-
1600	PY 63.3.65	SIGNATURE	09 755-771
1690	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 75-129
1691	PR00456	RIBOSOMAL PROTEIN PZ	PR00456E 3.06 7.281e-
		SIGNATURE	10 418-433 PR00456E
	ĺ		3.06 7.281e-10 419-434
	1		PR00456B 3.06 8.125e- 10 420-435
1692	PR00456	RIBOSOMAL PROTEIN P2	PR00456E 3.06 7.281e-
		SIGNATURE	10 487-502 PR00456B
	<b>'</b>		3.06 7.281e~10 488-503
		i	PR00456E 3.06 8.125e- 10 489-504
1693	BL00674	AAA-protein family	BL00674C 22.60 8.043e-
·		proteins.	24 274-317 BL00674B
		<del></del>	<del></del>

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		4.46 4.000e-23 241-263 BL00674D 23.41 8.560e- 18 338-385 BL00674E 15.24 1.720e-15 414- 434
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e- 10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466C 10.17 3.443e- 13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e- 09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e- 12 283-300 BL00028 16.07 3.769e-11 255- 272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e- 11 227-244 BL00028 16.07 1.600e-10 199- 216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e- 15 62-102 BL01019B 19.49 4.000e-15 107- 162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.484e- 12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558c- 14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.565e- 10 116-130 PR00019B 11.36 4.600e-09 113- 127 PR00019B 11.36 7.120e-09 204-21B
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e- 11 232-247 BL01159 13.85 5.408e-10 613- 628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e- 10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1714	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1715	BL01115 .	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 7.129e- 09 7-51
1718	BL00353	HMG1/2 proteins.	BL00353C 14.83 6.018e- 10 136-183 BL00353B 11.47 8.866e-09 86-136
1719	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.408e- 09 432-483
1721	BL00038	Myc-type, 'helix-loop- helix' dimerization domain proteins.	BL00038B 16.97 8.448e- 12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e- 09 418-428
1724	BL01279	Protein-L- isoaspartate(D- aspartate) 0- methyltransferase signa.	BL01279A 24.27 5.663c- 12 233-201
1728	BL00018	EP-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41
			4.176e-11 157-170

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1731	BL01160	Kinesin light chain	BL01160B 19.54 9.676e~
	2200	repeat proteins.	10 296-350
1732	BL01160	Kinesin light chain	BL01160B 19.54 9.676e-
1733	PF00850	repeat proteins. Histone deacetylase	10 316-370 PF00850F 15.70 4.349e-
1,33	F100050	family.	22 246-279 PF00850D
	- [		14.76 6.850e-20 177-
	1		201 PF00850E 8.88
	1		8.691e-18 209-235 PF00850G 22.75 4.098e-
			14 281-323
1734	BL00354	HMG-I and HMG-Y DNA-	BL00354C 6.61 5.932e
		binding domain proteins (Ahook)	09 292-307
1735	DM00179	w KINASE ALPHA ADHESION	DM00179 13.97 5.263e-
		T-CELL.	10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.188e-
		RAS SIGNATURE	11 5-27 PR00449D 10.79 2.241e-10 109-
			123 PR00449E 13.50
			9.289e-10 144-167
1744	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.188e-
		RAS SIGNATURE	11 5-27 PR00449D 10.79 2.241e-10 109-
	,		123 PRO0449E 13.50
			9.289e-10 144-167
1745	ВЬ00720	Guanine-nucleotide dissociation stimulators	BL00720B 16.57 8.297e- 15 136-160
		CDC25 family sign.	13 130-100
1746	PR00081	GLUCOSE/RIBITOL	PR00081B 10.38 6.727e-
	ľ	DRHYDROGENASE FAMILY	11 45-57 PR00081E
		SIGNATURE	17.54 3.935e-10 150-
1747	BL00439	Acyltransferases	BL00439H /18.24 8.435e-
	Ÿ	ChoActase / COT / CPT	14 65-91 BL00439G
1749	PR00819	family proteins.  CBXX/CFOX SUPERFAMILY	13.40 2.895e-12 3-14 PR00819B 10.83 7.158e-
2.25	1	SIGNATURE	11 4-20
1751	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 3.400e-
		METAL-BINDI.	14 33-46 PD00066 13.92 1.000e-13 89-102
	1		PD00066 13.92 7.000e-
	ì		FD00000 13.32 1.000c-
			13 61-74 PD00066
			13 61-74 PD00066 13.92 6.571e-12 117-
1753	BL01013	Oxysterol-binding	13 61-74 PD00066
		Oxysterol-binding protein family proteins.	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77
1753 1754	BL01013	protein family proteins. Receptor tyrosine kinase	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e-
		protein family proteins.	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I
		protein family proteins. Receptor tyrosine kinase	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e-
1754	BL00790	protein family proteins.  Receptor tyrosine kinase class V proteins.	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318
		protein family proteins. Receptor tyrosine kinase class V proteins.  PROTEIN ZINC PINGER	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e-
1754	BL00790	protein family proteins.  Receptor tyrosine kinase class V proteins.	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318
1754	BL00790	protein family proteins. Receptor tyrosine kinase class V proteins.  PROTEIN ZINC FINGER ZINC-FINGER METAL-	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09
1754	PD01066	protein family proteins.  Receptor tyrosine kinase class V proteins.  PROTEIN ZINC FINGER ZINC-FINGER METALBURDING NU.  GLIADIN.	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49  DM00406 7.73 7.600e-09 653-666
1754	BL00790	protein family proteins.  Receptor tyrosine kinase class V proteins.  PROTEIN ZINC FINGER ZINC-FINGER METALBURDING NU.  GLIADIN.  ADHESION GLYCOPROTEIN	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49  DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e-
1754	PD01066	protein family proteins.  Receptor tyrosine kinase class V proteins.  PROTEIN ZINC FINGER ZINC-FINGER METALBURDING NU.  GLIADIN.	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49  DM00406 7.73 7.600e-09 653-666
1754 1756 1758 1762	PD01066  DM00406  PD02929  PR00326	protein family proteins.  Receptor tyrosine kinase class V proteins.  PROTEIN ZINC PINGER ZINC-FINGER METAL-BINDING NU. GLIADIN.  ADHESION GLYCOPROTEIN PRECURSOR I.  GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49  DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167
1754 1756 1758	PD01066  DM00406  PD02929	protein family proteins. Receptor tyrosine kinase class V proteins.  PROTEIN ZINC PINGER ZINC-FINGER METAL-BINDING NU. GLIADIN.  ADHESION GLYCOPROTEIN PRECURSOR I. GTP1/OBG GTP-BINDING	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49  DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e-
1754 1756 1758 1762 1765	PD01066  DM00406  PD02929  PR00326  PF00023	protein family proteins.  Receptor tyrosine kinase class V proteins.  PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.  GLIADIN.  ADHESION GLYCOPROTEIN PRECURSOR I.  GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE  Ank repeat proteins.	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e- 14 523-539
1754 1756 1758 1762	PD01066  DM00406  PD02929  PR00326	protein family proteins.  Receptor tyrosine kinase class V proteins.  PROTEIN ZINC PINGER ZINC-FINGER METAL-BINDING NU. GLIADIN.  ADHESION GLYCOPROTEIN PRECURSOR I.  GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49  DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e-
1754 1756 1758 1762 1765 1775	PD01066  DM00406  PD02929  PR00326  PF00023  BL00942	protein family proteins.  Receptor tyrosine kinase class V proteins.  PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.  GLIADIN.  ADHESION GLYCOPROTEIN PRECURSOR I.  GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE Ank repeat proteins.  glpT family of transporters proteins.	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49  DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e- 14 523-539 BL00942F 15.07 4.343e- 10 371-389 BL00942B 20.36 8.040e-09 94-137
1754 1756 1758 1762 1765	PD01066  DM00406  PD02929  PR00326  PF00023	protein family proteins.  Receptor tyrosine kinase class V proteins.  EROTEIN ZINC FINGER ZINC-FINGER METALBURDING NU.  GLIADIN.  ADHESION GLYCOPROTEIN PRECURSOR I.  GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE ANK repeat proteins.	13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49  DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e- 14 523-539 BL00942F 15.07 4.343e- 10 371-389 BL00942B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134c-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.881e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

<sup>\*</sup> results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.
TRADOCS:1416223.1(%CRND1!.DOC)

TABLE 4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
2	ig	Immunoglobulin domain	-	SCORE
3	pkinase	Eukaryotic protein kinase	2.le-32	109.5
	-	domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	0	1090.4
8	fn3	Fibronectin type III domain	0	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	35.4
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH C	IMP dehydrogenase / GMP	1.6e-119	410.5
		reductase C terminus		1.20.5
21	IMPDH C	IMP dehydrogenase / GMP	4.3e-102	352.6
22		reductase C terminus	1	
46	pkinase	Eukaryotic protein kinase domain	2.4e-79	277.0
23	pkinase	Eukaryotic protein kinase domain	8.4e-74	258.6
25	RNA_pol_A	RNA polymerase alpha subunit	0	1077.7
26	Clq	Clq domain	1.9e-10	44.4
27	Ribosomal_L2	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L2	Ribosomal protein L23	le-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	Rts	Ets-domain	1.4e-56	182.1
45	Ets	Bts-domain	1.4e-56	182.1
46	LRR	Leucine Rich Repeat	1.7e-13	58.3
18	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
49	ITAM	Immunoreceptor tyrosine-based	1.4e-05	31.9
	111	activation mot		
50	OCH-5	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
52	ras	Ras family	8.5e-45	1-22-
		Phosphoribulokinase	8.5e-45 2.1e-65	162.3 230.7
53	PRK			1 / 311 /
	myb_DNA-	Myb-like DNA-binding domain	0.096	15.2
54	myb_DNA- binding	Myb-like DNA-binding domain	0.096	15.2
54	myb_DNA- binding voltage_CLC	Myb-like DNA-binding domain  Voltage gated chloride channels	0.096 3.3e-186	15.2 631.9
54 55 56	myb_DNA- binding voltage_CLC sugar_tr	Myb-like DNA-binding domain  Voltage gated chloride channels  Sugar (and other) transporter	0.096 3.3e-186 0.00015	15.2 631.9 -64.3
54 55 56	myb_DNA- binding voltage_CLC sugar_tr TBC	Myb-like DNA-binding domain  Voltage gated chloride channels  Sugar (and other) transporter  TBC domain	0.096 3.3e-186 0.00015 2.2e-37	15.2 631.9 -64.3 137.6
54 55 56 57	myb_DNA- binding voltage_CLC sugar_tr TBC ank	Myb-like DNA-binding domain  Voltage gated chloride channels  Sugar (and other) transporter  TBC domain  Ank repeat	0.096 3.3e-186 0.00015 2.2e-37 5.9e-25	15.2 631.9 -64.3
54 55 56 57 58	myb_DNA- binding voltage_CLC sugar_tr TBC ank ank	Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat	0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25	15.2 631.9 -64.3 137.6
54 55 56 57 58	myb_DNA- binding voltage_CLC sugar_tr TBC ank	Myb-like DNA-binding domain  Voltage gated chloride channels  Sugar (and other) transporter  TBC domain  Ank repeat	0.096 3.3e-186 0.00015 2.2e-37 5.9e-25	15.2 631.9 -64.3 137.6 96.3
54 55 56 57 58 59	myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi	Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family	0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49	15.2 631.9 -64.3 137.6 96.3 96.3
55 56 57 58 59 57	myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n	Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMR/MP20/Claudin family C2 domain	0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49 7.9e-54	15.2 631.9 -64.3 137.6 96.3 96.3 175.6
55 56 57 58 59 57	myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n C2 C2	Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family C2 domain C2 domain	0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49 7.9e-54 2.3e-54	15.2 631.9 -64.3 137.6 96.3 96.3 175.6
53 54 55 56 57 58 59 57	myb_DNA- binding voltage_CLC sugar_tr TBC ank PMP22_Claudi n C2	Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMR/MP20/Claudin family C2 domain	0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49 7.9e-54	15.2 631.9 -64.3 137.6 96.3 96.3 175.6

	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
NO:	<del></del>	1		SCORE
74	pkinase	domain Eukaryotic protein kinase	2.8e-38	140.6
/4	-^	domain	<b></b>	
76	zf- C4_Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92	laminin_G	Laminin G domain	6.le-27	98.5
93	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
95	pkinase	Eukaryotic protein kinase domain	1.4e-59	211.4
96	pkinase	Eukaryotic protein kinase domain	2.6e-51	183.9
97	adh short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various cellular act	6.8e-05	-5.2
104	pkinase	Eukaryotic protein kinase domain	2.7e-73	256.9
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductas e	FAD/NAD-binding Cytochrome reductase	7.7e-61	215.5
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
116	PH	PH domain	3.le-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty- acid binding pr	2.4e-14	53.5
118	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
120 .	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IP5_eIF4_eIF 2	eIF4-gamma/eIF5/eIF2-epsilon	le-32	122.2
124	ig	Immunoglobulin domain	6.5e-08	30.6
127	mito_carr	Mitochondrial carrier proteins	3e-16	58.6
128	PP2C	Protein phosphatase 2C	2.2e-71	250.6
129	ATP1G1_PLM_M AT8	ATPIGI/PLM/MATE family	3.1e-20	80.6
		meters develope complete advantage being an		
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133	ACBP	Acyl CoA binding protein	4.6e-22	86.7
133 134	ACBP EXM	Acyl CoA binding protein RNA recognition motif.	4.6e-22 1.2e-31	86.7 118.5
133	ACBP TXM TQ ATPIG1_PLM_M	Acyl CoA binding protein	4.6e-22	86.7
133 134 135	ACBP FXIII IQ	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome	4.6e-22 1.2e-31 2.6e-08	86.7 118.5 41.0
133 134 135 136	ACBP  IXM IQ ATPIG1_PLM_M AT8 WH2	Acyl CoA binding protein RNA recognition motif. TO calmodulin-binding motif ATPIGI/PLM/MATS family Wiskott Aldrich syndrome homology region 2	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067	86.7 118.5 41.0 85.7
133 134 135 136	ACBP  IXM IQ ATPIG1_PLM_M AT8 WH2  zf-C2H2 Peptidase_S2	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome	4.6e-22 1.2e-31 2.6e-08 9.3e-22	86.7 118.5 41.0 85.7
133 134 135 136 139 140	ACBP  IXM  IQ  ATPIG1_PLM_M  AT8  WH2  zf-C2H2  Peptidase_S2 6	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-02 5.7e-10	86.7 118.5 41.0 85.7 23.1 287.5 35.7
133 134 135 136 139 140 141	ACBP  IXm  IQ  ATPIG1_PLM_M  AT8  WH2  zf-C2H2  Peptidase_S2 6  arf	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I ADP-ribosylation factor family	1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10	86.7 118.5 41.0 85.7 23.1 287.5 35.7
133 134 135 136 139 140 141 143	ACBP  IXm  IQ  ATPIG1_PLM_M  AT8  WH2  Zf-C2H2  Peptidase_S2 6  arf  KRAB	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I ADP-ribosylation factor family KRAB box	1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10 1.2e-39 7.3e-30	86.7 118.5 41.0 85.7 23.1 287.5 35.7 145.2
133 134 135 136 139 140 141	ACBP  IXm  IQ  ATPIG1_PLM_M  AT8  WH2  zf-C2H2  Peptidase_S2 6  arf	Acyl CoA binding protein RNA recognition motif. TQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I  ADP-ribosylation factor family KRAB box Integral membrane protein DUF6 3'5'-cyclic nucleotide	1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10	86.7 118.5 41.0 85.7 23.1 287.5 35.7
133 134 135 136 139 140 141 143 146 148 149	ACBP  TXM  TQ  ATPIG1_PLM_M  AT8  WH2  zf-C2H2  Peptidase_S2 6  arf  KRAB  DUF6  PDEase	Acyl CoA binding protein RNA recognition motif. TO calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I  ADP-ribosylation factor family KRAB box Integral membrane protein DUF6 3'5'-cyclic nucleotide phosphodiesterase	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10 1.2e-39 7.3e-30 0.096 3.8e-80	86.7 118.5 41.0 85.7 23.1 287.5 35.7 145.2 112.6 8.0 231.1
133 134 135 136 139 140 141 143 146 148 149	ACBP  IXM IQ ATPIG1_PLM_M AT8 WH2  Zf-C2H2 Peptidase_S2 6 arf KRAB DUF6 PDEase	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MATS family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I ADP-ribosylation factor family KRAB box Integral membrane protein DUF6 3'5'-cyclic nucleotide phosphodiesterase S4 domain	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10 1.2e-39 7.3e-30 0.096 3.8e-80 1.1e-08	86.7 118.5 41.0 85.7 23.1 287.5 35.7 145.2 112.6 8.0 231.1
133 134 135 136 139 140 141 143 146 128 149	ACBP  IXM IQ ATPIG1_PLM_M AT8 WH2  zf-C2H2 Peptidase_S2 6 arf KRAB DUP6 PDEase  S4 tRNA-synt_1d	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I ADP-ribosylation factor family KRAB box Integral membrane protein DUF6 3'5'-cyclic nucleotide phosphodiesterase S4 domain tRNA synthetases class I (R)	1.2e-39 7.3e-30 0.096 1.2e-39 1.2e-39 7.3e-30 0.096 3.8e-80 1.1e-08 3.8e-103	86.7 118.5 41.0 85.7 23.1 287.5 35.7 145.2 112.6 8.0 231.1 42.3 356.1
133 134 135 136 139 140 141 143 146 148 149	ACBP  IXM IQ ATPIG1_PLM_M AT8 WH2  Zf-C2H2 Peptidase_S2 6 arf KRAB DUF6 PDEase	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MATS family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I ADP-ribosylation factor family KRAB box Integral membrane protein DUF6 3'5'-cyclic nucleotide phosphodiesterase S4 domain	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10 1.2e-39 7.3e-30 0.096 3.8e-80 1.1e-08	86.7 118.5 41.0 85.7 23.1 287.5 35.7 145.2 112.6 8.0 231.1

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SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PEAM
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
160	Zn carbOpept	Zinc carboxypeptidase	5e-138	471.9
165	pkinase	Eukaryotic protein kinase	5.1e-67	236.1
	-	domain		
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	27.0
168	Ribosomal_Sl	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	le-48	157:0
171	DUF59	Domain of unknown function	0.07	-17.4
172	pkinase	DUF59 Eukaryotic protein kinase	3.7e-15	58.6
	-	domain		
173	globin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	le-31	118.8
178	ATPIGI_PLM_M AT8	ATP1G1/PLM/MAT8 family	2.5e-17	71.0
179	2f-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y phosphatas e	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Bukaryotic protein kinase domain	6.5e-82	285.6
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent enzyme	2.5e-64	227.1
197	DnaJ	DnaJ domain	1.6e-38	141.4
199	RrnaAD	Ribosomal RNA adenine	0.00018	16.9
		dimethylases		
200	acid_phospha	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP- synt AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	vATP- synt AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	Clq	Clg domain	1.6e-70	247.7
212	UQ con	Ubiquitin-conjugating enzyme	7.4e-74	258.8
213	UQ con	Ubiquitin-conjugating enzyme	1e-53	191.9
215	DEAD	DEAD/DRAH box helicase	1.8e-43	140.4
216	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos_trans f 2	Glycosyl transferases	4e-21	83.6
219	ig	Immunoglobulin domain	0,092	10.7
222	WD4 D	WD domain, G-beta repeat	7.4e-23	89.4
	.1			
224 225	DnaJ CXXCXGX	TPR Domain DnaJ central domain (4 repeats)	1.2e-08 1.5e-38	141.5
226	G DnaJ CXXCXGX	DnaJ central domain (4 repeats)	1.5e-38	141.5
	G _			
229	HSP70	Hsp70 protein	2.4e-54	194.0
230	GSHPx	Glutathione peroxidases	3.4e-47	170.2
231	tsp_1	Thrombospondin type 1 domain	0.0075	17.1
233	cyclin	Cyclin	4.6e-144	492.0
234	ras	Ras family	4.8e-50	179.7
235	LRR	Leucine Rich Repeat	1.2e-30	115.3
236	LRR	Leucine Rich Repeat	6.7e-29	109.4
	PDZ	PDZ domain (Also known as DHR	1.7e-09	45.0
237			・ ふ、/ヒ・リフ	1 22.0

SEQ ID	PPAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORB
244	dCMP_cyt_dea m	Cytidine and deoxycytidylate deaminase	2.5e-05	31.1
245	ig	Immunoglobulin domain	6.7e-08	30.5
248	wnt	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito_carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekin ase	Adenylate kinase	1.8e-14	55.7
255	Cation_efflu x	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid transporter protein	2.6e-52	187.2
258	adenylatekin ase	Adenylate kinase	2.le-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial_PQ Q	PQQ enzyme repeat	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina se	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal_\$7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Bukaryotic protein kinase domain	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284 287	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
291	Exonuclease SAM	Exonuclease SAM domain (Sterile alpha	1.4e-67 0.034	238.0
292	SAM	motif) SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_trans f_4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)		294.8
305	KRAB	KRAB box	2e-44	161.0
306	rrm	RNA recognition motif.	2.7e-44	160.6
308	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA polymera	DNA polymerase X family	2.4e-64	227.2
	P-box	F-box domain.	9.5e-08	39.2
312 313	ig Ets	Immunoglobulin domain	6.8e-19	65.9
313	Kelch	Ets-domain	8.1e-60	192.3
315	arf	Kelch motif	1.3e-106	367.6
318	sugar tr	ADP-ribosylation factor family Sugar (and other) transporter	3.2e-35 0.0003	130.4
320	pkinase	Eukaryotic protein kinase	8.1e-83	-73.1
322	pkinase	domain  Bukaryotic protein kinase		288.6
		domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326 327	ARID HMG box	ARID DNA binding domain	5.1e-37	136.4
327	cadherin	HMG (high mobility group) box	6.7e-29	109.4
331	chromo	Cadherin domain   chromo' (CHRromatin	8.1e-81 4e-18	281.9 66.7
		Organization MOdifier)		
333	Peptidase M2	Glycoprotease family		467.4

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SEQ ID	PPAM NAME	DESCRIPTION	p-value	PFAM SCORE
335	vwa	von Willebrand factor type A	2.3e-07	37.9
339	ras	Ras family	7.8e-07	-59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	2f-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	ig	Immunoglobulin domain	0.0005	18.0
345			6.5e-65	
	pkinase ·	Rukaryotic protein kinase domain		229.1
347	pkinase	Bukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.1e-15	63.3
355	PHD	PHD-finger	3.2e-07	37.4
358	DUF6	Integral membrane protein DUF6	0.033	15.8
359	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	79.4
361	ank	Ank repeat	6.6e-34	126.1
362	ArfGap	Putative GTP-ase activating	4.7e-53	189.7
JU2 .	ALLOAD	protein for Arf	1.76-33	1 105.7
363	efhand	BF hand	5.46-10	46.6
363	LRR		8.8e-44	158.9
		Leucine Rich Repeat		1
368	laminin_G	Laminin G domain	1.5e-33	121.7
369	PP2C	Protein phosphatase 2C	5.3e-20	73.9
372	LIM	LIM domain containing proteins	9.9e-15	57.1
373	KRAB	KRAB box	4.8e-23	90.0 .
376	ion_trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase domain	1.6e-94	327.5
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin- transferase).	1.3e-07	-13.5
384	ank .	Ank repeat	2.5e-101	350.0
386	iq	Immunoqlobulin domain	9.5e-05	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.1e-21	83.6
396	spectrin	Spectrin repeat	2.1e-67	237.3
397	zf-C2H2	Zinc finger, C2H2 type	0.0066	237.3
399	fn3	Fibronectin type III domain	4.1e-102	352.6
400	WD40	WD domain, G-beta repeat	0.00049	26.8
			2	
401	El_dehydrog	Dehydrogenase B1 component	3e-119	1719.6
		Fibronectin type III domain	1_	
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGEF	RhoGEF domain	1.1e-23	92.1
411	P-box	P-box domain.	4.2e-06	33.7
412	SNF2_N	SNF2 and others N-terminal domain	5.8e-16	61.6
415	CPSase L cha	Carbamoyl-phosphate synthase (CPSase)	1.5e-172	586.6
	1 -	Leucine Rich Repeat	3.8e-24	93.6
418	LRR			
			20-58	207 5
419	DENN	DENN (AEX-3) domain	2e-58	207.5
419 420	DENN Rasgef	DENN (AEX-3) domain RasGEF domain	8.1e-43	155.7
419 420 421	DENN RasGEF ank	DENN (AEX-3) domain RasGEF domain Ank repeat	8.1e-43 1.4e-153	155.7 523.7
419 420 421 424	DENN RasGEF ank G-patch	DENN (AEX-3) domain RasGEF domain Ank repeat G-patch domain	8.1e-43 1.4e-153 1e-19	155.7 523.7 78.9
419 420 421 424 425	DENN RASGEF ank G-patch pkinase	DENN (AEX-3) domain RasGEF domain Ank repeat	8.1e-43 1.4e-153	155.7 523.7 78.9 117.1
419 420 421 424	DENN RasGEF ank G-patch	DENN (AEX-3) domain RasGEF domain Ank repeat G-patch domain Eukaryotic protein kinase	8.1e-43 1.4e-153 1e-19	155.7 523.7 78.9

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	<del> </del>			100.12
429	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	8.6e-11	39.2
431	DEAD	DEAD/DEAH box helicase	1e-66	214.0
432	SH3	SH3 domain	3.4e-16	67.2
433	GTP CDC	Cell division protein	2.1e-114	393.5
436	Collagen	Collagen triple helix repeat (20 copies)	4.6e-194	658.1
438	Ricin_B_lect	Similarity to lectin domain of	0.0085	10.5
441	Alpha_adapti	Alpha adaptin carboxyl-terminal	1.2e-256	866.0
442	Alpha_adapti	Alpha adaptin carboxyl-terminal	1.8e-235	795.7
443	PDZ	PDZ domain (Also known as DHR or GLGF).	1.9e-65	230.9
445	LON	ATP-dependent protease La (LON)	0.00012	-17.1
446	iq	Immunoqlobulin domain	0.00011	20.1
451	idaus	Sushi domain (SCR repeat)	1.4e-18	75.2
452	fn3	Fibronectin type III domain	1.5e-06	35.2
454	pyridoxal_de C	Pyridoxal-dependent decarboxylase conse	8.3e-14	50.3
456	kinesin	Kinesin motor domain	4.9e-217	734.4
457	neur_chan	Neurotransmitter-gated ion- channel	le-175	597.1
458	Josephin	Josephin	0.0002	18.7
468	bZIP	bZIP transcription factor	1.7e-07	31.8
470	NTP_transfer	Nucleotidyl transferase	6.3e-06	-26.3
471	WD40	WD domain, G-beta repeat	2e-28	107.9
473	LIM	LIM domain containing proteins	0.00021	20.7
477	zf-RanBP	Zn-finger in Ran binding protein and others.	0.028	21.0
479	WD40	WD domain, G-beta repeat	6.5e-18	73.0
480	KRAB	KRAB box	le-31	118.8
481	ArfGap	Putative GTP-ase activating protein for Arf	8.4e-66	232.0
485	SH2	Src homology domain 2	0.011	11.4
486 487	C1q daxm	Clq domain Double-stranded RNA binding motif	1.1e-47	259.6 171.9
489	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
490	Alpha_adapti	Alpha adaptin carboxyl-terminal domai	3.4e-222	751.6
492	SKI	Shikimate kinase	1.2e-10	48.8
497	KNV_polyprot	ENV polyprotein (coat polyprotein)	2.6e-22	77.6
498	abhydrolase_ 2	Phospholipase/Carboxylesterase	0.041	-48.1
500	rrm	RNA recognition motif.	5.4e-34	126.4
501	WW	WW domain .	4.6e-18	73.4
502	ig	Immunoglobulin domain	1.1e-10	39.5
504	abhydrolase	alpha/beta hydrolase fold	0.045	-3.6
505	vwa	von Willebrand factor type A domain	7.1e-62	219.0
508	Na_K_ATPase_C	Na+/K+ ATPase C-terminus	2.3e-145	496.3
509	Exonuclease	Exonuclease	1.3e-56	201.5
510	Glycos_trans f_1	Glycosyl transferases group 1	2.9e-06	27.0
511	Glycos_trans f_1	Glycosyl transferases group 1	2.9e-06	27.0
512	Glycos_trans f_1	Glycosyl transferases group 1	1.9e-09	38.5
514	pro_isomeras	Cyclophilin type peptidyl- prolyl cis-tr	1.8e-63	221.4

SEQ ID	PFAM NAME	I DECOMPTON		
NO:	PEAM NAME	DESCRIPTION	p-value	PFAM
515	1000			SCORE
L	EGF	EGF-like domain	1.9e-18	74.7
516	Surp	Surp module	4.3e-38	140.0
523	ig	Immunoglobulin domain	3.3e-06	25.0
526	UBX	UBX domain	1.1e-34	128.6
528	adh zinc	Zinc-binding dehydrogenases	2,7e-34	127.4
530	SAM	SAM domain (Sterile alpha	0.046	10.0
		motif)	0.046	10.0
531	adh short	short chain denydrogenase	2 222	
532		short charn denydrogenase	0.0025	-34.1
533	mito_carr	Mitochondrial carrier proteins	2.5e-81	281.7
1	mito_carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	PMO-like	Flavin-binding monooxygenase-	0	1153.7
ŀ		like		
536	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt 1	tRNA synthetases class I (I, L,	3.1e-136	466.0
!		M and V)	J.16-130	300.0
538	tRNA-synt 1	tRNA synthetases class I (I, L,	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	122-
]	cidos bytte_1	M and V)	3.1e-136	466.0
539	tRNA-synt 1			
339	CKNA-SYNC_I	tRNA synthetases class I (I, L,	1.9e-117	403.6
		M and V)	<u> </u>	
540	tRNA-synt_1	tRNA synthetases class I (I, L,	3.1e-136	466.0
		M and V)		
541	vATP-synt_E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	zf-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
544	DUF101	Protein of unknown function	8.5e-38	139.0
		DUF101	0.50 50	1 -37.0
545	TGFb_propept	TGP-beta propertide	1.1e-67	024 0
	ide	Tor Deta propepriae	1.16-07	238.2
547	WD40	WD domain, G-beta repeat	-	
548	RHD	WD domain, G-bela repeat	2.6e-32	120.8
549		Rel homology domain (RHD).	·1.6e-238	686.2
	MMR_HSR1	GTPase of unknown function	5.4e-67	236.0
551	HECT	HECT-domain (ubiquitin-	4.3e-127	435.6
ļ		transferase).		
554	MHC_II_alpha	Class II histocompatibility	3.5e-74	259.8
		antigen, alp	1	}
555	2f-UBR1	Putative zinc finger in N-	3.3e-16	67.3
		recognin	1	
556	Kelch	Kelch motif	5.5e-29	109.7
561	AMP-binding	AMP-binding enzyme	2.8e-06	-163.7
562	PABP	Poly-adenylate binding protein,	4.9e-38	139.8
	*	unique domai	4.50 30	132.0
564	Gag p30	Gag P30 core shell protein	1.2e-67	238.2
566	PWWP	PWWP domain		
567	SCAN	SCAN domain	8.1e-16	66.0
569	pkinase	· · · - · · · · · · · · · · · · ·	7.3e-68	238.9
309	pkinase	Rukaryotic protein kinase	1.5e-84	294.3
570	<del>  , , </del>	domain		·
570	pkinase	Bukaryotic protein kinase	1.5e-84	294.3
	-	domain .		
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin_head	Myosin head (motor domain)	0	1495.2
573	myosin_head	Myosin head (motor domain)	0	1490.4
575	Surp	Surp module	1.7e-23	91.5
576	Surp	Surp module	1.7e-23	91.5
577	DNA pol B	DNA polymerase family B	0 1.7e-23	
578	PDZ	PDZ domain (Also known as DHR		1138.6
	-~-		8.3e-09	42.7
579	IDD	or GLGP).		]
	LRR	Leucine Rich Repeat	4.9e-21	83.3
580	neur_chan	Neurotransmitter-gated ion-	5.9e-177	601.3
		channel		í
583	sushi	Sushi domain (SCR repeat)	0	1673.0
584	DRAD	DBAD/DEAH box helicase	7.3e-36	116.3
586	KH-domain	KH domain	2.9e-13	57.5
587	G-patch	G-patch domain		
589	LIM	LIM domain containing proteins	2.3e-14	61.2
590	bromodomain		2.3e-36	133.4
591		Bromodomain	6.6e-32	114.7
331	bromodomain	Bromodomain	6.6e-32	114.7

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			P varue	SCORE
592	hormone_rec	Ligand-binding domain of	3.5e-22	87.1
	_	nuclear hormone	1	
593	PHD	PHD-finger	3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase domain	5e-92	319.2
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_car=	Mitochondrial carrier proteins	6.3e-67	232.3
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PNWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_bind ing	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatas e	Protein-tyrosine phosphatase	1.4e-32	121.6
622	pkinase	Eukaryotic protein kinase domain	4.4c-40	146.6
623 .	BNR	BNR repeat	2.1a-11	51.3
624	molybdopteri n	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh_short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632 635	rrm pkinase	RNA recognition motif. Bukaryotic protein kinase	1.6e-104	30.5
636	Fork head	domain Fork head domain	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase	3.8e-70	246.5
642	TPR	TPR Domain	4.8e-08	40.1
643	efhand	EF hand	1.9e-27	104.6
647	SNF2 N	SNF2 and others N-terminal	1.3e-27	351.1
648	PseudoU synt	domain RNA pseudouridylate synthase	1.9e-55	197.6
	h_2		1	
650	zf-C2H2	Zinc finger, C2H2 type	0.0087	22.7
651	ank	Ank repeat	1.3e-17	71.9
652	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
653	neur_chan	Neurotransmitter-gated ion- channel	4.le-171	581.8
654	tsp_1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
661	pou	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
662	C2	C2 domain	6.7e-19	76.2
663	C2	C2 domain	6.7e-19	76.2
664	C2	C2 domain	6.7e-19	76.2
667	GST	Glutathione S-transferases.	9.3e-34	114.4
668	LRR	Leucine Rich Repeat	9.3e-31	115.6
670 671	spectrin	Spectrin repeat	4e-57	203.2
672	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
674	ABC_tran	ABC transporter WD domain, G-beta repeat	5.3e-60	212.8
0/3	1 110-20	wo domain, G-beta repeat	4.8e-24	93.3

SEQ ID	PPAM NAME	DESCRIPTION	p-value	PFAM
NO:	-		<u> </u>	SCORE
675	WD40	WD domain, G-beta repeat	4.8e-24	93.3
676	LRK	Leucine Rich Repeat	0.0015 2.6e-29	25.2 107.7
679	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type		
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
682	DSPC	Dual specificity phosphatase, catalytic doma	4.3e-43	156.6
683	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin	0	1890.8
689	PR55	Protein phosphatase 2A regulatory subunit PR	0	1038.8
691	homeobox	Homeobox domain	8.5e-30	112.4
696	Peptidase_M2	metallopeptidase family M24	2.6e-59	210.5
697	RhoGEF	RhoGEF domain	9.5e-35	128.9
698	PHD	PHD-finger	0.008	9.3
701	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
702	Sulfatase	Sulfatase	3e-231	781.6
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
707	Acyl_transf	Acyl transferase domain	1.1e-22	88.8
708	WD40	WD domain, G-beta repeat	4.8e-19	76.7
710	Ran_BP1	RanBP1 domain.	8.4e-06	-7.3
713	DEAD	DEAD/DRAH box helicase	9.9e-42	134.9
714	PH	PH domain	1.6e-09	39.0
715	DSPc	Dual specificity phosphatase, catalytic doma	1.5e-37	138.2
717	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
718	ig	Immunoglobulin domain	1e-29	100.8
719	integrin_B	Integrins, beta chain	0	1125.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	32.4
722	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
723	ig	Immunoglobulin domain	2.2e-05	22.4
724	P-box	F-box domain.	0.007	23.0
725	Nop	Putative snoRNA binding domain	8.1e-58	205.5
726	Nop	Putative snoRNA binding domain	8.1e-58	205.5
727	WD40	WD domain, G-beta repeat	7.5e-26	99.3
730	darm	Double-stranded RNA binding motif	0.027	12.1
731	dynamin	Dynamin family	4.2e-16	66.9
733	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.8e-10	41.7
735	CDP- OH_P_transf	CDP-alcohol phosphatidyltransferase	4.2e-26	100.1
738	DEAD	DRAD/DEAH box helicase	8.6e-57	182.5
739	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
742	ras	Ras family	2.2e-100	346.9
743	PMI_typeI	Phosphomannosc isomerase type I	1.2e-243	822.9
747	trypsin	Trypsin	6.4e-88	279.4
748	kazal	Kazal-type serine protease inhibitor domain	2.2e-52	187.4
749	efhand	EF hand	6.3e-06	33.1
751	PHD	PHD-finger	4.9e-16	66.7
752	zf-C2H2	Zinc finger, C2H2 type	3.2e-21	83.9
753	Hydrolase	haloacid dehalogenase-like hydrolase	6.le-11	49.8
754	Ribosomal_L3	Ribosomal L39 protein	0.00018	26.7
755	PH '	PH domain	3.6e-14	55.7
758	SCAN	SCAN domain	1.4e-53	191.5
759	PA	PA domain	0.0065	23.1
760	arf	ADP-ribosylation factor family	2.2e-19	77.8

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
762	histone	G 1572 / 100 / 100 / 100		SCORB
763	zf-MYND	Core histone H2A/H2B/H3/H4 MYND finger	9.9e-53	188.6
764	POU	Pou domain - N-terminal to	4.1e-14	60.3
		homeobox domain	1e-52	188.6
767	VWC	von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	BF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two · domains)	2.4e-53	181.6
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	le-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.le-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	G6PD ·	Glucose-6-phosphate dehydrogenase	1.5e-76	236.6
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito_carr	Mitochondrial carrier proteins	4.6e-57	198.5
782	SCAN	SCAN domain	1.3e-24	95.2
783	PDZ	PDZ domain (Also known as DHR or GLGF).	4.1e-07	37.1
785	DRAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase HII	Ribonuclease HII	2.5e-67	237.1
790	PI3_PI4_kina	Phosphatidylinositol 3- and 4-	5.4e-108	372.2
	se	kinases		1
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal-	Vertebrate galactoside-binding	4.1e-25	88.7
803	bind_lectin	lectin		
806	TBC	WD domain, G-beta repeat	0.00082	26.1
807	TBC	TBC domain	1.8e-26	101.4
808	CN hydrolase	Carbon-nitrogen hydrolase	1.8e-26	101.4
811	CBFD NFYB HM	Histone-like transcription	8.8e-80 6e-14	278.5 59.8
	F F	factor	96-14	59.8
812	adh short	short chain dehydrogenase	8.1e-20	79.3
614	IMP4	Domain of unknown function	3.3e-71	250.0
815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
816	Pept_tRNA_hy	Peptidyl-tRNA hydrolase	1.6e-37	138.0
817	ARID	ARID DNA binding domain	2.5e-18	74.3
826	IF5_eIF4_eIF	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
830	ArfGap	Putative GTP-ase activating protein for Arf	1.5e-53	191.3
831	LRR	Leucine Rich Repeat	2.1e-26	107 7
832	laminin_EGF	Laminin EGF-like (Domains III	2.1e-26 2e-57	204.2
839	rm	and V)	1. 25 55	L
840	Y_phosphatas	RNA recognition motif.	1.3e-22	88.5
	e	Protein-tyrosinc phosphatase	2.60-119	409:8
841	pkinase	Bukaryotic protein kinase domain	3.4e-100	346.3
844	Ribosomal_L2 2e	Ribosomal L22e protein family	1e-64	228.4
846	IBR	IBR domain	9e-15	62.5
849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.4e-07	26.5
850	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00016	18.9
				20.5
851	SET	SET domain	5e-30	113.2

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PPAM
110.	<del> </del>	rich domain	<del> </del>	SCORE
853	SRCR	Scavenger receptor cysteine- rich domain	0	1025.4
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit VIa	3.4e-58	206.7
B59	rrm	RNA recognition motif.	5.4e-45	162.9
861	PRK	Phosphoribulokinase	5.1e-62	219.4
863	mito_carr	Mitochondrial carrier proteins	2.9e-53	185.5
864	HSP90	Hsp90 protein	4.7e-158	538.5
866	ig	Immunoglobulin domain	4e-12	44.1
867	zf-C2H2	Zinc finger, C2H2 type	7e-135	461.5
872	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase_L_cha in	Carbamoyl-phosphate synthase (CPSase)	2.1e-218	739.0
879	Ribosomal_S1 2e	Ribosomal protein Sl2e	2.1e-98	340.3
882	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	1.2e-51	182.0
884	RA	Ras association (RalGDS/AF-6) domain	0.044	8.0
887	DUF92	Integral membrane protein DUF92	2.7e-12	54.3
889	sugar_tr	Sugar (and other) transporter	8.2e-63	222.1
893	DUF28	Domain of unknown function DUF28	1.3e-43	158.3
896	IP_trans	Phosphatidylinositol transfer protein	6.5e-98	338.7
898	DEAD	DEAD/DEAH box helicase	1.5e-48	156.5
899	KB2	KE2 family protein	7e-61	215.7
900	KB2	KB2 family protein	4.3e-51	183.2
901	zf-C2H2	Zinc finger, C2H2 type	2.7e-57	203.8
902 904	ras TPR	Ras family	2.3e-75	263.8
906	GBP	TPR Domain	3.2e-22	87.2
907	GBP	Guanylate-binding protein Guanylate-binding protein	8.9e-253	853.1
908	WD40	WD domain, G-beta repeat	1.1e-239	809.6
909	PH	PH domain	2.6e-26 1.3e-09	100.8
910	zf-C2H2	Zinc finger, C2H2 type	2.5c-39	39.4
913	Epimerase	NAD dependent	5e-07	-88.5
		epimerase/dehydratase family	J	
921 922	TBC WD40	TBC domain	1.5e-09	30.7
923	WD40	WD domain, G-beta repeat	1.6e-25	98.2
924	Hydrolase	WD domain, G-beta repeat haloacid dehalogenase-like	8.2e-07 2.9e-05	36.1 29.1
925	UQ con	hydrolase		I
926	CH CH	Ubiquitin-conjugating enzyme Calponin homology (CH) domain	0.00033 3.3e-53	-27.6
928	WD40	WD domain, G-beta repeat		190.2
929	zf-C3HC4	Zinc finger, C3HC4 type (RING	5.9e-48 3.1e-10	172.7 37.4
930	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase	7.2e-105	361.8
931	Ribul P 3 ep	Ribulose-phosphate 3 epimerase	1.2e-96	334.4
	im	family		L
936	C2			1 000
936 937	C2 NAP_family	C2 domain Nucleosome assembly protein	2.2e-62 1.1e-22	84.6
937	NAP_family	Nucleosome assembly protein (NAP)	1.1e-22	84.6
937 940	NAP_family abhydrolase	Nucleosome assembly protein (NAP) alpha/beta hydrolase fold	1.1e-22 0.011	3.1
937 940 944	NAP_family abhydrolase Tropomyosin	Nucleosome assembly protein (NAP) alpha/beta hydrolase fold Tropomyosins	0.011 3.2e-07	3.1 25.1
937 940 944 948	NAP_family abbydrolase Tropomyosin pkinase	Nucleosome assembly protein (NAP) alpha/beta hydrolase fold Tropomyosins Eukaryotic protein kinase domain	0.011 3.2e-07 3.4e-75	3.1 25.1 263.2
937 940 944	NAP_family abhydrolase Tropomyosin	Nucleosome assembly protein (NAP) alpha/beta hydrolase fold Tropomyosins Eukaryotic protein kinase	0.011 3.2e-07	3.1 25.1

SEQ ID NO:	PPAM NAME	DESCRIPTION	p-value	PFAM SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO IDH MOCA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-	CDP-alcohol	0.053	-22.2
	OH_P_transf	phosphatidyltransferase	Ì	)
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969	IF-2B	Initiation factor 2 subunit	8.4e-193	653.9
		family		,
970	RNase_PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L1 7	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestri	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase, 20 Kd sub	4.8e-63	222.9 ·
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA int end	tRNA intron endonuclease	0.0017	-34.2
	0			
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.012	11.6
1000	mito_carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6) domain	1.2e-15	65.4
1004	DUF81	Domain of unknown function DUF81	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family	3.7e-195	661.8
1008	TPR	TPR Domain	B.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	215.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.7e-15	53.1
1016	tRNA-synt 2c	tRNA synthetases class II (A)	2.3e-15	55.2
1018	RhoGAP	RhoGAP domain	1.6e-78	274.3
1022	PGAM	Phosphoglycerate mutase family	3.8e-18	69.7
1026	HMG box	HMG (high mobility group) box	8.4e-20	79.2
1027	TBC	TBC domain	7.3e-45	162.5
1028	UQ con	Ubiquitin-conjugating enzyme	1.4e-49	178.1
1032	PDZ	PDZ domain (Also known as DHR or GLGF).	0.028	16.3
1034	Hydrolase	haloacid dehalogenasc-like	2e-21	84.6
1037	KRAB	KRAB box	4.8e-06	32.4
1038	Cation_efflu	Cation efflux family	7.1e-42	152.5
1040	ART	NAD:arginine ADP- ribosyltransferase	4.7e-47	169.1
1042	WD40 -	WD domain, G-beta repeat	1.9e-18	74.7
	zf-C2H2		3.7e-24	93.7
1043	lectin c	Zinc finger, C2H2 type	1.9e-28	108.0
	_	Lectin C-type domain	0.00013	-25.1
1046	Glucosamine_ iso	Glucosamine-6-phosphate isomerase	0.00013	723.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	ig	Immunoqlobulin domain	1.7e-09	35.6
1050	Ribosomal L2	Ribosomal protein L24e	2e-33	124.5
1020	4e	RIOSOMAI PIOCEIN METE	20-33	124.5
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-44	159.2
1059	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1060	n homeobox	Homeobox domain	3,2e-31	117.2
1062	Acyltransfer	Acyltransferase	0.00065	10.5
1002	ase	Acyteransterase	20000,0	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1 OBG	GTP1/OBG family	4.8e-41	141.8
1071	ig	Immunoglobulin domain	8.4e-48	159.1
1072	PHD	PHD-finger	6.Be-07	36.3
1074	DENN	DENN (AEX-3) domain	8,3e-33	121.5
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1077	OLF	Olfactomedin-like domain	2,2e-66	234.0
1078	mito carr	Mitochondrial carrier proteins	1e-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
	DSPC	Dual specificity phosphatase,	3.3e-63	223.4
1093	DSPC	catalytic doma		223.4
1094	GSHPx	Glutathione peroxidases	9.6e-41	148.8
1095	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	.DUF25	Domain of unknown function	6e-75	262.4
		DUF25		<u> </u>
1105	Nitroreducta se	Nitroreductase family	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1.3e-179	610.1
1107	DAGKC	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating	9.7e-47	168.7
		protein for Arf	·	<u> </u>
1116	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14_17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolas	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase	1.4e-94	327.6
		domain		<del> </del>
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
1129	pro_isomeras e	Cyclophilin type peptidyl- prolyl cis-tr	2,2e-56	197.1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
1136	Adap_comp_su	Adaptor complexes medium	1.2e-256	866.0
1120	b	subunit family	2 5 250	709 9
1137	Adap_comp_su b	Adaptor complexes medium subunit family	2.5e-209	708.8
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase	9.4e-74	258.4
1152	Acyltransfer	domain Acyltransferase	1.2e-05	29.9
	ase			1
1153	IRS	PTB domain (IRS-1.type)	5.4e-55	196.1
1155	ig	Immunoglobulin domain	1.3e-31	106.9
1157	Asparaginase 2	Asparaginase	6.4e-72	252.3
1159	GMC_oxred	GMC oxidoreductases	4.7e-142	485.3
1160	zf-AN1	ANI-like Zinc finger	0.00021	27.9

OTTO YES	I Donald States	DESCRIPTION	p-value	PPAM
SEQ ID	PFAM NAME		b-Agrae	SCORE
1163	linker_histo	linker histone H1 and H5 family	3.8e-14	60.4
1164	DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	SAM domain (Sterile alpha motif)	0.04	10.5
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	ND domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1 MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGRF domain	1.7e-88	307.4
1185	mito carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn_DAP_Arg_ deC	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Secl	Secl family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation	0.022	-16.8
1203	adh short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie methylt	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm 3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP- synt AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	BF hand	3.2e-07	37.4
1219	rrm	RNA recognition motif.	2.1e-40	147.7
1220	DUF6	Integral membrane protein DUF6	0.015	21.5
1222	SCAN ·	SCAN domain	1.5e-71	251.1
1223	G-gamma	GCL domain	3.6e-36	129.5
1227	catalase	Catalase	0	1158.9
1232	PX	PX domain	2.2e-15	64.5
1233	PX	PX domain	2.2e-15	64.5
1236	FCH	Fes/CIP4 homology domain	3.3e-09	44.0
1241	Peptidase_M2 0	Peptidase family M20/M25/M40	2e-63	224.1
1243	WW	WW domain	0.044	17.9
1247	UPF0006	Metalloenzyme of unknown	6.3e-61	215.8
		function UPF0006		ſ
1248	Glycos_trans f_2	Glycosyl transferases	4.5e-10	46.9
1248			4.5e-10	46.9
	f_2	Glycosyl transferases		
1249	f_2 efhand	Glycosyl transferases  EF hand	4e-11	50.4
1249 1254	f_2 efhand UQ_con	Glycosyl transferases  BF hand Ubiquitin-conjugating enzyme	4e-11 2.1e-73	50.4 257.3
1249 1254 1255	f_2 efhand UQ_con ras formyl_trans	Glycosyl transferases  BF hand Ubiquitin-conjugating enzyme Ras family	4e-11 2.1e-73 2.2e-62	50.4 257.3 220.7
1249 1254 1255 1256	f_2 efhand UQ_con ras formyl_trans f	Glycosyl transferases  BF hand  Ubiquitin-conjugating enzyme Ras family  Formyl transferase  Zinc finger, C3HC4 type (RING	4e-11 2.1e-73 2.2e-62 4.9e-30	50.4 257.3 220.7 108.3
1249 1254 1255 1256	f_2 efhand UQ_con ras formyl_trans f Zf-C3HC4 DiHfolate_re	Glycosyl transferases  BF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase  Zinc finger, C3HC4 type (RING finger)	4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13	50,4 257,3 220,7 108.3
1249 1254 1255 1256 1259	f_2 efhand UQ_con ras formyl_trans f zf-C3HC4 DiHfolate_re d G_glu_transp	Glycosyl transferases  EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase  Zinc finger, C3HC4 type (RING finger) Dihydrofolate reductase	4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13	50.4 257.3 220.7 108.3 46.4

SEQ ID	PPAM NAME	DESCRIPTION	p-value	I PFAM
NO:			parae	SCORE
1266	SCP	SCP-like extracellular protein	6e-29	108.0
1267	K_tetra	K+ channel tetramerisation domain	2.8e-27	104.0
1269	ras	Ras family	1.3e-85	297.9
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine- binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1298	PIW	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1307	mito_carr	Mitochondrial carrier proteins	2.1e-53	186.0
1308	WD40	WD domain, G-beta repeat	1.6e-17	71.6
1310	UPAR_LY6	u-PAR/Ly-6 domain	7.le-20	75.5
1313	thiored	Thioredoxin	3.6e-05	21.6
1314	Aa_trans	Transmembrane amino acid transporter protein	1.5e-67	237.9
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L1 3	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_se	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_syntheta se	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
1335	UPP_syntheta 'se	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPC	Dual specificity phosphatase, catalytic doma	1,2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band 41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1347	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomera	0.086	-177.2
1348	BTB	BTB/POZ domain	5.3e-28	106.5
1349	DUF6	Integral membrane protein DUF6	0.033	15.8
1350	myosin_head	Myosin head (motor domain)	0	1088.7
1352	Nramp	Natural resistance-associated macrophage pro	1.2e-202	686.6
1353	S_100	S-100/ICaBP type calcium binding domain	5.3e-23	89.9
1355	DEAD	DEAD/DEAH box helicase	3.6e-65	209.0
1356	C2	C2 domain	2.4e-15	64.4
1357	RBD	Raf-like Ras-binding domain	4.2e-57	203.1
1360	zf-C2H2	Zinc finger, C2H2 type	7.4e-141	481.4
1361	HMG14 17	HMG14 and HMG17	7.9e-40	145.7

SEQ ID	PFAM NAME			
	}	DESCRIPTION	p-value	PFAM
1362	SIS	SIS domain		SCORE
1363	SIS		3.8e-30	113.6
1364		SIS domain	1.3e-28	108.5
1368	ig	Immunoglobulin domain	0.00026	19.0
1300	K_tetra	K+ channel tetramerisation domain	1.1e-16	68.9
1371	Collagen	Collagen triple helix repeat (20 copies)	2.2e-113	390.1
1372	DnaJ	DnaJ domain	<del> </del>	
1376	KRAB	KRAB box	6.6e-36	132.7
1378	ELM2	RIM2 domain	2.1e-38	141.0
1380	thiored		2e-23	91.3
1381	ank	Thioredoxin	1.2e-23	82.8
	1	Ank repeat	2.3e-83	290.4
1382	ВТВ	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.le-09	35.6
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	kinesin	Kinesin motor domain	7.8e-188	637.4
1394	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1398	KRAB	KRAB box	1.2e-49 5.1e-22	86.6
1402	bZIP	bZIP transcription factor		
1405	sugar tr	DELP CRAISCRIPTION FACTOR	0.035	13.1
1406	RhoGAP	Sugar (and other) transporter	0.003	-101.5
1407	rrm	RhoGAP domain	8.9e-47	168.8
1407	1	RNA recognition motif.	1e-35	132.1
	LRR	Leucine Rich Repeat	2.le-13	58.0
1409	Nebulin_repe at	Nebulin repeat	6e-54	192.6
1410	ank	Ank repeat	1.6e-17	71.6
1412	Ribosomal_L5	ribosomal L5P family C-terminus	8.2e-58	205.5
1415	1	Trimgin	A 70 0F	1270 4
1415	trypsin	Trypsin	4.7e-85	.270.4
1416	trypsin aminotran_1	Aminotransferases class-I	4.4e-05	-91.2
1416 1417	trypsin aminotran 1 S1	Aminotransferases class-I S1 RNA binding domain	4.4e-05 1.6e-07	-91.2 33.1
1416 1417 1419	trypsin aminotran 1 S1 WD40	Aminotransferases class-I Sl RNA binding domain WD domain, G-beta repeat	4.4e-05 1.6e-07 2.2e-09	7-91.2 33.1 44.6
1416 1417 1419 1422	trypsin aminotran_1 S1 WD40 cadherin	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain	4.4e-05 1.6e-07 2.2e-09 8.3e-42	7-91.2 33.1 44.6 152.3
1416 1417 1419 1422 1424	trypsin aminotran 1 S1 WD40 cadherin SH3	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80	-91.2 33.1 44.6 152.3 280.3
1416 1417 1419 1422 1424 1425	trypsin aminotran 1 S1 WD40 cadherin SH3	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17	-91.2 33.1 44.6 152.3 280.3
1416 1417 1419 1422 1424 1425 1426	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17	-91.2 33.1 44.6 152.3 280.3 70.6
1416 1417 1419 1422 1424 1425 1426	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17	-91.2 33.1 44.6 152.3 280.3
1416 1417 1419 1422 1424 1425 1426	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17	-91.2 33.1 44.6 152.3 280.3 70.6
1416 1417 1419 1422 1424 1425 1426	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8
1416 1417 1419 1422 1424 1425 1426 1427	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 le-26 3.9e-07	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8
1416 1417 1419 1422 1424 1425 1426 1427 1428	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase_C	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P	Aminotransferases class-I Sl RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol_P mito_carr C1q WD40	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins C1q domain WD domain, G-beta repeat	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol P mito carr C1q WD40 Inos-1- P_synth	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins C1q domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol P mito carr C1q WD40 Inos-1- P_synth rrm	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins C1q domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif.	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 inos-1- P_synth rrm ig G_Adapt_CT	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins C1q domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif.	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1436 1438 1440 1441	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 297.7 66.2 58.3 770.4 128.3 45.6
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1436 1440 1441 1443	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol_P mito_carr C1q WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1436 1438 1440 1441 1443 1446	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 3.4e-67	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1436 1440 1441 1443	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol_P mito_carr C1q WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-57 3.4e-67 0.00013	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1436 1438 1440 1441 1443 1446	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol P mito carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat. Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, C2H2 type	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1436 1438 1440 1443 1443	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol_P mito_carr C1q WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat. Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 297.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448	trypsin aminotran 1 s1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif.	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol P mito carr Clq WD40 inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 28.7 84.7 105.6 -145.1 82.9 146.7
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1446 1441 1443 1446 1447 1448 1455	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1440 1441 1443 1446 1447 1448 1455 1460	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1443 1446 1447 1448 1451 1455 1460 1461	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase C WD40 inositol P mito carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim C2	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat. Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase C2 domain	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-57 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35 4e-18	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2 131.2 73.6
1416 1417 1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1440 1441 1443 1446 1447 1448 1455 1460	trypsin aminotran 1 S1 WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim	Aminotransferases class-I S1 RNA binding domain WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase	4.4e-05 1.6e-07 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35	7-91.2 33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2

1474 D 1475 C x 1477 T 1478 T 1478 T 1480 T 1480 T 1485 Z 1486 P 1485 Z 1486 P 1489 D 1490 E 1491 S 1492 I 1495 Z 1497 P 1500 S 1502 h 1503 h 1505 E 1506 U 1511 P 1516 S 1518 a 1520 L 1521 R 1523 R 1523 R	BC rm g relo bind al ha if-C2H2 okinase melicase_C ours9	DENN (AEX-3) domain Cation efflux family  TBC domain RNA recognition motif. Immunoglobulin domain Telomere-binding protein alpha subuni Zinc finger, C2H2 type Eukaryotic protein kinase domain Helicases conserved C-terminal domain Protein of unknown function DUF89 Encyl-CoA hydratase/isomerase family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Bukaryotic protein kinase domain SH3 domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	1.3e-44 4.6e-49  Be-47 2e-21 5.5e-06 0.028 1.8e-68 9.5e-13 1.4e-15 0.079 5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28 1.9e-11	SCORE  161.6 176.4  169.0 84.6 24.3 -225.9  240.9 49.9  65.2 -132.4  149.7  166.1  77.2 36.3  85.8  27.2 13.8 13.8 90.8 84.2 101.8
1474 Di 1475 Ci x 1477 Ti 1478 Ti 1478 Ti 1480 Ti 1480 Ti 1481 Ti 1485 Zi 1486 Pi 1489 Di 1490 Ei 1491 Sp 1492 Li 1495 Zi 1497 Pi 1500 Si 1502 Li 1503 Li 1505 Ei 1506 Ui 1508 Pi 1511 Pi 1512 Si 1516 Si 1518 ai 1520 Li 1521 Ri 1523 Ri 1523 Ri 1528 Wi	ENN Cation_efflu C	Cation efflux family  TBC domain  RNA recognition motif.  Immunoglobulin domain  Telomere-binding protein alpha subuni  Zinc finger, C2H2 type  Eukaryotic protein kinase domain  Helicases conserved C-terminal domain  Protein of unknown function  DUF89  Enoyl-CoA hydratase/isomerase family  Adenylate and Guanylate cyclase catalyt  Leucine Rich Repeat  Zinc finger, C3HC4 type (RING finger)  Bukaryotic protein kinase domain  Homeobox domain  Homeobox domain  EGF-like domain  Ubiquitin carboxyl-terminal hydrolase family  Peptidase family M20/M25/M40  PX domain	4.6e-49  Be-47 2e-21 5.5e-06 0.028  1.8e-68 9.5e-13  1.4e-15 0.079  5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	176.4 169.0 84.6 24.3 -225.9 240.9 49.9 65.2 -132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
1475 C: x 1477 T: 1478 T: 1480 1: 480 1: 480 1: 485 2: 1486 P: 1485 2: 1486 P: 1489 D: 1490 E: 1491 P: 1495 2: 1497 P: 1500 S: 1502 h: 1503 h: 1505 E: 1506 U: 1508 P: 1512 S: 1516 S: 1518 a: 1520 1: 1521 R: 1522 R: 1523 R: 1528 W	ation_efflu  BC  Im  Gelo_bind_al  sha  if-C2H2  okinase  selicase_C  ours9  ccH  quanylate_cy  iRR  if-C3HC4  okinase	Cation efflux family  TBC domain  RNA recognition motif.  Immunoglobulin domain  Telomere-binding protein alpha subuni  Zinc finger, C2H2 type  Eukaryotic protein kinase domain  Helicases conserved C-terminal domain  Protein of unknown function  DUF89  Enoyl-CoA hydratase/isomerase family  Adenylate and Guanylate cyclase catalyt  Leucine Rich Repeat  Zinc finger, C3HC4 type (RING finger)  Bukaryotic protein kinase domain  Homeobox domain  Homeobox domain  EGF-like domain  Ubiquitin carboxyl-terminal hydrolase family  Peptidase family M20/M25/M40  PX domain	4.6e-49  Be-47 2e-21 5.5e-06 0.028  1.8e-68 9.5e-13  1.4e-15 0.079  5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	176.4 169.0 84.6 24.3 -225.9 240.9 49.9 65.2 -132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
X   1477   Ti   1478   Ti   1480   1484   Ti   1485   Zi   1486   Pi   1489   Di   1490   Ei   1491   Ei   1495   Zi   1497   Pi   1500   Si   1502   hi   1505   Ei   1506   Di   1508   Pi   1512   Si   1518   Ei   1518   Ei   1518   Ei   1521   Ri   1523   Ri   1528   W	GEC  TM  Gelo_bind_al  sha  If-C2H2  skinase  selicase_C  SUF89  SCH  suanylate_cy  screen  RR  If-C3HC4  skinase  SKINASE  SCH  SCH  SCH  SCH  SCH  SCH  SCH  S	TBC domain RNA recognition motif. Immunoglobulin domain Telomere-binding protein alpha subuni Zinc finger, C2H2 type Eukaryotic protein kinase domain Helicases conserved C-terminal domain Protein of unknown function DUF89 Enoyl-CoA hydratase/isomerase family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Bukaryotic protein kinase domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	8e-47 2e-21 5.5e-06 0.028 1.8e-68 9.5e-13 1.4e-15 0.079 5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	169.0 84.6 24.3 -225.9 240.9 49.9 65.2 -132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
1478 T. 1480 19 1480 19 1484 T. 1485 2. 1486 P. 1488 h. 1489 D. 1490 E. 1491 G. 1492 F. 1497 P. 1500 S. 1502 h. 1503 h. 1505 E. 1506 U. 1508 P. 1511 P. 1512 S. 1516 S. 1518 a. 1520 f. 1521 R. 1523 R. 1523 R.	rm  g elo_bind_al ha if-C2H2 bkinase  celicase_C  fUF89  cH ruanylate_cy kinase  skinase  skinase  chicase_C  furanylate_cy kinase  skinase	RNA recognition motif.  Immunoglobulin domain  Telomere-binding protein alpha subuni  Zinc finger, C2H2 type  Eukaryotic protein kinase domain  Helicases conserved C-terminal domain  Protein of unknown function DUF89  Encyl-CoA hydratase/isomerase family  Adenylate and Guanylate cyclase catalyt  Leucine Rich Repeat  Zinc finger, C3HC4 type (RING finger)  Eukaryotic protein kinase domain  SH3 domain  Homeobox domain  EGF-like domain  Ubiquitin carboxyl-terminal hydrolase family  Peptidase family M20/M25/M40  PX domain	2e-21 5.5e-06 0.028 1.8e-68 9.5e-13 1.4e-15 0.079 5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	84.6 24.3 -225.9 240.9 49.9 65.2 -132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2 101.8
1480 19 1484 70 1485 2: 1486 Pi 1488 h 1489 Di 1490 E 1491 G 1492 II 1495 Z 1497 Pi 1500 Si 1502 h 1503 h 1505 E 1506 U 1508 Pi 1512 S 1516 S 1518 ai 1520 f 1521 R 1523 R 1523 R 1528 W	g Telo_bind_al tha if-C2H2 okinase telicase_C TUF89 TCH TUANYlate_cy TRR OKINASE TOTAL TOT	Immunoglobulin domain Telomere-binding protein alpha subuni Zinc finger, C2H2 type Eukaryotic protein kinase domain Helicases conserved C-terminal domain Protein of unknown function DUF89 Encyl-CoA hydratase/isomerase family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Eukaryotic protein kinase domain SH3 domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	5.5e-06 0.028 1.8e-68 9.5e-13 1.4e-15 0.079 5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	24.3 -225.9 240.9 49.9 65.2 -132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2 101.8
1484 T. P. P. P. P. P. P. P. P. P. P. P. P. P.	elo_bind_al bha if-C2H2 ckinase delicase_C delicase_C delicase_C delicase_C delicase_C delicase_C delicase_C delicase_C delicase_C delicase_C delicase_C delicase_C delicase_C delicase_C delicase_d d	Telomere-binding protein alpha subuni Zinc finger, C2H2 type Eukaryotic protein kinase domain Helicases conserved C-terminal domain Protein of unknown function DUF89 Encyl-CoA hydratase/isomerase family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Bukaryotic protein kinase domain SH3 domain Homeobox domain Homeobox domain EGF-like domain Diquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	0.028  1.8e-68 9.5e-13  1.4e-15  0.079  5.2e-41  5.9e-46  3.4e-19 7.1e-10  1e-22  9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	-225.9 240.9 49.9 65.2 -132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
Pi   1485   2.   1486   Pi   1488   Pi   1488   Pi   1489   Pi   1490   Pi   1491   Pi   1495   Pi   1495   Pi   1500   Pi   1503   Pi   1505   Pi   1506   Pi   1508   Pi   1512   Pi   1512   Pi   1516   Pi   1518   Pi   1520   Pi   1521   Pi   1521   Pi   1521   Pi   1522   Pi   1523   Pi   1523   Pi   1523   Pi   1523   Pi   1523   Pi   1528   Pi   1528   Pi   1528   Pi   1523   Pi	hha if-C2H2 okinase  melicase_C ourse  ccH quanylate_cy ikr if-C3HC4 okinase  sH3 comeobox comeobox core core core core core core core core	subuni Zinc finger, C2H2 type Eukaryotic protein kinase domain Helicases conserved C-terminal domain Protein of unknown function DUF89 Encyl-CoA hydratase/isomerase family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Bukaryotic protein kinase domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	1.8e-68 9.5e-13 1.4e-15 0.079 5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	240.9 49.9 65.2 -132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
1486 P.  1488 h  1489 Di  1490 E  1491 G  1492 h  1495 Z  1497 Di  1500 Si  1502 h  1503 h  1505 E  1506 U  1511 P  1512 S  1516 S  1518 ai  1520 i  1521 R  1523 R  1528 W	celicase C  DUF89  CCH  FURANYLATE_CY  RR  FI-C3HC4  Okinase  GH3  COMMONDOWN	Eukaryotic protein kinase domain Helicases conserved C-terminal domain Protein of unknown function DUF89 Encyl-CoA hydratase/isomerase family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Bukaryotic protein kinase domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	9.5e-13 1.4e-15 0.079 5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	49.9 65.2 -132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
1488 ho 1489 Di 1490 E 1491 gr 1492 hr 1495 zr 1497 pr 1500 Si 1502 hr 1503 hr 1506 Dr 1508 pr 0 1511 pr 1512 Sr 1516 Sr 1518 ar 1520 ir 1521 R	celicase_C  DUF89  CH  ruanylate_cy  RR  rf-C3HC4  okinase  SH3  comeobox  c	domain Helicases conserved C-terminal domain Protein of unknown function DUF89 Encyl-CoA hydratase/isomerase family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Eukaryotic protein kinase domain SH3 domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	1.4e-15 0.079 5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	65.2 -132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
1489 Di 1490 E 1491 G 1491 G 1492 II 1495 Z 1497 P 1500 Si 1502 h 1503 h 1505 E 1506 U 1508 P 0 1511 P 1512 S 1516 S 1518 a 1520 i 1521 R 1523 R 1523 R	CCH  TUANYLATE_CY  RR  OF C3HC4  Okinase  SH3  LOMEODOX	domain Protein of unknown function DURB9 Encyl-CoA hydratase/isomerase family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Bukaryotic protein kinase domain SH3 domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	0.079 5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	-132.4 149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
1490 Ed 1491 G C C C C C C C C C C C C C C C C C C	CCH  Tuanylate_cy  IRR  If-C3HC4  Skinase  SH3  LOMEODOX	Encyl-CoA hydratase/isomerase family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Bukaryotic protein kinase domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	5.2e-41 5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	149.7 166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
1491 gr c 1492 h 1495 z: 1497 p 1500 Si 1502 h 1503 h 1506 U 1508 p 0 1511 p 1512 Si 1516 Si 1518 ai 1520 i 1521 R	ruanylate_cy  RR  RF-C3HC4  okinase  SH3  comeobox  comeobox  comeobox  CF  CH-2  Peptidase_M2  ox  Sulfatase	family Adenylate and Guanylate cyclase catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Eukaryotic protein kinase domain SH3 domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	5.9e-46 3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	166.1 77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
C   C   C   C   C   C   C   C   C   C	RR  if-C3HC4  okinase  sH3  comeobox	catalyt Leucine Rich Repeat Zinc finger, C3HC4 type (RING finger) Bukaryotic protein kinase domain SH3 domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	3.4e-19 7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	77.2 36.3 85.8 27.2 13.8 13.8 90.8 84.2
1495 z.  1497 p.  1500 Si 1500 h.  1503 h.  1505 E.  1506 U.  1508 p.  1511 p.  1512 S.  1516 S.  1518 a.  1520 i.  1521 R.  1523 R.  1528 W.	okinase SH3 LOMEODOX LOMEODOX LOMEODOX LOF LOF-2 Peptidase_M2 DX Sulfatase	Zinc finger, C3HC4 type (RING finger) Bukaryotic protein kinase domain SH3 domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	7.1e-10 1e-22 9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	36.3 85.8 27.2 13.8 13.8 90.8 84.2
1497 P1 1500 Si 1502 h 1503 h 1505 E 1506 U 1508 P 1511 P 1512 S 1516 S 1518 at 1520 i 1521 R 1523 R 1528 W	okinase  GH3  Anomeobox  Anomeobox  GF  JCH-2  Peptidase_M2  ON  GUIFATARE	finger) Rukaryotic protein kinase domain SH3 domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	85.8 27.2 13.8 13.8 90.8 84.2
1500 Si 1502 h 1503 h 1505 E 1506 U 1508 P 0 1511 P 1512 S 1516 S 1518 at 1520 i 1521 R 1523 R 1523 R	SH3 LOMEODOX LOMEODOX LUSF LUST LUST LUST LUST LUST LUST LUST LUST	domain SH3 domain Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	9.3e-05 0.084 0.084 2.7e-23 2.7e-21 2.8e-28	27.2 13.8 13.8 90.8 84.2
1502 h 1503 h 1505 E 1506 U 1508 P 0 1511 P 1512 S 1516 S 1518 a 1520 i 1521 R 1523 R 1528 W	nomeobox nomeobox SGF JCH-2 Peptidase_M2 DCH-SULfatase	Homeobox domain Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	0.084 0.084 2.7e-23 2.7e-21	13.8 13.8 90.8 84.2
1503 h 1505 E 1506 U 1508 P 0 1511 P 1512 S 1516 S 1518 ai 1520 i 1521 R 1523 R 1528 W	omeobox CGF JCH-2 Peptidase_M2 O	Homeobox domain EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	0.084 2.7e-23 2.7e-21 2.8e-28	13.8 90.8 84.2
1505 E 1506 U 1508 P 0 1511 P 1512 S 1516 S 1518 at 1520 i 1521 R 1523 R 1528 W	OGF OCH-2 Peptidase_M2 O OCK Sulfatase	EGF-like domain Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	2.7e-23 2.7e-21 2.8e-28	90.8
1506 U 1508 P 0 1511 P 1512 S 1516 S 1518 at 1520 i 1521 R 1523 R 1528 W	OCH-2 Peptidase_M2 OCH-2 Sulfatase	Ubiquitin carboxyl-terminal hydrolase family Peptidase family M20/M25/M40 PX domain	2.7e-21 2.8e-28	101.8
1508 P. 0 1511 P. 1512 S. 1516 S. 1518 at 1520 i. 1521 R. 1523 R. 1528 W.	Peptidase M2 ) PX Sulfatase	hydrolase family Peptidase family M20/M25/M40 PX domain	2,8e-28	101.8
0 1511 P. 1512 S 1516 S 1518 au 1520 i. 1521 R 1523 R 1528 W	o Sulfatase	PX domain	l	L
1512 S 1516 S 1518 at 1520 i. 1521 R 1523 R 1528 W	Gulfatase		1.9e-11	
1516 S 1518 at 1520 i. 1521 R 1523 R 1528 W			~	51.5
1518 au 1520 i 1521 R 1523 R 1528 W	Syntaxin	Sulfatase	2.8e-35	130.7
1520 i. 1521 R 1523 R 1528 W		Syntaxin	0.011	-62.3
1521 R 1523 R 1528 W	minotran_3	Aminotransferases class-III pyridoxal-pho	9.7e-106	305.6
1523 R 1528 W	g	Immunoglobulin domain	0.075	11.0
1528 W	l'A	Ras association (RalGDS/AF-6) domain	0.013	13.3
	hoGAP	RhoGAP domain	2.5e-05	18.7
1535 I	7D40	WD domain, G-beta repeat	5.4e-24	93.1
	MS	impB/mucB/samB family	7.8e-95	328.5
1538 F	YYVE	PYVE zinc finger	3.2e-27	101.5
1539 D	DAGKC	Diacylglycerol kinase catalytic domain	6e-07	36.5
1540 O	Cular_alb	Ocular albinism type 1 protein	0	1184.7
1653 S	SAP	SAP domain	6e-06	33.2
1654 A	mino_oxidas	Flavin containing amine oxidase	3.2e-43	157.0
1655 A	mino_oxidas	Plavin containing amine oxidase	3.2e-43	157.0
1656 R	Rhoger	RhoGEF domain	1.4e-24	95.1
1657 M	MR HSRI	GTPase of unknown function	0.0011	-45.5
	ICH-2	Ubiquitin carboxyl-terminal hydrolase family	2.5e-11	51.1
1660 a	ctin	Actin	6.6e-21	69.9
	BAH	BAH domain	1.7e-82	287.5
	rwa	von Willebrand factor type A	0	1909.4
1663 W		WD domain, G-beta repeat	1.4e-67	237.9
	VD4 0		1,3e-93	324.4
	VD40 xf-C2H2			344-4
1671 S	rf-C2H2 Vol1_Nop2_Su	Zinc finger, C2H2 type NOL1/NOP2/sun family	1.3e-93 1.3e-23	84.3

SRQ ID	PFAM NAME	DESCRIPTION	p-value	PPAM
NO:		252 date: 1201	P vazac	SCORE
1672	chromo	'chromo' (CHRromatin	2.1e-18	67.7
	1	Organization MOdifier)	)	
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	0.0025	17.6
		type	1	1
1676	Glyco_hydro_ 47	Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1681	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1683	MMR HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduc	Ferric reductase like	8.4e-82	285.2
1698	Perric reduc	Ferric reductase like	3.5e-53	190.1
_0,0	t t	transmembrane com	3.se-53	130.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP EFTU	Elongation factor Tu family	0.014	11.4
1703	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	derm	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine	0.045	9.2
		dimethylases	0.043	]
1725	CIDE-N	CIDE-N domain	5.9e-40	145.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EP hand	5.1e-20	79.9
1733	Hist_deacety	Histone deacetylase family	1.7e-104	360.6
1735	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.0023	16.1
1743	ras	Ras family	3.7e-10	-21.3
1744	ras	Ras family	3.7e-10	-21.3
1745	Rascep	RasGEF domain	3.2e-49	176.9
1746	adh_short	short chain dehydrogenase	7.1e-08	34.6
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	142.2
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758		RNA recognition motif.	0.017	21.2
1760	rm			
	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1761	Nop Nop	Putative snoRNA binding domain Putative snoRNA binding domain	6.1e-95 6.1e-95	328.8 328.8
1761 1765	Nop Nop MMR_HSR1	Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function		328.8 149.4
1761 1765 1769	Nop Nop MMR_HSR1 CN_hydrolase	Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase	6.1e-95 6.4e-41 3e-06	328.8 149.4 -43.9
1761 1765 1769 1775	Nop Nop MMR HSR1 CN hydrolase ank	Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase Ank repeat	6.1e-95 6.4e-41 3e-06 4.1e-07	328.8 149.4 -43.9 37.1
1761 1765 1769 1775 1779	Nop Nop MMR_HSR1 CN_hydrolase ank Oxysterol_BP	Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase Ank repeat Oxysterol-binding protein	6.1e-95 6.4e-41 3e-06 4.1e-07 4.7e-56	328.8 149.4 -43.9 37.1 199.6
1761 1765 1769 1775	Nop Nop MMR HSR1 CN hydrolase ank	Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase Ank repeat	6.1e-95 6.4e-41 3e-06 4.1e-07	328.8 149.4 -43.9 37.1

SEQ ID	PFAM NAME	DESCRIPTION .	p-value	PFAM
NO:				SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN01!.DOC)

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1	1-21	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.982	0.901
10	1-21	0.991	0.955
11	1-23	0.989	
12	1-25		0.899
13		0.955	0.803
	1-18	0.932	0.625
14	1-18	0.938	0.876
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.953	0.840
20	1-20	0.935	0.701
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	0.976
32	1-22	0.998	0.909
35	1-33	0.949	0.736
36	1-33	0.949	0.736
46	1-19	0.970	0.951
67	1-25	0.968	0.848
71	1-18	0.949	0.845
72	1-30	0.991	0.919
75	1-29	0.958	0.854
88	1-20	0.986	0.834
94	1-33	0.994	0.943
97	1-46	0.964	
103	1-49		0.595
108		0.983	0.570
	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
162	1-25	0.937	0.729
168	1-16	0.939	0.826
171	1-27	0.964	0.777
178	1-21	0.945	0.825
180	1-27	0.981	0.941
187	1-28	0.982	
190	1-19		0.936
196	1-22	0.953	0.840
		0.975	0.916
197	1-22	0.963	0.936

SEQ ID NO:	POSITION OF SIGNAL IN AMINO	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
	ACID SEQUENCE	SCORE)	SCOKE)
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211 216	1-29	0.971	0.849
218	1-33	0.961	0.956
219	1-19	0.970	0.871
221 (	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.955
248	1-30	0.970	0.722
249	1-23	0.976 ~	0.935
252	1-18	0.971	0.940
261	1-24	0.883	0.587
265	1-18	0.939	0.868
272	1-24	0.953	0.739
283	1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302 304	1-28	0.980	0.893
312	1-16	0.907	0.635
313	1-17	0.993	0.976
323	1-22	0.998	0.753
324	1-17	0.982	0.954
328	1-19	0.971	0.865
329	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.920	0.712
332	1-24	0.975	0.881
333 334	1-19	0.984	0.941
335	1-20	0.899	0.567
336	1-20	0.942	0.813
337	1-38	0.942	0.653
338	1-27	0.973	0.772
339	1-36	0.979	0.804
340	1-27	0.888	0.597
343	1-19	0.971	0.865
344	1-22	0.994	0.928
345	1-17	0.966	0.687
346	1-19	0.936	0.822
349	1-22	0.963	0.924
351	1-24	0.982	0.966
352	1-31	0.918	0.815
354	1-31	0.974	0.839
355	1-29	0.932	0.632
356	1-15	0.994	0.969
357	1-33	0.935	0.726
360	1-27	0.938	0.827
361	1-25	0.954	0.674
362	1-22	0.929	0.788
363	1-21	0.881	0.715
364	1-33	0.978	0.841
365	1-33	0.978	0.841

SEQ ID NO:	POSITION OF	Maxs (MAXIMUM	MeanS (MEAN
	SIGNAL IN AMINO ACID SEQUENCE	SCORE)	SCORE)
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370	1-24	0.920	0.712
371	1-24	0.961	0.773
372	1-27	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388 389	1-30	0.989	0.868
390	1-19	0.984	0.782
392	1-20	0.981	0.782
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408 409	1-39	0.976	0.551
410	1-33	0.897	0.570
411	1-38	0.990	0.962
412	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	0.940
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-22	0.889	0.785
422	1-48	0.982	0.862
424	1-19	0.979	0.933
428 430	1-38	0.942	0.653
430	1-18	0.947	0.595
433	1-33	0.957	0.789
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
443	1-15	0.966	0.940
448	1-36	0.979	0.804
453	1-41	0.958	0.609
455	1-33	0.943	0.606
457	1-27	0.888	0.597
462	1-16	0.925	0.681
486	1-27	0.972	0.845
495	1-24	0.917	0.636
498 .	1-26	0.993	0.890
505	1-20	0.976	0.926
507	1-17	0.966	0.687
510	1-23	0.930	0.593

SEQ ID NO:	POSITION OF	Maxs (MAXIMUM	Monne /METAN
DEG ID NO:	SIGNAL IN AMINO	SCORE)	Means (MEAN
1	ACID SEQUENCE	SCORD/	SCORE)
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	0.966
550	1-30	0.933	0.713
552	1-21	0.973	0.912
554	1-23	0.969	0.784
571	1-21	0.918	0.815
574	1-31	0.988	0.912
580	1-39	0.925	0,556
594	1-31	0.974	0.839
608	1-29	0.932	0.632
609	1-29	0.532	0.632
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.935	0.726
653	1-27	0.938	0.827
668	1-22	0.929	0.788
677	1-16	0.948	0.807
685	1-21	0.861	0.715
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.860	0.562
713	1-25	0.966	0.743
718	1-19	0.936	0.822
719	1-20	0.961	0.824
729	1-29	0.972	0.874
735	1-46	0.903	0.598
746	1-14	0.916	0.730
747	1-22	0.965	0.876
748	1-29	0.968	0.785
759	1-24	0.961	0.773
767	1-27	0.919	0.768
768	1-33	0.900	0.585
773	1-42	0.959	0.702
797	1-19	0.986	0.945
798	1-19	0.944	0.759
820	1-17	0.900	0.568
827	1-17	0.995	.I.—
848	1-20	0.9/1	0.749
864	1-20	0.928	0.782
866	1-19	0.986	0.782
873	1-23	0.948	0.886
881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
950	1-29	0.957	0.845
963	1-20	0.981	0.900
964	1-20	0.886	0.558
973	1-16	0.968	0.890
980	1-34	0.961	0.749
981	1-20	0.953	0.822
984	1-12	0.938	0.780
1015	1-22	0.938	0.854
1040	1-46	0.977	0.698
1052	1-18	0.969	0.842
1059	1-20	0.927	0.867
1065	1-33	0.983	0.918
1069	1-22	0.993	0.935
		1 4 . 3 2 3	V.933

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	Means (MEAN SCORE)
1075	1-27	0.992	0.934
1080	1-19	0.931	0.829
1092	1~19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-38	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
	· L	0.967	
1189	1-35		0.839
1192	1-46	0.993	0.638
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	0.789
1380	1-26	0.979	0.904
1397	1-27	0.962	0.777
1399	1-23	0.997	0.960
1404	1-24	0.998	0.977
1410	1-15	0.946	0.845
1414	1-24	0.913	0.588
1415	1-19	0.982	0.929
1416			
• • • •	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588 .
1428	1-25	0.957	0.899
1430	1-34	0.977	0.819
1431	1-28	0.979	0.923
1432	1-36	0.957	0.613
1433	1-32	0.921	0.753
1434	1-39	0.983	0.621
1435	1-25	0.910	0.631
1436	1-42	0.988	0.868
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12		0.753
1462		0.931	
	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	0.891
1561	1-25	0.967	0.899
1580	1-17	0.923	0.824

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

TABLE 6					
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide sequence		sequence	priority application	
1	1787	3573	5359	784CIP2 1	1103
1 2	1788	3574	5360	784CIP2_1	2673
3	1789	3575	5361	784CIP2_2	4117
4	1790	3576	5362	784CIP2 4	5556
5	1791	3577	5363	784CIP2 5	5562
6	1792	3578	5364	784CIP2 6	5562
<del></del>	1793	3579	5365	784CIP2 7	5562
8	1794	3580	5366	784CIP2 8	5562
<del>- 9</del>	1795	3581	5367	784CIP2 9	5563
10	1796	3582	5368	784CIP2 10	5564
11	1797	3583	5369	784CIP2 11	5565
12	1798	3584	5370	784CIP2 12	5689
13	1799	3585	5371	784CIP2 13	5729
14	1800	3586	5372	784CIP2_14	5745
15	1801	3587	5373	784CIP2_15	5777
16	1802	3588	5374	784CIP2_16	5777
17	1803	3589	5375	784CIP2_17	5789
18	1804	3590	5376	784CIP2_18	5792
19	1805	3591	5377	784CIP2_19	5804
20	1806	3592	5378	784CIP2_20	5805
21	1807	3593	5379	784CIP2_21	5805
22	1808	3594	5380	784CIP2_22	5844
23	1809	3595	5381	784CIP2_23	5844
24	1810	3596	5382 5383	784CIP2_24 784CIP2_25	5850 5867
26	1811	3597 3598	5383	784CIP2_25 784CIP2_26	5973
27	1812	3599	5385	784CIP2 27	5995
28	1814	3600	5386	784CIP2 28	5995
29	1815	3601	5387	784CIP2 29	6005
30	1816	3602	5388	784CIP2 30	6007
31	1817	3603	5389	784CIP2 31	6007
32	1818	3604	5390	784CIP2 32	6009
33	1819	3605	5391	784CIP2 33	6012
34	1820	3606	5392	784CIP2_34	6015
35	1821	3607	5393	784CIP2_35	6016
36	1822	3608	5394	784CIP2_36	6016
37	1823	3609	5395	7B4CIP2_37	6018
38	1824	3610	5396	784CIP2_38	6018
39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828 1829	3614 3615	5400 5401	784CIP2 42 784CIP2 43	6081
				784CIP2_43 784CIP2_44	
44	1830 1831	3616	5402 5403	784CIP2_44 784CIP2_45	6118
46	1831	3617 3618	5404	784C1P2 45	6130
45	1833	3619	5405	784CIP2_46	6177
48	1834	3620	5406	784CIP2 48	6189
49	1835	3621	5407	784CIP2_48	6191
50	1836	3622	5408	784CIP2 50	6204
51	1837	3623	5409	784CIP2 51 ·	6204
52	1838	3624	5410	784CIP2 52	6284
53	1839	3625	5411	784CIP2 53	6367
54	1840	3626	5412	784CIP2 54	6436
55	1841	3627	5413	784CIP2 55	6442
56	1842	3628	5414	784CIP2 56	6445
57	1843	3629	5415	784CIP2 57	6457
58	1844	3630	5416	784CIP2 58	6458
59	1845	3631	5417	784CIP2 59	6458
		L	L		<u></u>

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO: in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
60	sequence			application	
61	1846	3632	5418	784CIP2_60	6462
62	1847	3633	5419	784CIP2_61	6472
63	1848	3634	5420	784CIP2_62	6499
	1849	3635	5421	784CIP2_63	6499
64	1850	3636	5422	784CIP2_64	6505
65 66	1851	3637	5423	784CIP2_65	6534
	1852	3638	5424	784C1P2_66	6534
67 68	1853	3639	5425 5426	784CIP2_67	6540
	1854	3640		784C1P2_68	6550
69 70	1855	3641	5427	784CIP2_69	6550
70	1856 1857	3642	5428	784CIP2_70	6592
72		3643	5429	784CIP2_71	6645
73	1858 1859	3644	5430	784CIP2_72	6671
74	1860	3645 3646	5431 5432	784CIP2_73 784CIP2_74	6763
75	1861	3647	5432		6763
76	1862	3648	5434	784CIP2_75 784CIP2_76	6786
77	1863	3649	5435	784CIP2_76 784CIP2_77	6824 6830
78	1864	3650	5435 5436	784C1P2_77 784C1P2_78	6831
79	1865	3651	5437	784CIP2_78	6832
80	1866	3652	5438	784CIP2 80	6834
81	1857	3653	5439	784CIP2 81	6834
82	1858	3654	5440	784C1P2 82	6835
83	1869	3655	5441	784CIP2 83	6837
84	1870	3656	5442	784CIP2 84	6843
85	1871	3657	5443	784CIP2 85	6859
86	1872	3658	5444	784CIP2 86	6915
87	1873	3659	5445	784CIP2 B7	6932
88	1874	3660	5446	784CIP2 88	6957
89	1875	3661	5447	784CIP2 89	6961
90	1876	3662	5448	784C1P2 90	6973
91	1877	3663	5449	784CIP2_91	6973
92	1878	3664	5450	784CIP2_93	7007
93	. 1879	3665	5451	784CIP2_94	7018
94	1880	3666	5452	784CIP2_95	7019
95	1881	3667	5453	784CIP2_96	7020
96	1882	3668	5454	784CIP2_97	7020
97	1883	3669	5455	784CIP2_98	7021
98	1884	3670	5456	784CIP2_99	7023
99	1885	3671	5457	784CIP2_100	7027
100	1886	3672	5458	784CIP2_101	7028
101	1887	3673	5459	784CIP2_102	7029
102	1888	3674	5460	784CIP2_103	7031
103	1889	3675	5461	784CIP2_104	7032
104	1890	3676	5462	784CIP2_105	7033
105	1891	3677	5463	784CIP2_106	7035
106	1892	3678	5464	784CIP2_107	7036
107	1893	3679	5465	784CIP2_108	7039
108	1894	3680	5466	784CIP2_109	7043
109	1895	3681	5467	784CIP2_110	7044
110	1896	3682	5468	784CIP2_111	7046
111	1897	3683	5469	784CIP2_112	7054
112	1898	3684	5470	784CIP2_113	7061
113	1899	3685	5471	784CIP2_114	7077
114	1900	3686	5472	784CIP2_115	7092
115	1901	3687	5473	784CIP2_116	7094
116	1902	3688	5474	784CIP2_117	7106
117	1903	3689	5475	784CIP2_118	7107
118	1904	3690	5476	784CIP2_119	7111
119	1905	3691	5477	784CIP2_120	7123
120	1906	3692	5478	784CIP2_121	7142
121	1907	3693	5479	784CIP2_122	7142

SEQ ID NO:	SEQ ID	SEQ ID NO:	TSRO ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	No:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	i
	sequence			application	
122	1908	3694	5480	784CIP2_123	7154
123	1909	3695	5481	784CIP2_124	7160
124	1910	3696	5482	784CIP2_125	7169
126	1911	3697	5483	784CIP2_126	7185
126	1912	3698 3699	5484	784CIP2 127	7197
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164	1950	3736	5522	784CIP2_165	7493
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168	1954	3740	5526	784CIP2_169	7520
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178	1964	3749	5535	784CIP2_178	7615
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197	1983	3769	5555	784CIP2_199	7737
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	306	2092				
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424 425 426 427 428	2208 2209 2210 2211 2212 2213 2214	3995 3996 3997 3998 3999 4000	5781 5782 5783 5784 5785 5786	784CIP2B 97 784CIP2B 98 784CIP2B 99 784CIP2B 100 784CIP2B 101 784CIP2B 101 784CIP2B 102	2818 2819 2943 3137 3137 3160

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450	2236 2237	4022 4023	5809	784CIP2B_124 784CIP2B_125	4321
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455	2241	4027	5813	784CIP2B 129	5569
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471	2257	4043	5829	784CIP2B_145	5617
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477	2263	4049	5835	784CIP2B_151	5627
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. 483	2269	4055	5841	784CIP2B_157	5643
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486	2272	4058	5844	784CIP2B_160	5658
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488	2274	4060	5846	784CIP2B_162	5667
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500	2286	4072	5858	784CIP2B 174	5720
501	2287	4073	5859	784CIP2B 175	5727
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513	2299	4085	5871	784CIP2B_187	5761
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516	2302	4088	5874	784CIP2B_190	5773
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550	2336	4122	5908	784CIP2B 225	5939
551	2337	4123	5909	784CIP2B_225	5945
	2338	4124	5910	784CIP2B 227	5946
552		3464	3210	/04CIE2D_A4/	2240
552 553	2339	4125	5917	784CTD20 220	5947
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558	2344	4130	5916	784CIP2B_234	5978
559	2345	4131	5917	784CIP2B_235	5979
560	2346	4132	5918 5919	784CIP2B_236 784CIP2B_237	5980
561	2347	4133			5988
562	2348	4134	5920	784CIP2B 238 784CIP2B 239	5989 5991
563	2349	4135	5921 5922		5991
564	2350	4136		784CIP2B_240	1
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566	2352	4138	5924	784CIP2B_242	6003
567	2353	4139	5925	784CIP2B_243	6004
568	2354	4140	5926 5927	784CIP2B_244	6013 6028
569	2355	4141		784CIF2B_245	6028
570	2356	4142	5928	784CIP2B_246 784CIP2B_247	6028
571	2357	4143	5929	784CIP2B 247 784CIP2B 248	6031
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573 574	2359 2360	4145	5931	784CIP2B_249 784CIP2B_250	6032
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576	2362	4148	5934	784CIP2B 252	6037
577	2363	4149	5935	784CIP2B_252 784CIP2B_253	6043
578	2364	4150	5936	784CIP2B 254	6044
579	2365	4151	5937	784CIP2B 255	6046
580	2366	4152	5938	784CIP2B 256	6048
581	2367	4153	5939	784CIP2B 257	6049
582	2368	4154	5940	784CIP2B 258	6051
583	2369	4155	5941	784CIP2B 259	6053
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585	2371	4157	5943	784CIP2B 261	6063
586	2372	4158	5944	784CIP2B 262	6066
. 587	2373	4159	5945	784CIP2B 263	6067
588	2374	4160	5946	784CIP2B 264	6068
589	2375	4161	5947	784CIP2B 265	6073
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613	2399	4185	5971	784CIP2B 290	6145
614	2400	4186	5972	784CIP2B 291	6146
615	2401	4187	5973	784CIP2B 292	6148
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622	2408	4194	5980	784CIP2B_299	6172
623	2409	4195	5981	784CIP2B_300	6173
624	2410	4196	5982	784CIP2B_301	6190
625	2411	4197	5983	784CIP2B_302	6194
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	2416	4202	5988	784CIP2B_308	6214
631	2417	4203	5989	784CIP2B_309	6215
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634	2419	4205	5991	784CIP2B_311	6226
635	2420 2421	4206 4207	5992 5993	784CIP2B_312	6229
636	2422 2422			784CIP2B 313 784CIP2B 314	6234
637	2423	4208 4209	5994 5995	784CIP2B_314 784CIP2B 315	6237 6238
638	2424	4210	5995	784CIP2B_315	6239
639	2425	4211	5997	784CIP2B_316	6239
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642	2428	4214	6000	784CIP2B 320	6244
643	2429	4215	6001	784CIP2B 321	6245
644	2430	4216	6002	784CIP2B 322	6250
645	2431	4217	6003	784CIP2B 323	6252
646	2432	4218	6004	784CIP2B 324	6252
647	2433	4219	6005	784CIP2B 325	6256
64B	2434	4220	6006	784CIP2B 326	6260
649	2435	4221	6007	784CIP2B 327	6261
650	2436	4222	6008	784CIP2B 328	6264
651	2437	4223	6009	784CIP2B 329	6265
652	2438	4224	6010	784CIP2B 330	6266
653	2439	4225	6011	784CIP2B_331	6270
654	2440	4226	6012	784CIP2B_332	6271
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656	2442	4228	6014	784CIP2B_335	6276
657	2443	4229	6015	784CIP2B_336	6281
658	2444	4230	6016	784CIP2B_337	6281
659	2445	4231	6017	784CIP2B_338	6288
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661	2447	4233	6019	784CIP2B_340	6294
662	2448	4234	6020	784CIP2B_343	6312
663	2449	4235	6021	784CIP2B 344	6312
664	2450	4236	6022	784CIP2B_345	6312
665	2451	4237	6023	784CIP2B_346	6322
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667	2453	4239	6025	784CIP2B_349	6329
668	2454	4240	6026	784CIP2B_350	6331
669	2455	4241	6027	784CIP2B_351	6333
670	2456	4242	6028	784CIP2B_352	6334
671	2457	4243	6029	784CIP2B_353	6337
672	2458	4244	6030	784CIP2B_354	6339
673	2459	4245	6031	784CIP2B_355	6346
674	2460	4246	6032	784CIP2B_356	6348
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676	2462	4248	6034	784CIP2B_358	6350
677	2463	4249	6035	784CIP2B_359	6351
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684	2470	4256	6042	784CIP2B_366	6379
685	2471	4257	6043	784CIP2B_367	6380
686	2472	4258	6044	784CIP2B_368	6381
687	2473	4259	6045	784CIP2B_369	6392
688	2474	4260	6046	784CIP2B_370	6395
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693	2479	4265	6051	784CIP2B_375	6411
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695 696	2481	4267	6053 6054	784CIP2B_377	6416
697	2482 2483	4268 4269	6055	784CIP2B 378	6418
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699	2484	4271	6057	784CIP2B_380 784CIP2B_381	6423 6426
700	2486	4272	6058	784CIP2B 382	6427
701	2487	4273	6059	784CIP2B_382 784CIP2B_383	6428
702	2458	4274	6060	784CIP2B 384	6429
703	2489	4275	6061	784CIP2B 385	6430
704	2490	4276	6062	784CIP2B 386	6432
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706	2492	4278	6064	784CIP2B 388	6438
707	2493	4279	6065	784CIP2B 389	6441
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711	2497	4283	6069	784CIP2B_394	6461
712	2498	4284	6070	784CIP2B_395	6467
713	2499	4285	6071	784CIP2B_396	6468
714	2500	. 4286	6072	784CIP2B_397	6487
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716	2502	4288	6074	784CIP2B_399	6506
717	2503	4289	6075	784CIP2B_401	6514
718	2504	4290	6076	784CIP2B_402	6519
719	2505	4291	6077	784CIP2B_403	6521
720	2506	4292	6078	784CIP2B_404	6532
721	2507	4293	6079	784CIP2B_405	6536
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725	2511	4297	6083	784CIP2B_409	6551
726	2512	4298	6084	784CIP2B_410	6551
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	2514	4300	6086	784CIP2B_412	6554
729	2515	4301	6087	784CIP2B_413	6556
730	2516	4302	6088	784CIP2B_414	6560
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	2519	4305	6091	784CIP2B_417	6567
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736	2522	4308	6094	784CIP2B_420	6577
737	2523	4309	6095	784CIP2B_421	6593
738	2524	4310	6096	784CIP2B_422	6595
770			E007 1	-/4///TD3D /33 (	6599
739	2525	4311	6097	784CIP2B_423	
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744	2530	4316	6102	784CIP2B_428	6631
745	2531	4317	6103	784CIP2B_429	6632
746	2532	4318	6104	784CIP2B_430	6633
747	2533	4319	6105 6106	784CIP2B_431	6634
748 749	2534 2535	4320 4321	6105	784CIP2B_432 784CIP2B_433	6638 6641
750	2536	4322	6108	784CIP2B 433	6644
750	2537	4323	6109	784CIP2B_434 784CIP2B_435	6646
752	2538	4324	6110	784CIP2B 436	6648
753	2539	4325	6111	784CIP2B 437	6652
754	2540	4326	6112	784CIP2B 438	1 6654
755	2541	4327	6113	784CIP2B 439	6657
756	2542	4328	6114	784CIP2B 440	6658
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758	2544	4330	6116	784CIP2B 442	6664
·759	2545	4331	6117	784CIP2B 443	6668
760	2546	4332	6118	784CIP2B_444	6669
761	2547	4333	6119	784CIP2B 445	6673
762	2548	4334	6120	784CIP2B 446	6685
763	2549	4335	6121	784CIP2B_447	6687
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765	2551	4337	6123	784CIP2B_449	6693
766	2552	4336	6124	784C1P2B_450	6698
767	2553	4339	6125	784CIP2B_451	6699
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769	2555	4341	6127	784CIP2B_453	6711
770	2556	4342	6128	784CIP2B_454	6713
771 772	2557	4343 4344	6129 6130	784CIP2B 455 784CIP2B 456	6716 6725
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774	2560	4346	6132	784CIP2B_457	6727
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776	2562	4348	6134	784CIP2B 460	6730
777	2563	4349	6135	784CIP2B 461	6730
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781	2567	4353	6139	784CIP2B 465	6745
782	256B	4354	6140	784CIP2B_466	6751
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787	2573	4359	6145	784CIP2B_471	6768
788	2574	4360	6146	784CIP2B_472	6773
789	2575	4361	6147	784CIP2B_473	6776
790	2576	4362	6148	784CIP2B_474	6796
791	2577	4363	6149	784CIP2B_475	6798
792	.2578	4364	6150	784CIP2B_476	6823
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794	2580	4366	6152	784CIP2B_478	6826
795	2581	4367	6153	784CIP2B 479	6839
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797	2583	4369	6155	784CIP2B_482	6849
798 799	2584	4370	6156	784CIP2B_483	6854
800	2585	4371	6157	784CIP2B_484	6857
801	2586	4372	6158	784CIP2B_485	6861 6873
802	2587 2588	4373	6159	784CIP2B_486	6873
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808	2594	4380	6166	784CIP2B_493	6894
809	2595	4381	6167	784CIP2B_494	6901
810	2595	4382	6168	784CIP2B_495	6904
811	2597	4383	6169	784CIP2B_496	6907
812	259B	4384	6170	784C1P2B_497	6914
813	2599	4385	6171	784CIP2B_498	6917
814	2600	4386	6172	784CIP2B_499	6923
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816	2602	4388	6174	784CIP2B_501	6931
817	2603	4389	6175	784CIP2B_502	6935
818	2604	4390	6176	784CIP2B_503	6940
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821	2607	4393	6179	784CIP2B_506	6947
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825	2611	4397	6183	784CIP2B_510	6962
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828	2614 2615	4400	6186	784CIP2B_513	6983
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658	2644	4430	6216	784CIP2B_543	7121
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· 870	2656	4442	6228	784CIP2B_555	7191
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876	2662	4448	6234	784CIP2B_561	7216
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	2673	4459 4460	6246	784C1P2B_572 784C1P2B_573	7275
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925	2711	4497	6283	784CIP2B_612	7410
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933	2719	4505	6291	784CIP23_620	7424
934	2720	4506	6292	784CIP2B_621	7426
935	2721	4507	6293	784CIP29_622	7427
936	2722	4508	6294	784CIP2B_623	7428
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980	2766	4552	6338	784CIP23_667	7569
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1010   2796		<u></u>			<u> </u>	
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1012   2798					1	
1013   2799   4585   6371   784CIP2B_701   7694     1014   2800   4586   6372   784CIP2B_702   7715     1015   2801   4587   6373   784CIP2B_703   7716     1016   2802   4588   6374   784CIP2B_704   7718     1017   2803   4589   6375   784CIP2B_705   7721     1018   2804   4590   6375   784CIP2B_705   7721     1018   2804   4590   6376   784CIP2B_706   7723     1019   2805   4591   6377   784CIP2B_707   7729     1020   2806   4592   6378   784CIP2B_708   7733     1021   2807   4593   6379   784CIP2B_709   7735     1022   2808   4594   6380   784CIP2B_709   7735     1023   2809   4595   6381   784CIP2B_710   7741     1023   2809   4595   6381   784CIP2B_711   7743     1024   2810   4596   6382   784CIP2B_711   7749     1025   2811   4597   6383   784CIP2B_713   7749     1026   2812   4598   6384   784CIP2B_713   7749     1027   2813   4599   6385   784CIP2B_714   7750     1029   2814   4600   6386   784CIP2B_716   7759     1029   2815   4601   6387   784CIP2B_716   7759     1030   2816   4602   638B   784CIP2B_717   7760     1031   2817   4603   6389   784CIP2B_719   7764     1032   2818   4604   6390   784CIP2B_719   7766     1033   2819   4605   6391   784CIP2B_72   77777     1036   2822   4608   6392   784CIP2B_72   77777     1037   2823   4609   6395   784CIP2B_72   77777     1038   2824   4610   6396   784CIP2B_72   7777     1039   2825   46611   6397   784CIP2B_72   7777     1039   2825   46611   6396   784CIP2B_72   7777     1039   2825   4611   6397   784CIP2B_72   7777     1039   2825   4611   6397   784CIP2B_72   7777     1039   2825   4611   6397   784CIP2B_72   7778     1040   2826   4612   6398   784CIP2B_72   7777     1037   2823   4609   6395   784CIP2B_72   7777     1038   2824   4610   6396   784CIP2B_72   7778     1040   2826   4611   6397   784CIP2B_72   7778     1040   2826   4612   6398   784CIP2B_73   7782     1041   2827   4613   6495   784CIP2B_73   7781     1040   2826   4616   6402   784CIP2B_73   7781     1040   2826   4616   6402   784CIP2B_73   7782     1041   2829   4615   6401						
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1020						
1021   2807						
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1024						
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1049 2835 4621 6407 784CIP2B 737 7824 1050 2836 4622 6408 784CIP2B 738 7826			4619	6405	784CIP2B_735	7808
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1330	3116	4902	6688	784CIP2B_1020	8942
1331	3117	4903	6689	784C1P2B_1021	8994
1332	3118	4904	6690	784CIP2B_1022	9023
1333	3119	4905	6691	784CIP2B 1023	9028
1334	3120	4906	6692	784CIP2B_1024	9058
1335	3121	4907	6693	784CIP2B_1025	9058
1336	3122	4908	6694	784CIP2B 1026	9079
1337	3123	4909	6695	784CIP2B 1027	9079
1338	3124	4910	6696	784CIP2B 1028	9082
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1340	3126	4912	6698	784CIP2B 1030	9093
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1353	3139	4925	6711	784CIP2B_1043	9276
1354	3140	4926	6712	784CIP2B_1044	9345
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1373	3159	4945	6731	784CIP2B_1063	9623
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1375	3161	4947	6733	784CIP2B_1065	9747
1376	3152	4948	6734	784CIP2B_1066	9773
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1381	3167	4952	6738 6739	784CIP2B_1070 784CIP2B 1071	9843 9854
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1419	3205	4991	6777	784CIP2C_6	953
1420	3206	4992	6778	784CIP2C_7	980
1421	3207	4993	6779	784CIP2C_8	1595
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1434	3220	5006	6792	784CIP2C_21	2959
1435	3221	5007	6793	784CIP2C_22	2965
1436	3222	5008	6794	784CIP2C_23	2966
1437	3223	5009	6795	784CIP2C_24	2970
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1598	3384	5170	6956	784CIP2C_190	6057
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1626	3412	5198			7509
1627	3413	5199	6985	784CIPZC_219	1
1628	3414	5200	6986	784CIP2C_220	7544
1629	3415	5201	6987	784CIP2C_221	7564
1630	3416	5202	6988	784CIP2C_222	7568
1631	3417	5203	6989	784CIP2C_223	7631
1632	3418	5204	6990	784CIP2C_224	7813
1633	3419	5205	6991	784CIP2C_225	7831
1634	3420	5206	6992	784CIP2C_226	7843
1635	3421	5207	6993	784CIP2C_227	7907
1636	3422	5208	6994	784CIP2C_228	7943
1637	3423	5209	6995	784CIP2C_229	8175
1638	3424	5210	6996	784CIP2C_230	8216
1639	3425	5211	6997	784CIP2C 231	8225
1640	3426	5212	6998	784CIP2C 232	8271
1641	3427	5213	6999	784CIP2C 233	8397
1642	3428	5214	7000	784CIP2C 234	8466
1643	3429	5215	7001	784CIP2C 235	8503
1644	3430	5216	7002	784CIP2C 236	8953
1645	3431	5217	7003	784CIP2C 237	9106
1646	3432	5218	7004	784CIP2C 238	9139
1647	3433	5219	7005	784CIP2C 239	9555
	3434	5220	7006	784CIP2C 240	9650
1648				784CIP2C_240	9889
1649	3435	5221	7007	784CIP2C_241	9933
1650	3436	5222	7008	1	
1651	3437	5223	7009	784CIP2C_243	9953
1652	3438	5224	7010	784CIP2C_244	9981
1653	3439	5225	7011	784CIP2D_1	746
1654	3440	5226	7012	784C1P2D_2	3558
1655	3441	5227	7013	784CIP2D_3	3558
1656	3442	522B	7014	784CIP2D_4	3633
1657	3443	5229	7015	784CIP2D_5	3658
1658	3444	5230	7016	784C1P2D_6	3732
1659	3445	5231	7017	784CIP2D_7	4004
1660	3446 .	5232	7018	784CIP2D 8	4700
1661	3447	5233	7019	784C1P2D 9	4703
1662	3448	5234	7020	784CIP2D 10	4774
1663	3449	5235	7021	784CIP2D 11	4894
1664	3450	- 5236	7022	784CIP2D 12	4918
					5159
1665	3451	5237	7023	784CIP2D_13	
1666	3452	5238	7024	784CIP2D 14	7443
1667	3453	5239	7025	784CIP2D_15	8673
1668	3454	5240	7026	784CIP2D_16	8679
7.60	3455	5241	7027	784CIP2D 17	8727
1669		<u> </u>			
1670	3456	5242	7028 7029	784CIP2D_18	8734 8756

of full- length nucleotide sequence    1672   3458   5244   7930   784C1P2D   20     1673   3459   5245   7931   784C1P2D   21     1674   3456   5246   7932   784C1P2D   22     1675   3461   5247   7933   784C1P2D   22     1676   3465   5248   7931   784C1P2D   22     1677   3463   5248   7931   784C1P2D   22     1678   3461   5247   7933   784C1P2D   22     1679   3464   5250   7935   784C1P2D   24     1679   3464   5250   7935   784C1P2D   24     1679   3464   5250   7935   784C1P2D   24     1679   3464   5250   7935   784C1P2D   24     1679   3465   5251   7937   784C1P2D   24     1679   3465   5251   7937   784C1P2D   24     1681   3467   5253   7938   784C1P2D   24     1683   3468   5255   7937   784C1P2D   27     1683   3468   5255   7939   784C1P2D   27     1684   3470   5355   7941   794C1P2D   30     1686   3472   5253   7943   784C1P2D   30     1686   3474   5257   7943   794C1P2D   32     1688   3474   5267   7946   794C1P2D   37     1688   3474   5267   7946   794C1P2D   37     1689   3476   5262   7948   794C1P2D   37     1691   3477   5263   7948   794C1P2D   37     1692   3478   5264   7963   794C1P2D   37     1693   3478   5264   7963   794C1P2D   37     1694   3486   5267   7948   794C1P2D   37     1695   3488   5267   7948   794C1P2D   37     1696   3488   5277   7968   794C1P2D   37     1697   3488   5277   7968   794C1P2D   37     1698   3488   5277   7968   794C1P2D   37     1699   3488   5277   7968   794C1P2D   37     1700   3488   5277   7968   794C1P2D   37     1701   3489   5278   7968   794C1P2D   37     1701   3489   5279   7968   794C1P2D   37     1701   3489   5279   7968   794C1P2D   37     1701   3489   5280   7968   794C1P2D   37     1701   3489   5280   7968   794C1P2D   37     1701   3489   5279   7968   794C1P2D   37     1701   3489   5279   7968   794C1P2D   37     1702   3489   5279   7968   794C1P2D   37     1703   3499   5279   7968   794C1P2D   37     1704   3499   5279   7968   794C1P2D   37     1705   3499   5279   7968   794C1P2D   37     1701   3499   5288   7978   7	SEO ID NO:	SEQ ID	SEO ID NO:	SEQ ID	Priority	SEQ ID
Inspite   Insp						, -
nuclectide gequence geptide gequence geptimes ge			, –		_	
Bequence   3458   5244   7030   RedCIP2D 20   8018		length	sequence		SEQ ID NO: in	09/488,725
1672 3458 5244 7030 784C1P2D 20 8018 1673 3459 5245 7031 784C1P2D 21 8644 1674 3460 5246 7032 784C1P2D 22 8846 1675 3462 5248 7034 784C1P2D 22 8936 1676 3462 5248 7034 784C1P2D 23 8912 1676 3462 5248 7034 784C1P2D 24 8912 1677 3463 5249 7035 784C1P2D 25 8918 1678 3464 5250 7036 784C1P2D 25 8918 1679 3465 5251 7037 784C1P2D 27 8941 1660 3466 5252 7038 784C1P2D 27 8941 1661 3467 5253 7039 784C1P2D 29 8931 1662 3468 5254 7040 784C1P2D 29 8931 1663 3465 5255 7040 784C1P2D 29 8931 1663 3465 5255 7041 784C1P2D 31 9012 1684 3470 5256 7042 784C1P2D 31 9012 1685 3471 5257 7043 784C1P2D 33 9025 1686 3472 5258 7044 784C1P2D 33 9025 1686 3472 5258 7044 784C1P2D 35 9035 1687 3473 5259 7045 784C1P2D 35 9035 1688 3474 5260 7046 784C1P2D 35 9035 1689 3475 5261 7047 784C1P2D 35 9034 1689 3477 5262 7048 784C1P2D 35 9034 1690 3476 5262 7048 784C1P2D 38 9134 1691 3477 5263 7049 784C1P2D 38 9134 1691 3477 5263 7049 784C1P2D 38 9134 1693 3479 5264 7050 784C1P2D 38 9134 1694 3480 5266 7052 784C1P2D 44 9223 1695 3491 5266 7052 784C1P2D 44 9223 1696 3497 5266 7055 784C1P2D 44 9223 1696 3497 5266 7055 784C1P2D 44 9223 1697 3481 5267 7055 784C1P2D 44 9223 1698 3491 5267 7055 784C1P2D 44 9223 1698 3491 5267 7055 784C1P2D 49 9233 1699 3476 5262 7048 784C1P2D 38 9134 1691 3497 5262 7048 784C1P2D 38 9134 1691 3497 5264 7050 784C1P2D 34 9223 1693 3498 5264 7050 784C1P2D 34 9223 1696 3492 5268 7055 784C1P2D 44 9223 1697 3491 5266 7055 784C1P2D 49 9233 1698 3491 5267 7055 784C1P2D 49 9233 1698 3491 5267 7055 784C1P2D 49 9233 1698 3491 5267 7055 784C1P2D 59 9394 1700 3486 5272 7058 784C1P2D 59 9315 1700 3486 5272 7058 784C1P2D 59 9315 1701 3493 5269 7055 784C1P2D 59 9349 1702 3488 5274 7060 784C1P2D 59 9349 1703 3493 5265 7055 784C1P2D 59 9349 1704 3490 5266 7052 784C1P2D 59 9349 1705 3493 5295 7065 784C1P2D 59 9349 1707 3493 5295 7065 784C1P2D 59 9349 1708 3495 5285 7077 784C1P2D 59 9449 1709 3495 5281 7077 784C1P2D 59 9349 1709 3495 5281 7077 784C1P2D 59 9449 1710 3496 5282 7078 784C1P2D 59 9449 1711 3497 5283 7069 784C1P2D 59 9660 1712 3508 5	sequence	peptide	-	веquence	priority	
1673   3459   5245   7051   784C[P2D_21]   8844   1675   3461   5247   7033   784C[P2D_22]   8916   1675   3461   5247   7033   784C[P2D_22]   8918   1676   3462   5248   7035   784C[P2D_22]   8918   1677   3463   5249   7035   784C[P2D_23]   8918   1679   3464   5250   7036   784C[P2D_26]   8918   1679   3465   5251   7037   784C[P2D_26]   8918   1680   3466   5252   7038   784C[P2D_27]   8941   1680   3466   5252   7038   784C[P2D_27]   8941   1681   3467   5253   7039   784C[P2D_27]   8951   1682   3468   5253   7059   784C[P2D_29]   8951   1682   3468   5254   7040   784C[P2D_20]   9007   1683   3465   5254   7040   784C[P2D_20]   9007   1683   3465   5255   7041   784C[P2D_20]   9007   1684   3470   5256   7042   784C[P2D_23]   9013   1686   3472   5255   7041   784C[P2D_33]   5025   1686   3472   5258   7044   784C[P2D_33]   5025   1686   3472   5258   7044   784C[P2D_33]   5025   1686   3472   5258   7044   784C[P2D_34]   9053   1689   3475   5261   7047   784C[P2D_37]   9113   1690   3476   5262   7048   784C[P2D_37]   9113   1691   3477   5263   7049   784C[P2D_39]   9152   1693   3479   5265   7054   784C[P2D_39]   9152   1693   3479   5265   7051   784C[P2D_39]   9152   1693   3479   5265   7051   784C[P2D_34]   9213   1694   3480   5266   7052   7048   784C[P2D_34]   9213   1694   3480   5266   7055   784C[P2D_44]   9211   1695   3481   5267   7053   784C[P2D_44]   9211   1696   3486   5272   7053   784C[P2D_44]   9213   1696   3484   5266   7055   784C[P2D_44]   9213   1696   3486   5272   7053   784C[P2D_44]   9213   1696   3480   5266   7055   784C[P2D_44]   9213   1696   3480   5266   7055   784C[P2D_44]   9213   1696   3480   5266   7055   784C[P2D_44]   9213   1696   3480   5266   7055   784C[P2D_44]   9213   1696   3480   5266   7055   784C[P2D_44]   9213   1696   3480   5266   7055   784C[P2D_45]   9339   1700   3486   5277   7053   784C[P2D_45]   9339   1700   3486   5277   7056   784C[P2D_45]   9334   1706   3490   5276   7056   784C[P2D_56]   9326   1706   3490   5276   7056   784C[P2D_		sequence		l	application	
1674   3460   5246   7032   784CIP2D 22   8846   1675   3461   5247   7033   784CIP2D 23   8912   1676   3462   5248   7034   784CIP2D 24   8918   1677   3463   5249   7035   784CIP2D 25   8918   1678   3464   5250   7036   784CIP2D 27   8941   1679   3465   5251   7037   784CIP2D 27   8941   1680   3466   5252   7038   784CIP2D 27   8941   1680   3466   5252   7038   784CIP2D 27   8941   1680   3466   5252   7038   784CIP2D 29   8951   1681   3467   5253   7039   784CIP2D 29   8951   1682   3468   5254   7040   784CIP2D 29   8951   1683   3465   5255   7041   784CIP2D 31   9012   1684   3470   5256   7042   784CIP2D 31   9012   1684   3470   5256   7042   784CIP2D 31   9012   1685   3471   5257   7043   784CIP2D 33   9025   1687   3473   5259   7044   784CIP2D 33   9025   1687   3473   5259   7045   784CIP2D 36   9055   1689   3476   5262   7046   784CIP2D 37   9056   1689   3476   5262   7048   784CIP2D 37   9056   1689   3476   5262   7048   784CIP2D 37   9051   1691   3477   5263   7049   784CIP2D 38   9134   1691   3479   5264   7050   784CIP2D 38   9134   1693   3479   5264   7050   784CIP2D 38   9134   1693   3479   5264   7050   784CIP2D 34   9223   1693   3479   5266   7052   784CIP2D 34   9223   1693   3491   5267   7055   784CIP2D 34   9223   1693   3491   5267   7055   784CIP2D 34   9223   1696   3491   5267   7055   784CIP2D 34   9223   1696   3491   5267   7055   784CIP2D 34   9223   1696   3491   5267   7055   784CIP2D 34   9223   1696   3491   5267   7055   784CIP2D 34   9223   1696   3491   5267   7055   784CIP2D 34   9223   1696   3491   5267   7055   784CIP2D 34   9223   1696   3491   5267   7055   784CIP2D 34   9223   1696   3491   5267   7055   784CIP2D 34   9223   1696   3491   5267   7055   784CIP2D 34   9223   1696   3495   5266   7055   784CIP2D 35   9236   1696   3495   5266   7052   784CIP2D 35   9236   1696   3495   5266   7052   784CIP2D 35   9236   1696   3495   5266   7052   784CIP2D 35   9236   1696   3495   5266   7055   784CIP2D 35   9236   1696   3495   5266   7055   784CIP2	1672	3458	5244	7030	784CIP2D_20	8818
1675   3461   5247   7033   784CIPZD 23   8912   1676   3462   5248   7035   784CIPZD 25   8918   1677   3463   5249   7035   784CIPZD 25   8918   1678   3464   5250   7036   784CIPZD 26   8941   1679   3465   5251   7037   784CIPZD 28   8951   1680   3466   5252   7038   784CIPZD 28   8951   1681   3467   5253   7039   784CIPZD 28   8951   1681   3467   5253   7039   784CIPZD 28   8951   1682   3468   5254   7040   784CIPZD 30   9007   1683   3469   5255   7041   784CIPZD 30   9007   1683   3469   5255   7041   784CIPZD 30   9007   1683   3469   5255   7041   784CIPZD 31   9012   1684   3470   5256   7042   784CIPZD 32   9013   1685   3471   5257   7043   784CIPZD 32   9013   1686   3472   5258   7044   784CIPZD 34   9053   1687   3473   5257   7045   784CIPZD 34   9053   1688   3474   5260   7046   784CIPZD 34   9053   1689   3475   5261   7047   784CIPZD 36   9054   1689   3476   5262   7048   784CIPZD 37   9013   1690   3476   5262   7048   784CIPZD 37   9013   1691   3477   5263   7049   784CIPZD 37   9013   1692   3478   5264   7050   784CIPZD 39   9152   1693   3479   5264   7050   784CIPZD 39   9152   1694   3480   5266   7052   784CIPZD 39   9152   1695   3481   5267   7053   784CIPZD 40   9152   1695   3481   5267   7053   784CIPZD 41   9211   1694   3480   5266   7052   784CIPZD 44   9231   1696   3482   5268   7051   784CIPZD 44   9231   1697   3488   5271   7057   784CIPZD 47   9303   1701   3486   5272   7058   784CIPZD 48   9314   1702   3488   5271   7057   784CIPZD 49   9314   1703   3489   5275   7061   784CIPZD 50   9316   1704   3490   5276   7062   784CIPZD 50   9316   1706   3492   5286   7055   784CIPZD 50   9316   1707   3493   5287   7063   784CIPZD 50   9316   1708   3494   5287   7066   784CIPZD 50   9316   1709   3498   5277   7063   784CIPZD 50   9316   1700   3486   5272   7058   784CIPZD 50   9316   1701   3498   5281   7067   784CIPZD 50   9316   1702   3498   5287   7061   784CIPZD 50   9316   1703   3499   5280   7070   784CIPZD 50   9317   1704   3499   5280   7070   784CIPZ	1673	3459	5245	7031	784C1P2D_21	
1676	1674	3460	5246	7032		
1677 3463 5229 7035 784CIP2D 25 8948 1678 3464 5250 7635 784CIP2D 27 8941 1679 3465 5251 7037 784CIP2D 27 8941 1660 3466 5252 7038 784CIP2D 28 8951 1661 3467 5253 7039 784CIP2D 29 8951 1662 3468 5252 7038 784CIP2D 29 8951 1662 3468 5255 7041 784CIP2D 30 9007 1663 3469 5255 7041 784CIP2D 30 9007 1663 3469 5255 7041 784CIP2D 32 9013 1664 3470 5255 7042 784CIP2D 32 9013 1665 3471 5257 7043 784CIP2D 32 9013 1666 3472 5258 7044 784CIP2D 34 9053 1667 3473 5259 7045 784CIP2D 34 9053 1669 3475 5261 7047 784CIP2D 35 9054 1669 3475 5262 7046 784CIP2D 37 9054 1669 3475 5262 7046 784CIP2D 37 9113 1690 3476 5262 7048 784CIP2D 37 9113 1690 3478 5264 7050 784CIP2D 39 9152 1691 3478 5264 7050 784CIP2D 39 9152 1692 3478 5264 7050 784CIP2D 39 9152 1693 3478 5265 7051 784CIP2D 40 9152 1694 3480 5266 7052 784CIP2D 40 9223 1696 3482 5268 7051 784CIP2D 41 9211 1697 3483 5269 7055 784CIP2D 42 9223 1696 3484 5270 7053 784CIP2D 44 9231 1697 3483 5269 7055 784CIP2D 44 9231 1697 3483 5269 7055 784CIP2D 44 9231 1697 3483 5269 7055 784CIP2D 44 9231 1697 3489 5267 7053 784CIP2D 44 9231 1697 3489 5277 7053 784CIP2D 48 9236 1698 3484 5270 7055 784CIP2D 48 9236 1699 3485 5271 7057 784CIP2D 48 9236 1698 3484 5270 7056 784CIP2D 48 9236 1699 3485 5271 7057 784CIP2D 48 9231 1700 3486 5272 7058 784CIP2D 48 9231 1701 3487 5273 7059 784CIP2D 59 9314 1702 3488 5274 7060 784CIP2D 59 9314 1703 3489 5275 7061 784CIP2D 59 9314 1704 3490 5276 7062 784CIP2D 59 9314 1705 3491 5277 7063 784CIP2D 59 9314 1706 3495 5281 7067 784CIP2D 59 9315 1707 3493 5279 7066 784CIP2D 59 9316 1708 3499 5275 7061 784CIP2D 59 9316 1709 3498 5276 7062 784CIP2D 59 9316 1709 3498 5277 7063 784CIP2D 59 9317 1701 3496 5287 7079 784CIP2D 59 9461 1703 3499 5276 7062 784CIP2D 59 947 1704 3498 5276 7062 784CIP2D 59 947 1705 3491 5277 7063 784CIP2D 59 947 1707 3493 5279 7068 784CIP2D 59 947 1708 3498 5280 7066 784CIP2D 59 947 1709 3498 5280 7066 784CIP2D 59 947 1709 3498 5280 7066 784CIP2D 59 9461 1709 3495 5281 7077 784CIP2D 69 9561 1714 3500 5286 7087 784CIP2D 69 9561 1715 3501 5299 70	1675	3461	5247	7033	784CIP2D_23	8912
1678	1676	3462	5248	7034	l	
1679 3465 5281 7037 784CIP2D 27 8941 1680 3466 5282 7038 784CIP2D 28 8951 1681 3467 5253 7039 784CIP2D 28 8951 1682 3468 5284 7040 784CIP2D 30 9007 1683 3469 5285 7041 784CIP2D 30 9007 1683 3469 5285 7041 784CIP2D 32 9013 1684 3470 5285 7042 784CIP2D 32 9013 1685 3471 5287 7043 784CIP2D 34 9053 1686 3472 5288 7044 784CIP2D 34 9053 1686 3472 5288 7044 784CIP2D 34 9053 1687 3473 5289 7045 784CIP2D 34 9053 1689 3475 5261 7047 784CIP2D 36 9054 1689 3475 5261 7047 784CIP2D 37 9113 1690 3476 5262 7048 784CIP2D 37 9113 1690 3476 5262 7048 784CIP2D 39 9152 1691 3477 5263 7049 784CIP2D 39 9152 1692 3478 5264 7050 7046 784CIP2D 39 9152 1693 3478 5266 7050 784CIP2D 40 9152 1693 3479 5266 7051 784CIP2D 41 9211 1694 3480 5266 7052 784CIP2D 41 9221 1695 3481 5267 7053 784CIP2D 43 9223 1695 3481 5267 7053 784CIP2D 43 9223 1696 3482 5268 7054 784CIP2D 44 9231 1697 3483 5269 7055 784CIP2D 47 9303 1700 3486 5272 7056 784CIP2D 47 9303 1701 3489 5275 7057 784CIP2D 49 9314 1702 3488 5274 7060 784CIP2D 48 9309 1701 3489 5275 7061 784CIP2D 59 9314 1702 3498 5275 7062 784CIP2D 59 9314 1703 3489 5275 7063 784CIP2D 48 9309 1704 3490 5276 7062 784CIP2D 59 9316 1706 3491 5277 7063 784CIP2D 59 9314 1707 3439 5276 7062 784CIP2D 59 9314 1708 3491 5277 7063 784CIP2D 59 9314 1709 3495 5281 7067 784CIP2D 59 9314 1709 3495 5281 7067 784CIP2D 59 9314 1709 3495 5281 7067 784CIP2D 59 9314 1709 3495 5281 7067 784CIP2D 59 9326 1701 3497 5277 7063 784CIP2D 59 9493 1704 3490 5276 7062 784CIP2D 59 9493 1705 3491 5277 7063 784CIP2D 59 9493 1706 3496 5287 7069 784CIP2D 59 9493 1707 3493 5279 7063 784CIP2D 59 9493 1708 3499 5275 7061 784CIP2D 59 9493 1709 3495 5281 7067 784CIP2D 59 9493 1709 3495 5281 7067 784CIP2D 59 9493 1709 3495 5281 7067 784CIP2D 59 9493 1709 3495 5281 7069 784CIP2D 59 9493 1709 3495 5281 7069 784CIP2D 59 9493 1709 3495 5281 7069 784CIP2D 59 9493 1701 3496 5282 7068 784CIP2D 59 9493 1702 3498 5289 7079 784CIP2D 69 9564 1711 3503 5289 7099 784CIP2D 69 9564 1712 3508 5299 7068 784CIP2D 79 9499 1723 3509 5298 7091 784CIP2D 79 9499 1724 3	1677	3463	5249	7035		L
1680	1678	3464	5250			
1681   3467   5253   7039   784CHP2D_29   8951   1682   3468   5254   7040   784CHP2D_30   9007   1683   3469   5255   7041   784CHP2D_31   9012   1684   3470   5256   7042   784CHP2D_32   9013   1685   3471   5257   7043   784CHP2D_32   9013   1686   3472   5258   7044   784CHP2D_32   9053   1687   3473   5259   7045   784CHP2D_35   9054   1688   3474   5260   7046   784CHP2D_36   9054   1689   3475   5261   7047   784CHP2D_36   9054   1699   3475   5262   7048   784CHP2D_38   9134   1690   3476   5262   7048   784CHP2D_38   9134   1691   3477   5263   7049   784CHP2D_38   9134   1692   3478   5264   7050   784CHP2D_39   9152   1693   3479   5265   7051   784CHP2D_39   9152   1693   3479   5266   7051   784CHP2D_40   9152   1694   3480   5266   7051   784CHP2D_42   9223   1695   3481   5267   7053   784CHP2D_42   9223   1695   3481   5267   7053   784CHP2D_44   9223   1698   3464   5270   7056   784CHP2D_45   9236   1698   3464   5270   7056   784CHP2D_46   9236   1700   3466   5272   7058   784CHP2D_46   9236   1700   3468   5271   7057   784CHP2D_47   9303   1701   3487   5273   7059   784CHP2D_48   9309   1701   3487   5273   7059   784CHP2D_50   9314   1702   3489   5275   7061   784CHP2D_51   9319   1703   3489   5275   7061   784CHP2D_51   9319   1704   3490   5276   7062   784CHP2D_55   9316   1705   3491   5277   7063   784CHP2D_55   9316   1706   3492   5278   7066   784CHP2D_55   9316   1707   3493   5279   7065   784CHP2D_56   9326   1708   3499   5285   7071   784CHP2D_56   9356   1710   3496   5291   7067   784CHP2D_56   9551   1706   3492   5278   7066   784CHP2D_56   9551   1707   3493   5279   7065   784CHP2D_56   9551   1708   3499   5285   7071   784CHP2D_56   9551   1709   3495   5281   7067   784CHP2D_56   9551   1710   3496   5292   7068   784CHP2D_56   9551   1711   3500   5296   7072   784CHP2D_56   9568   1711   3500   5296   7071   784CHP2D_56   9551   1712   3498   5285   7071   784CHP2D_56   9556   1713   3500   5296   7077   784CHP2D_57   9459   1714   3500   5296   7077   784CHP2		3465				
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1683   3469   5255   7041   784CIP2D_31   9012     1684   3470   5256   7042   784CIP2D_32   9013     1685   3471   5257   7043   784CIP2D_33   9025     1686   3472   5258   7044   784CIP2D_33   9025     1687   3473   5259   7044   784CIP2D_35   9054     1688   3474   5259   7045   784CIP2D_35   9054     1689   3475   5261   7047   784CIP2D_36   9054     1689   3476   5262   7048   784CIP2D_36   9054     1690   3476   5262   7048   784CIP2D_37   9113     1690   3476   5262   7048   784CIP2D_38   9134     1691   3477   5263   7049   784CIP2D_38   9134     1692   3478   5264   7050   784CIP2D_39   9152     1693   3479   5265   7051   784CIP2D_40   9152     1693   3479   5266   7052   784CIP2D_40   9152     1694   3480   5266   7052   784CIP2D_42   9223     1695   3481   5267   7053   784CIP2D_42   9223     1697   3483   5265   7051   784CIP2D_44   9221     1697   3483   5265   7054   784CIP2D_44   9231     1698   3464   5270   7056   784CIP2D_45   9236     1699   3485   5271   7057   784CIP2D_48   9309     1700   3486   5272   7058   784CIP2D_48   9309     1701   3487   5275   7061   784CIP2D_51   9314     1702   3489   5274   7060   784CIP2D_51   9314     1703   3499   5275   7061   784CIP2D_52   9348     1705   3491   5277   7063   784CIP2D_52   9348     1706   3492   5278   7064   784CIP2D_55   9346     1708   3494   5280   7066   784CIP2D_55   9347     1708   3494   5280   7066   784CIP2D_55   9491     1709   3495   5281   7067   784CIP2D_56   9414     1709   3495   5281   7067   784CIP2D_56   9414     1709   3495   5281   7067   784CIP2D_56   9419     1710   3496   5282   7068   784CIP2D_56   9419     1711   3497   5283   7069   784CIP2D_56   9459     1712   3498   5280   7066   784CIP2D_56   9419     1713   3499   5265   7071   784CIP2D_56   9551     1716   3502   5288   7075   784CIP2D_56   9551     1716   3502   5288   7077   784CIP2D_56   9551     1716   3503   5287   7073   784CIP2D_56   9551     1716   3505   5291   7077   784CIP2D_56   9557     1720   3506   5292   7078   784CIP2D_76   9759     1721						
1684 3470 5256 7042 784CIP2D_32 9013 1685 3471 5257 7043 784CIP2D_34 9053 1686 3472 5258 7044 784CIP2D_34 9053 1687 3473 5258 7045 784CIP2D_35 9054 1688 3474 5250 7046 784CIP2D_35 9054 1689 3475 5261 7047 784CIP2D_37 9113 1690 3476 5262 7048 784CIP2D_37 9113 1691 3477 5263 7049 784CIP2D_38 9134 1691 3477 5263 7049 784CIP2D_38 9134 1691 3477 5263 7049 784CIP2D_39 9152 1692 3478 5264 7050 784CIP2D_40 91.52 1693 3479 5265 7051 784CIP2D_40 91.52 1693 3479 5266 7052 784CIP2D_42 9221 1694 3460 5266 7052 784CIP2D_42 9221 1695 3481 5267 7053 784CIP2D_43 9221 1696 3482 5268 7055 784CIP2D_43 9223 1696 3482 5268 7055 784CIP2D_44 9231 1697 3483 5269 7055 784CIP2D_45 9236 1699 3485 5271 7057 784CIP2D_46 9330 1700 3486 5272 7056 784CIP2D_46 9314 1700 3486 5272 7056 784CIP2D_48 9309 1701 3487 5273 7059 784CIP2D_48 9309 1701 3487 5273 7059 784CIP2D_48 9314 1702 3488 5274 7060 784CIP2D_59 9314 1703 3489 5275 7061 784CIP2D_59 9314 1705 3491 5277 7063 784CIP2D_59 9339 1704 3490 5276 7062 784CIP2D_59 9314 1705 3491 5277 7063 784CIP2D_59 9314 1706 3496 5278 7066 784CIP2D_59 9314 1707 3493 5276 7062 784CIP2D_59 9314 1708 3494 5280 7066 784CIP2D_56 9326 1709 3495 5281 7067 784CIP2D_56 9316 1709 3495 5281 7067 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_56 9511 1711 3497 5283 7069 784CIP2D_56 9511 1712 3498 5284 7070 784CIP2D_56 9551 1714 3500 5286 7072 784CIP2D_56 9568 1714 3500 5286 7072 784CIP2D_56 9561 1715 3501 5287 7073 784CIP2D_59 9493 1710 3496 5292 7078 784CIP2D_56 9561 1711 3503 5287 7073 784CIP2D_59 9493 1712 3498 5284 7070 784CIP2D_56 9561 1713 3599 5285 7071 784CIP2D_57 9493 1710 3496 5282 7068 784CIP2D_56 9568 1711 3503 5287 7073 784CIP2D_56 9568 1712 3503 5289 7075 784CIP2D_57 9493 1713 3509 5296 7081 784CIP2D_57 9493 1710 3506 5292 7078 784CIP2D_57 9493 1711 3503 5289 7079 784CIP2D_59 9493 1712 3509 5295 7081 784CIP2D_59 9493 1713 3509 5295 7081 784CIP2D_79 9649 1725 3511					L	
1685   3471   5257   7043   784CIP2D_33   9025     1686   3472   5258   7044   784CIP2D_34   9053     1687   3473   5259   7045   784CIP2D_35   9054     1688   3474   5260   7046   784CIP2D_36   9054     1688   3474   5260   7046   784CIP2D_36   9054     1689   3475   5261   7047   784CIP2D_37     1690   3476   5262   7048   784CIP2D_37   9113     1690   3476   5262   7048   784CIP2D_39   9135     1691   3477   5263   7049   784CIP2D_39   9135     1692   3478   5264   7050   784CIP2D_40   9152     1693   3479   5265   7051   784CIP2D_40   9152     1693   3479   5265   7051   784CIP2D_41   9211     1694   3480   5266   7052   784CIP2D_41   9221     1695   3481   5267   7053   784CIP2D_41   9223     1695   3481   5267   7053   784CIP2D_44   9231     1697   3483   5269   7055   784CIP2D_44   9231     1698   3484   5270   7056   784CIP2D_46   9236     1699   3485   5271   7057   784CIP2D_46   9236     1699   3486   5272   7058   784CIP2D_48   9309     1700   3486   5272   7058   784CIP2D_48   9309     1701   3487   5273   7059   784CIP2D_50   9314     1702   3488   5274   7060   784CIP2D_50   9326     1703   3489   5275   7061   784CIP2D_50   9326     1704   3490   5276   7062   784CIP2D_51   9339     1706   3491   5277   7063   784CIP2D_52   9348     1707   3493   5279   7063   784CIP2D_52   9348     1708   3494   5280   7066   784CIP2D_53   9349     1709   3495   5281   7067   784CIP2D_56   9341     1709   3495   5281   7067   784CIP2D_56   9341     1709   3495   5281   7067   784CIP2D_56   9341     1701   3496   5282   7068   784CIP2D_56   9341     1702   3498   5279   7063   784CIP2D_56   9341     1703   3499   5275   7061   784CIP2D_56   9341     1704   3496   5282   7068   784CIP2D_56   9359     1705   3491   5277   7063   784CIP2D_56   9348     1707   3493   5285   7071   784CIP2D_57   9359     1708   3494   5280   7066   784CIP2D_56   9359     1709   3495   5281   7067   784CIP2D_56   9359     1710   3496   5292   7078   784CIP2D_56   9359     1711   3503   5295   7061   784CIP2D_56   9359     1712   3506					, <u> </u>	
1686   3472   5258   7044   784CIP2D 34   9053     1687   3473   5259   7045   784CIP2D 35   9054     1688   3474   5265   7046   784CIP2D 36   9054     1689   3475   5261   7047   784CIP2D 37   9054     1689   3476   5262   7048   784CIP2D 37   9113     1690   3476   5262   7048   784CIP2D 38   9134     1691   3477   5263   7049   784CIP2D 38   9134     1691   3477   5263   7049   784CIP2D 39   9152     1692   3478   5264   7050   784CIP2D 40   9152     1693   3479   5265   7051   784CIP2D 41   9221     1694   3480   5266   7052   784CIP2D 42   9223     1695   3481   5267   7053   784CIP2D 42   9223     1696   3482   5268   7054   784CIP2D 44   9231     1697   3483   5269   7055   784CIP2D 45   9236     1699   3484   5270   7056   784CIP2D 45   9236     1699   3484   5270   7056   784CIP2D 47   9303     1700   3486   5272   7058   784CIP2D 48   9309     1701   3487   5273   7059   784CIP2D 49   9314     1702   3488   5274   7060   784CIP2D 50   9326     1703   3489   5275   7061   784CIP2D 50   9326     1704   3490   5276   7062   784CIP2D 50   9326     1706   3492   5278   7061   784CIP2D 51   9339     1706   3492   5278   7064   784CIP2D 53   9376     1707   3438   5279   7065   784CIP2D 51   9382     1708   3494   5280   7066   784CIP2D 54   9382     1709   3495   5281   7067   784CIP2D 59   9438     1701   3487   5279   7063   784CIP2D 59   9346     1707   3439   5279   7065   784CIP2D 59   9349     1708   3494   5280   7066   784CIP2D 54   9382     1709   3495   5281   7067   784CIP2D 56   9316     1701   3498   5282   7068   784CIP2D 56   9316     1703   3498   5282   7068   784CIP2D 66   9581     1701   3498   5282   7068   784CIP2D 66   9581     1701   3498   5282   7068   784CIP2D 66   9581     1703   3500   5286   7072   784CIP2D 66   9581     1703   3500   5286   7072   784CIP2D 66   9581     1703   3500   5286   7072   784CIP2D 66   9588     1703   3500   5290   7076   784CIP2D 66   9588     1708   3500   5290   7076   784CIP2D 67     1728   3510   5290   7066   784CIP2D 70   9669     1726   3512		l				
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1696 3482 5268 7054 784CIP2D_44 9231 1697 3483 5269 7055 784CIP2D_45 9236 1698 3484 5270 7056 784CIP2D_46 9236 1699 3485 5271 7057 784CIP2D_47 9303 1700 3486 5272 7058 784CIP2D_48 9309 1701 3487 5273 7059 784CIP2D_48 9309 1702 3488 5274 7060 784CIP2D_49 9314 1702 3488 5274 7060 784CIP2D_50 9326 1703 3489 5274 7060 784CIP2D_50 9326 1703 3489 5275 7061 784CIP2D_51 9339 1704 3490 5276 7062 784CIP2D_51 9339 1705 3491 5277 7063 784CIP2D_53 9376 1706 3492 5278 7064 784CIP2D_53 9376 1707 3493 5279 7065 784CIP2D_54 9382 1708 3494 5280 7066 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_56 9414 1709 3495 5281 7067 784CIP2D_57 9439 1710 3496 5282 7068 784CIP2D_59 9493 1711 3497 5283 7069 784CIP2D_59 9493 1712 3498 5284 7070 784CIP2D_59 9493 1713 3499 5285 7071 784CIP2D_60 9501 1714 3500 5286 7072 784CIP2D_62 9526 1715 3501 5287 7073 784CIP2D_63 9551 1716 3502 5288 7073 784CIP2D_63 9551 1716 3502 5288 7073 784CIP2D_66 9511 1718 3504 5290 7076 784CIP2D_66 9588 1719 3505 5291 7077 784CIP2D_66 9588 1719 3505 5291 7077 784CIP2D_66 9588 1719 3505 5291 7077 784CIP2D_66 9588 1719 3505 5291 7077 784CIP2D_66 9588 1719 3505 5291 7077 784CIP2D_66 9588 1719 3505 5291 7077 784CIP2D_66 9588 1719 3507 5289 7075 784CIP2D_66 9588 1719 3507 5289 7076 784CIP2D_66 9588 1719 3507 5289 7077 784CIP2D_66 9588 1719 3507 5289 7078 784CIP2D_66 9588 1719 3507 5293 7079 784CIP2D_66 9588 1719 3507 5293 7079 784CIP2D_66 9588 1719 3507 5293 7079 784CIP2D_66 9588 1719 3507 5293 7079 784CIP2D_67 9597 1720 3506 5292 7078 784CIP2D_67 9597 1721 3507 5293 7079 784CIP2D_67 9527 1722 3508 5294 7080 784CIP2D_70 9649 1723 3509 5296 7082 784CIP2D_70 9649 1724 3510 5296 7082 784CIP2D_70 9649 1725 3511 5297 7083 784CIP2D_70 9649 1726 3514 5300 7086 784CIP2D_77 9787 1729 3515 5301 7087 784CIP2D_70 9649 1729 3515 5301 7087 784CIP2D_70 9649 1729 3515 5301 7087 784CIP2D_70 9649 1731 3516 5302 7088 784CIP2D_70 9642 1732 3518 5301 7087 784CIP2D_70 9787						
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1699 3485 5271 7057 784CIF2D 47 9303 1700 3486 5272 7058 784CIF2D 48 9309 1701 3487 5273 7059 784CIF2D 48 9309 1701 3487 5273 7059 784CIF2D 49 9314 1702 3488 5274 7060 784CIF2D 50 9326 1703 3489 5275 7061 784CIF2D 51 9339 1704 3490 5276 7062 784CIF2D 52 9348 1705 3491 5277 7063 784CIF2D 53 9376 1706 3492 5278 7064 784CIF2D 53 9376 1707 3493 5279 7065 784CIF2D 55 9407 1708 3494 5280 7066 784CIF2D 55 9407 1709 3495 5281 7067 784CIF2D 57 9414 1709 3496 5282 7068 784CIF2D 57 9439 1710 3496 5282 7068 784CIF2D 59 9493 1711 3497 5283 7069 784CIF2D 59 9493 1712 3498 5284 7070 784CIF2D 60 9501 1713 3499 5285 7071 784CIF2D 61 9526 1714 3500 5286 7072 784CIF2D 61 9526 1716 3501 5287 7073 784CIF2D 62 9526 1716 3502 5288 7074 784CIF2D 63 9551 1716 3502 5289 7075 784CIF2D 64 9557 1717 3503 5289 7075 784CIF2D 64 9557 1718 3504 5290 7076 784CIF2D 66 9588 1719 3505 5291 7077 784CIF2D 64 9557 1710 3506 5292 7078 784CIF2D 69 9591 1712 3508 5294 7079 784CIF2D 69 9591 1712 3508 5297 7073 784CIF2D 66 9588 1718 3501 5287 7073 784CIF2D 64 9557 1716 3502 5288 7074 784CIF2D 64 9557 1717 3503 5289 7075 784CIF2D 64 9557 1718 3501 5287 7073 784CIF2D 64 9557 1719 3505 5291 7077 784CIF2D 66 9588 1719 3505 5291 7077 784CIF2D 68 9615 1720 3506 5292 7078 784CIF2D 69 9628 1721 3507 5293 7079 784CIF2D 69 9628 1722 3508 5294 7080 784CIF2D 70 9649 1723 3509 5295 7081 784CIF2D 71 9652 1724 3510 5296 7082 784CIF2D 72 9660 1725 3511 5297 7083 784CIF2D 73 9662 1726 3512 5298 7084 784CIF2D 71 9652 1727 3513 5299 7085 784CIF2D 73 9662 1728 3514 5300 7086 784CIF2D 75 9746 1728 3515 5301 7087 784CIF2D 79 9746						
1700   3486   5272   7058   784CIP2D_48   9309   1701   3487   5273   7059   784CIP2D_49   9314   1702   3488   5274   7060   784CIP2D_50   9326   1703   3489   5275   7061   784CIP2D_51   9339   1704   3490   5276   7062   784CIP2D_52   9348   1705   3491   5277   7063   784CIP2D_52   9348   1706   3492   5278   7064   784CIP2D_54   9382   1707   3493   5279   7065   784CIP2D_54   9382   1707   3493   5279   7065   784CIP2D_55   9407   1708   3494   5280   7066   784CIP2D_55   9414   1709   3495   5281   7067   784CIP2D_57   9419   1710   3496   5282   7068   784CIP2D_58   9485   1711   3497   5283   7069   784CIP2D_59   9493   1712   3498   5284   7070   784CIP2D_60   9501   1713   3499   5285   7071   784CIP2D_60   9501   1714   3500   5286   7072   784CIP2D_60   9501   1715   3501   5287   7073   784CIP2D_62   9526   1716   3502   5288   7074   784CIP2D_64   9557   1716   3503   5289   7075   784CIP2D_66   9588   1718   3504   5290   7076   784CIP2D_66   9588   1718   3504   5290   7076   784CIP2D_66   9588   1718   3504   5290   7076   784CIP2D_66   9588   1712   3506   5292   7078   784CIP2D_66   9587   1720   3506   5292   7078   784CIP2D_68   9628   1722   3508   5294   7080   784CIP2D_68   9628   1722   3508   5294   7080   784CIP2D_68   9628   1724   3510   5297   7079   784CIP2D_68   9628   1724   3510   5297   7078   784CIP2D_69   9628   1724   3510   5295   7081   784CIP2D_79   9649   1724   3510   5296   7082   784CIP2D_79   9652   1724   3510   5296   7082   784CIP2D_79   9652   1724   3510   5296   7082   784CIP2D_79   9652   1724   3510   5296   7082   784CIP2D_79   9660   1725   3511   5297   7083   784CIP2D_79   9662   1725   3511   5297   7083   784CIP2D_79   9746   1728   3515   5301   7087   784CIP2D_79   9746   1728   3515   5301   7087   784CIP2D_79   9746   1728   3515   5301   7087   784CIP2D_79   9746   1728   3515   5301   7087   784CIP2D_79   9746   1728   3515   5301   7087   784CIP2D_79   9746   1728   3515   5301   7087   784CIP2D_79   9746   1729   3515   5301   7087   784CIP2		L			·	
1701         3487         5273         7059         784CIP2D_49         9314           1702         3488         5274         7060         784CIP2D_50         9326           1703         3489         5275         7061         784CIP2D_51         9339           1704         3490         5276         7062         784CIP2D_52         9348           1705         3491         5277         7063         784CIP2D_53         9376           1706         3492         5278         7064         784CIP2D_54         9382           1707         3493         5279         7065         784CIP2D_55         9407           1708         3494         5280         7066         784CIP2D_56         9414           1709         3495         5281         7067         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_59         9493           1711         3498         5284         7070         784CIP2D_59         9493           1711         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526			·			
1702         3488         5274         7060         784CIP2D_50         9326           1703         3499         5275         7061         784CIP2D_51         9339           1704         3490         5276         7062         784CIP2D_52         9348           1705         3491         5277         7063         784CIP2D_53         9376           1706         3492         5278         7064         784CIP2D_54         9382           1707         3493         5279         7065         784CIP2D_55         9407           1708         3494         5280         7066         784CIP2D_56         9414           1709         3495         5281         7067         784CIP2D_56         9414           1709         3495         5281         7067         784CIP2D_58         9485           1711         3496         5282         7068         784CIP2D_59         9493           1712         3498         5283         7069         784CIP2D_59         9493           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501						
1703         3489         5275         7061         784CIP2D_51         9339           1704         3490         5276         7062         784CIP2D_52         9348           1705         3491         5277         7063         784CIP2D_53         9376           1706         3492         5278         7064         784CIP2D_54         9382           1707         3493         5279         7065         784CIP2D_55         9407           1708         3494         5280         7066         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_57         9439           1711         3496         5282         7068         784CIP2D_59         9433           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526			1	1		
1704         3490         5276         7062         784CIP2D_52         9348           1705         3491         5277         7063         784CIP2D_54         9376           1706         3492         5278         7064         784CIP2D_54         9382           1707         3493         5279         7065         784CIP2D_55         9407           1708         3494         5280         7066         784CIP2D_55         9414           1709         3495         5281         7067         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_59         9431           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_61         9526           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1717         3503         5289         7074         784CIP2D_66         9588						
1705         3491         5277         7063         784CIP2D_53         9376           1706         3492         5278         7064         784CIP2D_54         9382           1707         3493         5279         7065         784CIP2D_55         9407           1708         3494         5280         7066         784CIP2D_56         9414           1709         3495         5281         7067         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_58         9485           1711         3496         5282         7068         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9588	l	I				
1706         3492         5278         7064         784CIP2D_54         9382           1707         3493         5279         7065         784CIP2D_55         9407           1708         3494         5280         7066         784CIP2D_56         9414           1709         3495         5281         7067         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_58         9485           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9588           1718         3504         5290         7076         784CIP2D_67         9597		<u> </u>		* *		1
1707         3493         5279         7065         784CIP2D_55         9407           1708         3494         5280         7066         784CIP2D_56         9414           1709         3495         5281         7067         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_58         9485           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9588           1719         3505         5291         7077         784CIP2D_66         9588           1719         3506         5292         7078         784CIP2D_68         9615		I	L			
1708         3494         5280         7066         784CIP2D_56         9414           1709         3495         5281         7067         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_58         9485           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_66         9587           1720         3506         5292         7078         784CIP2D_68         9615						
1709         3495         5281         7067         784CIP2D_57         9439           1710         3496         5282         7068         784CIP2D_58         9485           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_65         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_70         9649						
1710         3496         5282         7068         784CIP2D_58         9485           1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649						
1711         3497         5283         7069         784CIP2D_59         9493           1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_65         958           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_66         9588           1719         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652				1		
1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_66         9588           1719         3506         5292         7078         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652			l	7069	784CIP2D 59	9493
1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5296         7081         784CIP2D_70         9652           1724         3510         5296         7082         784CIP2D_72         9660	l			l	784CIP2D 60	9501
1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_68         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725				1		9526
1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_68         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746		3500		7072	784CIP2D_62	9526
1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_70         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1730         3516         5302         7088         784CIP2D_77         9787		3501	5287	7073	784CIP2D_63	9551
1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787	1716	3502	5288	7074	784CIP2D_64	9557
1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842	1717	3503	5289	7075	784CIP2D_65	9568
1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842	1718	3504	5290	7076	784CIP2D_66	9588
1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5296         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842	1719	3505	5291	7077	784CIP2D_67	9597
1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842	1720	3506	5292	7078	784CIP2D_68	9615
1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842	1721	3507	5293	7079		
1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842	1722	3508	5294	7080	784CIP2D_70	9649
1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842	1723	3509	5295	7081	784CIP2D_71	9652
1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842	1724	3510	5296	7082	784CIP2D_72	9660
1727         3513         5299         7085         784CIP2D 75         9746           1728         3514         5300         7086         784CIP2D 76         9777           1729         3515         5301         7087         784CIP2D 77         9787           1730         3516         5302         7088         784CIP2D 78         9790           1731         3517         5303         7089         784CIP2D 79         9842           1732         3518         5304         7090         784CIP2D 80         9842	1725	3511	5297	7083	784CIP2D_73	9662
1728         3514         5300         7086         784CIP2D 76         9777           1729         3515         5301         7087         784CIP2D 77         9787           1730         3516         5302         7088         784CIP2D 78         9790           1731         3517         5303         7089         784CIP2D 79         9842           1732         3518         5304         7090         784CIP2D 80         9842	1726	3512	5298	7084	784CIP2D_74	9725
1729         3515         5301         7087         784CIP2D 77         9787           1730         3516         5302         7088         784CIP2D 78         9790           1731         3517         5303         7089         784CIP2D 79         9842           1732         3518         5304         7090         784CIP2D 80         9842	1727	3513	5299	7085	784CIP2D_75	9746
1730         3516         5302         7088         784CIP2D 78         9790           1731         3517         5303         7089         784CIP2D 79         9842           1732         3518         5304         7090         784CIP2D_80         9842	1728	3514	5300	7086	784CIP2D_76	9777
1731 3517 5303 7089 784CIP2D 79 9842 1732 3518 5304 7090 784CIP2D_80 9842	1729	3515 .	5301	7087	784CIP2D_77	9787
1732 3518 5304 7090 784CIP2D_80 9842	1730	3516	5302	7088	784CIP2D_78	9790
	1731	3517	5303	7089	784CIP2D_79	9842
1733 3519 5305 7091 784CIP2D_81 9848	1732	3518	5304	7090	784CIP2D_80	9842
	1733	3519	5305	7091	784CIP2D_81	9848

SEO ID NO:	I SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	Jequence	sequence	priority	09/900,725
	sequence	i	Doquedoo	application	ł
1734	3520	5306	7092	784CIP2D 82	9867
1735	3521	5307	7093	784CIP2D 83	10010
1736	3522	5308	7094	784CIP2D 84	10011
1737	3523	5309	7095	784CIP2D 85	10052
1738	3524	5310	7096	784CIP2D 86	10057
1739	3525	5311	7097	784CIP2D 87	10085
1740	3526	5312	7098	784CIP2D 89	10139
1741	3527	5313	7099	784CIP2D 90	10142
1742	3528	5314	7100	784CIP2D 92	10165
1743	3529	5315	7101	784CIP2D 93	10173
1744	3530	5316	7102	784CIP2D 94	10173
1745	3531	5317	7103	784CIP2D 95	10273
1746	3532	5318	7104	784CIP2B 1	3121
1747	3533	5319	7105	784CIP2B 2	3628
1748	3534	5320	7106	784CIP2B 4	3673
1749	3535	5321	7107	784CIP2E 5	4018
1750	3536	5322	7108	784CIP2E 6	4467
1751	3537	5323	7109	784CIP2E 7	4865
1752	3538	5324	7110	784CIP2E 8	4916
1753	3539	5325	7111	784CIPZE 9	4923
1754	3540	5326	7112	784CIP2B 10	4926
1755	3541	5327	7113	784CIP2B 11	4962
1756	3542	5328	7114	784CIP2R 12	4963
1757	3543	5329	7115	784CIP2B 13	4964
1758	3544	5330	7116	784CIP2B 14	4988
1759	3545	5331	7117	784CIP2B 15	5835
1760	3546	5332	7118	784CIP2B 16	7682
1761	3547	5333	7119	784CIP2B 17	7682
1762	3548	5334	7120	784CIP2B_18	7699
1763	3549 ,	5335	7121	784CIP2E 19	7707
1764	3550	5336	7122	784CIP2E 20	7707
1765	3551	5337	7123	784CIP2E_21	7752
1766	3552	5338	7124	784CIP2E_22	8357
1767	3553	5339	7125	784CIP2E_23	9065
1768	3554	5340	7126	784CIP2B_24	9324
1769	3555	5341	7127	784CIP2P_1	2976
1770	3556	5342	7128	784CIP2F_2	3559
1771	3557	5343	7129	784CIP2F_3	4021
1772	3558	5344	7130	784CIP2F_4	4474
1773	3559	5345	7131	784CIP2F_5	4566
1774	3560	5346	7132	784CIP2F_6	4705
1775	3561	5347	7133	784CIP2F_7	4707
1776	3562	5348	7134	784CIP2F_8	4712
1777	3563	5349	7135	784CIP2F_9	5008
1778	3564	5350	7136	784CIP2F_10	5009
1779	3565	5351	7137	784CIP2F_11	5015
1780	3566	5352	7138	784CIP2F_12	5015
1781	3567	5353	7139	784CIP2F_13	7724
1782	3568	5354	7140	784CIP2F_14	7725
1783	3569	5355	7141	784CIP2F_15	8828
1784	3570	5356	7142	784CIP2F_16	8830
1785	3571	5357	7143	784CIP2F_17	9739
1786	3572	5358	7144	784CIP2F_18	9896

TRADOCS:1416247.1(%CS7011.DOC)

TABLE 7

	DLE /		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location		H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	
]	corresponding	to first	L-Leucine; M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1			
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	sequence		\=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPG
3333	1 33,	1	
1	ŀ	1	BTVYYSVEYQGEYESLYTSHIWIPSSNCSLTEGPECDVTDDITA
í			TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
1	Į.		TKDGFHLVIBLEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
t		1	VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
1	ł	i	
]	}	)	VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW
	•	ì	KITQF
5360	2	1115	PRVRSSGCQRDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
1 3300	1 -	1	
1	1	ĺ	CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
}	ì	ł	SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
	İ	1	FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
i .	}	<b>1</b>	VVLPTGDVWSRPDGSYLNKLLITRARQDDAGNYICLGANTMGYS
i	i	<b>f</b>	·-
1	1	j.	FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
1	1	Į	GTLLLWLCQAQKKPCTPAPAPPLPGHR?PGTARDRSGDKDLPSL
1	<b>!</b>		AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS
	1	I .	TPHTYTHPPPSCOLNSSHS
E2.53	<del></del>	000	
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
I			SSKELWYMPEBYIRQGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
1		1	PKHIQLROLLRELMEKRGLDSCLSPLDKKVPPCPRNFSAKLFCL
1		}	AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
[		ſ .	
i	ľ	ł	PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPPEC
1			SQSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSQD
1	<b>!</b>		LRPYKVNIDPSSEAPGHSCRSRPVBSSCSSKFSWDEYEQYKKE
5362	2	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQXA
3302	1 -	1 .0,,	
I	1	}	NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
)			VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ
1			MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSL?AESSSIDL
•	{	[	FPSPADSGTNSVPSQLENNTNHYSSQIEGNTNSSFLKGGNGENA
1		i	VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
	1		
i .	ţ		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
1 .	j		EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
	· ·		PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
ŀ	<u> </u>		ETAGIPSTPEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
	1		
1			TVCHPNTLLINQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
1			GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
1			ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH
;			SNVIPTCEPOSLVENLTOKLANVNNOLFMIDVKENFKISLESHT
1			
i '	1		VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISHDNVIQNFEKT
1			LEIIKTAMNSQILEVKSG9QGAGETSQNAQINYNIQLPSVNTVQ
1			NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
I			QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
1			MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPR
i			
1	•		MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT
1			EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTBENKKESQ
] .			PALELRAETONTHSNVAVIPEKOLIEKKSPDKTESSLQVITVTS
Į l	l i		BOCNTNALTNTOTKGRKIRRHKKEKBEKKRKKPVSOSLEFPTRY
i	l l		
			SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAKVEE
į į			ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
1	i i		HEMTPEEIESMTASVDVGKFPCDQLECKSSFTTYLNYVVHLRAD
1	}		HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
[			HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
1			KMPKTKRKKKNNLENKNAKIVQIBENKPYSLKRGKHVYSIKARN
1	[ i		DALSECTSRFVTQYPCMIKGCTSVVTSBSNIIRHYKCHKLSKAF
1			
l I	!		TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND
	}		NSRTIATVSQKEVBKNE*DEMDELTELFITKLINEDSTSVBTQA
]			NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE
1	,		Karpasaaelssvrkeetavaiqtiebiipasfdwssfkpmgpe
1			VSFLKFLERSAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV
1 1			TSGNHVCPCKESETFVQFANPSQLQCSDNVKIVLDKNLKDCTEL
			·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid. B=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
í	residue of	amino acid -	W=Tryptophan, Y=Tyrcsine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1			PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLMML
1			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
1			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1'			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGBWT
			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
1		•	ITCTSRNRCNDODTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
1			EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
( )			DSGVVYSVGMQLA+KTQGNKQML\CTCLGNGVSCQBTAVTOTYG
		9	GNSNGEPCVLPFTYNGRTFYSCTTEGRODGHLWCSTTSNYEODO
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
			DNMKWCGTTQNYDADQKFGFCPMAAHERICTTNEGVMYRIGDOW
			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1			DTFHKRHEEGHMLNCTCPGQGRGRWKCDPVDQCQDSETGTPYQI
1			GDSWEKYVHGVRYQCYCYGRGIGBWHCQPLQTYPSSSGPVEVPI
			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQKVTRFDFTTTSTST
			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1		•	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1 - 1			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
•			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
} ;			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AKN
			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1		•	ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
]			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1 1		•	TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1 1			LEANPOTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1		•	HADOSSCTF\DNLEVPGLEYNVSVYTVKDDKESVP1SDT11PAV
] ]			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNB
1 1			GRMLQSLSIPPLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1 1			\LEGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
i i			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLINLTPGTEYVV
1 1			SIVALNGRRESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1 1			APAVTVRYYRITYGETGGNSFVQEFTVPGSKSTATISGLKPGVD
1 1	1		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSOMQVTDVQDNS
1 1	j		ISVKNLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
[ ]			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
[			BLQGLRPGSEYTVSVVALHDDMRSOPLIGTOSTAIPAPTDLKFT
1	Ì		QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKKINLAPDGS
1 1			SVVVSGLMVATKYEVSVYALKDTLTSRPAGGVVTTLENVSPPRR
] }	1		ARVIDATETTITISWRIKTETITGFQVDAVPANGOTPIQRITKP
			DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1 1			NLRFLATTPNSLLVSWOP?RARITGYIIKYEKPGSPPREVVPRP
-			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
	i		QLVTLPHPNLHGPRILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1 1			SGQQPSVGQQMIFERHGFRRTTPPTTATPIRHRPRPYPPNVGOR
1 1		ł	ALSQTTISWAPFQDTSEYIISCHPVGTDBEPLQFRVPGTSTSAT
1	}		LTGLTRGATYNIIVEALKDOORHKVREEVVTVGNSVNEGLNOPT
1	ì		DDSCFDPYTVSHYAVGDEWERMSESGFKLLCOCLGFGSGHFRCD
] [			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
<b>!</b> [			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
	i		RPGGBPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVO
			ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
	,-	, •••	PPSWRRQPPGGIRRDFSRRLRRBANLVATCLPVRASLPHRLNML
	į	1	RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
			THE PERSON NAMED AND ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATION OF THE PERSON NAMED ASSOCIATI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
TD.	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid residue of	P-Proline, Q-Glutamine, R-Arginine,
1	residue of	amino acid	S-Serine, T-Threonine, V-Valine,
l	amino acid	sednence	W-Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
i	sequence	acquence	\=possible nucleotide insertion)
			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
	ľ		PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
f	ĺ		CTLANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
1	ł		ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
ł			BWKCERHTSVOTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
ſ		•	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
Ĭ.			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
			KYSPCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1			DNMKWCGTTQNYDADQKFGFCPMAAH3EICTTNEGVMYRIGDQW
1	j		DKQHDMGHMMRCTCVGNGRGEWTC1AYSQLRDQCIVDDITYNVN
	. :		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
	ł		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
	•	•	GHLNSYTIKGLKPGVVYBGQLISIQQYGHQEVTRFDFTTTSTST
l .			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVEWVSASDTV
ł			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
			VYQISEDCEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRNSR
			PQAPITGYRIVYSPSVEGSSTBLNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNOESPKATGVFTTLOPGSSIPPYN
			TEVTETTIVITWTPAPRIGFKLGVRPSQGGBAPREVTSDSGSIV
			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
			LEANPOTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
			PPPTDLRFTN/IIGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
	•		GRMLQSLSIFFLSDN\AVVLTNLLPGTZYVVSVSSVYEQHESTP
	•		\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1 :			YTITVYAVTGRGDSPASSKPISINYRTRIDKPSQMQVTDVQDNS
1			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1			EGLOPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAPTDV
			DVDSIKIAWESPQGQVSRYRVTYSSPRDGIHELFPAPDGREDTA
1			BLQGLRPGSEYTVSVVALHDDMBSQPLIGTQSTAIPAPTDLKFT
			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKBINLAPDSS
			SVVVSGLMVATKYBVSVYALXDTLTSRPAQGVVTTLENVSPPRR
			ARVIDATETTITISWRTKTETITGPQVDAVPANGQTPIQRTIKP
	1		DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTFNSLLVSWOPPRARITGYIIKYEKPGSPPREVVPRP
4	1		RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
<u> </u>			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
	]		SGQQPSVGQQMIFEEHGPRRTTPPTTATPIRHRPRPYPPNVGQB
-	·		ALSOTTISWAPFODTSEYIISCHPVGTDBEPLQFRVPGTSTSAT
			LTGLTRGATYNIIVEALKDQQRHKVRBEVVTVGNSVNEGLNQPT
			DDSCPDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHPRCD
1	1	1	SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
)			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
5365	9066	702	ADREDSRE
2305	8066	703	RICCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
	ĺ		PPSWRRQPPGGTRRDFSRRLRREANLVATCLPVRASLPHRLNMI.
1 1		}	RGFGFGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK
1	ľ	i	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
	1		CTIANRCHEGGQSYKIGDTWRRPHRTGGYMLECVCLGNGKGEWT
]			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVVDCTCLGEGSGR
·			

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No: nucleotide corresponding to first amino acid residue of maino acid residue of maino acid residue of maino acid seduce of maino acid	SEQ	Predicted	Predicted end	
corresponding to first amino acid residue of mino acid residue of mino acid amino acid sequence sequen	1			
to first amino acid residue of seidu	NO:			
amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acquence  ###TYPEOphan, Y=TyTosine, X=Unknom, *=Stop Codon, /=possible mucleotide delction)  ####TYPEOphan, Y=TyTosine, X=Unknom, *=Stop Codon, /=possible mucleotide delction  #####TYPEOphan, Y=TyTosine, X=Unknom, *=Stop Codon, /=possible mucleotide delction  ####TYPEOphan, Y=TyTosine, X=Unknom, *=Stop BMCREHTSVOTTSGSCSPFTUVAPAVYOOPHROPPYCHTOT GRINGSPCVIPTYTHORTCRYSCTTBGRQDGHMCGTYTOTTGGG GRINGSPCVIPTYTHORTCRYSCTTBGRQDGHMCGTYTOTTGGG REGISTER DEMCACES TO THE TIME	}	1		•
### amino acid	1			
maino acid gequence    Marthyptophan, Y-Tyxosine, X-Unknown, *=Stop   Codon, '-possible mucleotide delction,   Apossible mucleotide delction,   Apossible mucleotide delction,   Apossible mucleotide delction,   Trissencoportess'(Elightessempsella/Clictosese   BRKCREHTSVOTTSGSSOPTIVES/REGITOSEKOMSSEMS/CSCPTAVYCOTG   GENGEBCVLPFTYNGRTCFSSCTTSBRQDGHMCGTTSNTEGDO   KYSCTCHTWIAUTRGSSNSQALCHFPET/KHRHTYDCTSBRQDGHMCGTTONTDDQRFGCTWAAAWS(GCPTAVYCOTG)   GENGEBCVLPFTYNGRTCFSSCTTSBRQDGHMCGTTSNTEGDO   KYSCTCHTWIAUTRGSSNSQALCHFPET/KHRHTYDCTSBQDG   KYSCTCHTWIAUTRGSSNSQALCHFPET/KHRHTYDCTSBQDG   KYSCTCHTWIAUTRGSSNSQALCHFPET/KHRHTYDCTSBQDG   KYSCTCHTWIAUTRGSNSQALCHFPET/KHRHTYDCTSBQDG   KYSCTCHTWIAUTRGSNSQALCHFPET/KHRHTYDCTSCNSQATTSNTEGDO   KYSCTCHTWIAUTRGSNSQALCHFPET/KHRHTYDCTSCNSQATTSNTEGDO   KYSCTCHTWIAUTRGSNSQALCHFPET/KHRHTYDCTSCNSQATTSNTEGDO   KYSCTCHTWIAUTRGSNGACHTTUNGCTTSSSSCTPVOI   GENNSBURGLIAISTSGTTADDAPDSTVOIDUDISTSVORMS   GENNSBURGLIAISTSGTTADDAPDSTVOIDUDISTSVORMS   COMPANY TO A CONTINUE A CONTIN	[	to first	amino acid	
amino acid sequence  Codon, /-possible nucleotide disection	1	amino acid	residue of	
Appearable mucleotide insertion	ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Appealable mucleotide insertion	1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ITCISENCEMOTIFISTRICION WERDERCHILCULTURARICE BRKCHITSUOTISSESGEPTUMANUPOPOPHOLOPY CHICUT DEGUVYSUGHOLA *CIQCRICGHIA (CTLCIAGUSCGETAVTOTY) GENERGEVU, PETVINGTETYS CTISERGOGIALMESTERINSEDO RYGECTORITUJOTROGISMALA CHEPFLYININITOCTSEGRE BRKCHICTUJOTROGISMALA EPFLYININITOCTSEGRE BRKCHICTUJOTROGISMA CHEPFLYININITOCT CHEPFLYININITOCT CHEPFLYININITOCT CHEPFLY CHEPFLYININITOCT CHEPFLY CH	1			\=possible nucleotide insertion)
BRKCERHTSVOTTSSGSGEPTUDRANVOROPHROPPYCHICUT  BGGVVSVGWOGNA FROCRIKGM, CTCLAGWSCGGTAVTOTTG  GRSNGEPCULPTUTNGTPSGCTTSGRQOGHAMCSTTSNYSQDQ  XYSGCTCHTULVGTGGSSNAGALGPEFTVJNINTNTCTSGRR  DMMKGCTTGNYDADQKSGCFCPMAMBERICTTMSGWAYARIGOOM  ROQMORGEMERICTUCKGGGSWGRACDSGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	ļ	- Dodgeston		
DEGUVYSUGOLA-KTQCANGAL-(TELGANGSCGETAVTQTYG GRSGEPCVL)PPITVAGTREGTSCTAGEGGGGALGGETSTNYEDGO AYGCTCHTVIJQTRGGSSNALACGEPFLYNINTTOCTSEGER DBMAGGGTTONTADORSPCPC-PMANER CITTERGYMY IGOAM DEGUDMGSBRETTUCHGGGGSSTCLAYSOLADGCTVDD.TYAVA TETHEREGGHALACTEPGGGGGGSGETCLAYSOLADGCTVDD.TYAVA DEGUDMGSBRETTUCHGGGGGSTCLAYSOLADGCTVDD.TYAVA TETHEREGGHALACTEPGGGGGGSGETCLAYSOLADGCTVDD.TYAVA THEOGRAPH CONTROL OF THE CON	1	1		
GISNIGEPCULPHYNRGEPSECTTRORQUORILAGSTENNYEQUO NYSECTEDITULOUTGENSNAGALOFFEYNINNINTOCTSEGRE INMINGCITIONYDADORSPOREPCHANNERS LITTERGUMYRIGOOM DEQUAMBERMENT CURRORGERSWICTUS GOLOGOUS PROFESSOL DEQUAMBERMENT CURRORGERSWICTUS GOLOGOUS PROFESSOL DESCRIPTION OF THE SERVICE OF	1			
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SCQOPSVGQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVRBEVVTVCHNSVHBGINOPT DDSCFDPYTVSHYAVGDEWERMSESCFKLLCQLGFGSGHFRCD SSRWCHDMGVNYKLGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGBQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGBPSPEGTTGQSYNQXSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRB  5366 8066 703 RLCCTGGGGGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLREANLVATCLPVRASLPHRINML RGPGFGLLLLAVLCLGTAVPSTGASKSKRQAQOMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIHDCTCIGAGRGRIS CTIANRCHEGGGSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIABKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKDDNRGNLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGSCCETAVTQTYG	1	1		
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LTGLTRGATYNI IVEALKDQQRHKVRBEVVTVGNSVNBGLNQPT DDSCPPPYTVSHYAVGDEWRRMSESGPKLLCQCLGFGSGHFRCD SSRWCHDMGVNYKIGEKWDRQGENGQMMSCTCLGNIGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGGRGWRCDNCR RPGGBPSPEGTTGQSYNQXSQRYHQRTNTNVNCFIECFMPLDVQ ADREDSRB  5366 8066 703 RLCCTGGGGBGTPGASGKRGPAATTSLVLCIPSVPPPVPPPTLMP PSWRRQPPGGIRRDFSRRLRRBANLVATCLPVRASLPHRLNML RGPGFGLLLLAVLCLGTAVPSTGASKSKRQAQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWRRTYLGNALVCTCYGGSRGFNCESK PEAESTCEDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGMLECVCLGNGKGEWT CKPIARKCFPHAAGTSYVVGETWKKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKIDNRGNLCQCITGNGRG EWKCERHTSVOTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCOETAVTQTYG	1	1		ALSOTTISWAPPODTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
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CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCPDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPPTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA+KTQGNKQML\CTCLGNGVSCQETAVTQTYG	1	1		
CKPIABKCPDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA+KTQGNKQML\CTCLGNGVSCQETAVTQTYG	1	<b>\</b>		PEAFETCPDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
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ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPPTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA+KTQGNKQML\CTCLGHGVSCQETAVTQTYG	1	İ		
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SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
: OW.	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1 1	amino acid	sequence	\=possible nucleotide insertion)
	sequence		KYSPCTDHTVLVQTRGGNSNGALCHFPPLYNNHNYTDCTSEGRR
1 1			DNMKWCGTTQNYDADQKFGFCPMAAHBEICTTNEGVMYRIGDQW
l f			DKQHDMGHMMRCTCVGNGRGBWTCIAYSQLRDQCIVDDITYNVN
1 1		·	DTFHKRHEEGHMLNCTCFGOGRGRWKCDPVDQCDDSETGTFYQI
1			GDSWEKYVHGVRYOCYCYGRGIGEWHCOPLOTYPSSSGPVEVFI
1 1			TETPSOPNSHPIOWNAPOPSHISKYLLRWRPKNSVGRWKEATIP
1 1			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1 1			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1 1		Ì	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1 1			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1			PQAPITGYRIVYSPSVEGSSTELNLPZTANSVTLSDLQPGVQYN
]		· ·	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1 1	,		KVTIMWTPPRSAVTGYRYDVIPVNLPGEHGQRLPLSRNTF\AEN
			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1		ļ	ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1			PLRNLQPASBYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TRVTETTIVITNTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1 [			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1 1			LEANPOTCYLTVEWERSTTPDITGYRITTTPTNGQQGNSLEEVV
3	:		
1 1			PPPTDLRFIN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNR
			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYBQHESTP
1 1		}	\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1 1	!		TGYRIR\HHPRHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1 1			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1 1			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1 1			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1 1		ļ	ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDOTEMTI
1 1	•		BGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHBLPPAPDGEEDTA
1			BLOGLRPGSBYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1 [		[	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1 1			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1 1			ARVIDATEITITISWRIKTETITGFQVDAVPANGQTPIQRTIKP
1 1		}	DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1 1			nlrplattpnsllvswqppraritgy11kykkpgspprevvprp
1 1		ì	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1 1		1	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
		1	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQPRVPGTSTSAT LTGLTRGATYNIIVRALKDQQRHKVREEVVTVGNSVNEGLNQPT
1		{	DDSCPDPYTVSHYAVGDEWERMSESGPKLLCQCLGFGSGHFRCD
			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1 1		Ì	HEATCYDDGKTYHVGEOWOKEYLGAICSCTCFGGORGWRCDMCR
]	·		RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
1 1		16.	ADREDSRE
5367	235	3591	KKILNMLCKKNIVIEYLADILYBYLYGFCPSGIKKYLIIHVLRL
	,		1LBLWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKEMRHHLQIM
] 1			EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQPGEKRLV
			KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ
) * {			GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM
1 1			SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEIANYPIYKI
		ļ	
1			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI
			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCBIQEAVSRI LYSPATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG
			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCBIQEAVSRI LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG KGYPSAVPKDKDRQCPKLRQGIDKKIVIYVQQTTNKELAIERCP
			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCBIQEAVSRI LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG KGYPSAVPKDKDRQCPKLRQGIDKKIVIYVQQTTNKELAIERCP GLLLSPGKDVRNSDMHLLDLBSMGKSSDGKSYVITGSWNPKSPH
			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCBIQEAVSRI LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG KGYPSAVPKDKDRQCPKLRQGIDKKIVIYVQQTTNKELAIERCP GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH FQVVNEBTPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP
			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG KGYPSAVPKDKDRQCPKLKQGIDKKIVIYVQQTTNKELAIERCP GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSMNPKSPH FQVVNBETPKDKVLFMTTAVDLVITBVQEPVRFLLETKVRVCSP NERLPWPFSKRSTTENFFLKLKQIKQRBRKNNTDILYEVVCLBS
			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG KGYPSAVPKDKORQCFKLRQGIDKKĮVIYVQQTTNKELAIERCP GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH FQVVNEETPKDKVLFMTTAVDLVITBVQEPVRFLLETKVRVCSP NERLFWPFSKRSTTENFFIKLKQIKQRERKNNTDILYEVVCLES ESEREKRKTTASPSVRLPQSGSQSSVIPSPPRDDEBEDNDEPLL
			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG KGYPSAVPKDKDRQCPKLKQGIDKKIVIYVQQTTNKELAIERCP GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSMNPKSPH FQVVNBETPKDKVLFMTTAVDLVITBVQEPVRFLLETKVRVCSP NERLPWPFSKRSTTENFFLKLKQIKQRBRKNNTDILYEVVCLBS

mcLectida cortesponding cortesponding cortesponding to first to first to first saino acid anino acid anino acid sequence  ### Heilatiding, La-Typycsine, X-Typycsine, L-Leucine, M-Methiodine, N-Myghide, L-Leucine, M-Methiodine, N-Myghide, L-Leucine, M-Methiodine, N-Myghide, L-Leucine, M-Methiodine, N-Myghide, L-Leucine, M-Methiodine, N-Myghide, Sequence  ### Heilatiding, L-Typycsine, X-Typycsine, sequence  ### Heilatiding, L-Typycsine, X-Typycsine, Sequence  ### Heilatiding, L-Typycsine, X-Typycsine, Sequence  ### Heilatiding, L-Typycsine, X-Typycsine, Sequence  ### Heilatiding, L-Typycsine, X-Typycsine, Sequence  ### Heilatiding, L-Typycsine, X-Typycsine, Sequence, L-Leucine, M-Methiodine, N-Myghide, Sequence, L-Leucine, M-M	SEQ	Predicted	Predicted end	
Mo: location corresponding to first anino acid residue of amino acid manino acid residue of amino acid sequence residue of acid sequence residue of acid se		ž .	3	Amino acid segment containing signal peptide
Cortesponding to first   anino acid   residue of   set   residue of   set				(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
Cortesponding to first   anino acid   residue of   set   residue of   set	NO:			Glutamic Acid, F-Phenylalanine, G-Glycine,
b first anino acid residue of santo acid residue of santo acid sequence  ##################################	1	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of sequence	į.	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
anino acid residue of amino acid sequence  8-Serine, T-Thrronine, V-Valine, amino acid sequence  8-Serine, T-Thrronine, V-Valine, amino acid sequence  8-Serine, T-Thrronine, V-Valine, amino acid sequence  8-Serine, T-Thrronine, V-Valine, amino acid sequence  8-Serine, T-Thrronine, V-Valine, amino acid sequence  8-Serine, T-Thrronine, V-Valine, AVALLARD SERINE, Color of Serine, AVALLARD SERINE, Color of Serine, AVALLARD SERINE, COLOR SERINE, COLOR SERINE, COLOR SERINE, COLOR SERINE, COLOR SERINE, COLOR SERINE, COLOR SERIES, COLOR	1	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
residue of amino acid sequence  ###Tryptophan, Y-Tyrosine, X-Uukhoom, *-\$Etop Codon, /-possible mucleotide eletion (	1	amino acid	residue of	S=Serine, T=Threonine V-Valine
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PETGHLVPLSGHBLGFAHKSVITGMVMSSTFEDDGEVJRBITKERK TVWSBIGKGFLOSGLDRWITKKGYTEDLANGLSVURBITKERK GRBFSGHTPIDSLVGONIANDQILLEDSMIFSLASCIITAKLCTW AIMPLITSERVQKKLYBEINQVFGNGPVITBEKTQLRVCQHVLC ETVRTAKLTPVSAQLQDIECKTDRFIIFRETIMLYALLGVVLQDP MTMPSPHKPDDREDDGLVMKTTSSLGFSGTQSCCPELPAYMVT TVLSSVIVARHLLLSVBGQVLTETKYELLVTSSREAMITVSKRY  5369  1 6622  PRILCPSIMABANAVLADGGURRHRRILGTMSASFVPRGASLED CRCHAPCLADITGINKRYVWQOPTSAPITYSEDELISSS RCLKADVIG/VMRROQRERRENLATTSREAMITVSKRY QKKOMECCRNDFPMNAVLCPSKAVINILLERCLMNRRIPKIGKMF RCLKADVIG/VMRROQRERRENLATTMGGAFKANSEDATKK LIGEWGGPY PISCCLKMRBSEKGENDMOBENTKSVELINGIGPVY LLSERHITLAQQSNSPFQVILCPFGINGTLTGGAFKANSEDATKK LIGEWGGPY PISCCLKMRBSEKGENDMOBENTKSVELINGIGPY LLSERHITLAQQSNSPFQVILCPFGINGTLTGGAFKANSEDATKK LIGEWGGPY PISCCLKMRBSEKGENDMOBENTKSVELINGIGPY MIPPACPVILVPQSDIPTSSVGSTTKGSSCLGVHQVPASTRDPA MSSVTLTPPTSPEWQTTVDGSVGKWNFSDGFNSGTSHH GGKIPFRLAMHVVDBVMQBCCMMRRAQNIRKYSASSGLCBEATA AKVASNDPVEATORINGSCLGLRKRILKSRNAGQQGABFLOQQQ ILPRIKITKRKQKKSKKQRRPLTPPHHREVSDDWGMD\ADS\A SGRLV\1SAP\DSQVQVRSNIR\TNDVAK\TPQMRGTERMANSEQ PPLSP\HIPPOLDSDKYMTPSTTPQGGHTPDTPLVSKM BERIBSLGGSPPPQVGRAVSPTVYVGTAVALBEBRANTAKYYK FPRKKDVEPLPPOLLSDKYPTSTPQGGHTPDTPLVSKM BERIBSLGGSPPPQVGRAVSPTVYVGTAVALBEBRANTAKYYK FPRKKDVEPLPPOLLSDKYRDDVGPFGGDEFDELIDYAFVEGDESP LEPHKKDVEPLPPOLLSDKYRDDVGPFGGDFTDFLVFRVGGER PLKYSDELVQQYJLKNQCLSATASDABGEPKIDPYAFVEGDESP LEQHTMGFSRMANNKKYGKNDTTGGGTVLTGENSSTGAPPKIE VDEGFCSRKSSIKDDFAVVKPRNCJLVSCSMFAPLKTLPSQY LEHILLIPEGCLTRQSHVVGRLALLASGFSVEPTERGGGSNMOPE VGTAYTPQTHTSCGMPPSSAPPSNGAGILPSSTPTTCRFTPTPTPT RTHTTRRAAGGRARDGSVKYNDSDLUSPSRSTSTCAUNSVEP ATVPSIEPARISTYVALLLESSFMMLFRGONSGLFFDELID LIGNTDGGGRARRFFRELIKATSARHVWGGTSRGKISSKLINSVEP ATVPSIEPARAFSARHVWGGTSRGKISSKLINSVEP ATVPSIEPARAFSARHVWGGTSRGKISSKLINSVEP ATVPSIEPARAFSARHVWGGTSRGKISSKLINSVEP ATVPSIEPARAFSARHVWGGTSRGKSKRGSTGGT LDGAFGRAFFFRELITATICHTSSTSSTSTNATHSTUTTRATSSSSS SHASGVSSNKLPSFPFGSMSNAAGSMSTQANTVYSMCXGLJOG CRYDLGPYLASSESSLITPOPHDVNSTNDRKVGIPTOGESS LTGGARVGSLASSESSLITPOPHPONDSKVGIPTOGFSH NTPSATLASASSTWTTSGASSSSATANNTUTTROTALTSCSSSS SNLASGVSSNKLPSFPFGSMSNAAGSMS	1			MNOCE AND ODARI ADADICALIZATION PRANCES IN ANTICOLOR AND ADADICALIZATION OF ANTICALIZATION OFFICIALIZATION OFFICIALIZATI
TVWSEIGIGFLDESLDENMTRIKQTEDAMICHSULRNIIKEREK GRRYSCHIPT DISLUGGINDOLLDESHI SLASCIITAKLICTW AIMPLTTSEEVQKKLYEEINQVFGMCPVTPEKIEQLRYCQHVIC ETVRTAKLTEVSAQLQDIEGKIDEFIIPRITUKLAGGVVIQDE MTØPSPHKEPDDRRDDELMTMTFSSLEPSGTDECERERAYMYT TVLLSVILVERLHLISVEGQVIETKYELVTSSEERAMITVSKRY TVLLSVILVERLHLISVEGQVIETKYELVTSSEERAMITVSKRY TVLLSVILVERLHLISVEGQVIETKYELVTSSEERAMITVSKRY TVLLSVILVERLHLISVEGQVIETKYELVTSSEERAMITVSKRY PRSILCPSIMARAAVLANGGIRRERELLFATSSEERGASFEVDRGSEED CHCHLPCLADLTGIKWKRYVMGGPTSAPILPPVTEEDPIISSPS RCLKADVIG/VWRRDGIRRERELLF-IFWGGMSSEEDGENGE RCLKADVIG/VWRRDGRPERREL-LF-IFWGGGMSSEPORGSETK ULSEBLITLAQGSNSPPQVILCPFCLAGTITTQAFKMSDEATKK LIGEMKQPYPISCLKEMSBEKGEMMMEDDSLAAVEVUVAGVR MIPPACPVULVOSDIPTPSPVUSTTLOSTITATAPKMSDEATKK LIGEMKQPYPISCLKEMSBEKGEMMMEDDSLAAVEVUVAGVR MISVYLTPPTSPEBVQTVDRQSVQKWVKPSSVSGERNSDSTSHH GGKIPRILAMINVDRVWGECMMRAQMIKKKYSASSGLICEFATA AKVASMDPVERTQTTRICSCLHERMLKSRQGGABSIGOQQ ILPHKITMKYGKRSEKPQRFLITPFHHRVSVSDDVGMDAJSA SQRLVI ISAPPJSGLVRSNIRT\NTDMCQGGABSIGOQQQ ILPHKITMKYGKRSEKPQRFLITPFHHRVSVSDDVGMDAJSA SQRLVI ISAPPJSGLVRSNIRT\NTDMCQGGABSIGOQQQ ILPHKITMKYGKRSEKPQRFLTPFHHRVSVSDDVGMPTDPLVPSKPM EDRIDSLGGRPPPQVQRAVEPTVVVTANNIEBBRAILMHTVTX PFRKENDVEFLPPQLESDRYNDDFVQFPCGESTVTVLHWQCKK PLKVSDELVQQYQIKNGCLSALASDABGERTDPJFAVEGDEF LFPDKKDRGNSERAAKHKWLGGTSVVVLSHEDAMSLFPSS IKODAPRTSEARPPSTSLITDSDLAVSTVLLSHEDAMSLFPSS IKODAPRTSEARPPSTSLITDSDLAVSTVLLSHEDAMSLFPSS IKODAPRTSEARPPSTSLITDSDLAVSTVLLSHEDAMSLFPSS IKODAPRTSEARPPSTSLITDSDLAVSTVLLSHEDAMSLFPSS IKODAPRTSEARPPSTSLITDSDLAVSTVLLSHEDAMSLFPSS IKODAPRTSEARPPSTSLITDSDLAVSTLLDLINSSEIGQPKIE VDESCSPKSBERKGERKRYGLEGLESSTSTCERPINSVP RTHTTPRAGGGABAGGRAVKENSDLAVSTDLINFSSUEDBLIT RTHTTPRAGGGABAGGRAVKENSDLAVSTSCLIPHTMSVP RTHTTPRAGGGABAGGARAFFROULTSHTWSPP RTHTTPRAGGGABAGGARAFFROULTSHTWSPP RTHTTPRAGGGABAGGARAFFROULTSHTWSPP RTHTTPRAGGGABAGGARAFFROULTSHTWSPP RTHTTPRAGGGABAGGARAFFROULTSHTWSPP RTHTTPRAGGABAGGARAFFROULTSHTWSPP RTHTTPRAGGABAGGARAFFROULTSHTWSPP RTHTTPRAGGABAGGARAFFROULTSHTWSPP RTHTTPRAGGABAGGARAFFROULTSHTWSPP RTHTTPRAGGABAGGARAFFROULTSHTWSP RTHTTPRAGGABAGGARAFFROULTSHTWSP RTHTT	1			DELON AND COME CONTROL
GRNFSCHIFIDSLUÇGINLADOQUILDESMIFSLASCITITALICITM AIMPLITESEWQKIKLUEERINQVERGEVIPEXIEQLAYCQHULC ETVRTAKLTPVSAQLQDIECKIDER I IPERTIVLYALGUVICQDE MTWPSPHKEDPDIRKDELMMRTPSSLEPSGTQECCELEPAYMVT TULLSULVARIHLLSUNGQUIRKRRELLEGTMSASEVDRGASLED TULLSULVARIHLLSUNGQUIRKRRELLEGTMSASEVDRGASLED CHCHECLADUTGIKKRYVWQGPTSAPILPPVTEEDPILSPS RCLKADVIG/VWRROGPERRE\\\\^\*\^\*\^\*\^\*\^\*\^\*\^\*\^\*\^\*	1			
AIMPLITESEVOJKKLYEETNOUTENGEVTPETEIBLARYCQHULC ETVRTAKLTUPVSALG DIE GKIDRP I PERSTUTUKALGUVILODD MTWPSPHKFDPDRFDDELVMKTPSSLGPSGTQECEBERPAYMVT TULLSVILVERLHELSVEGGVIETKYELVTSSEERMITYJSKR.  PRSLCPSIMARANALDAGGIKRRERLJKGTMSASFVPNGASLED CHCHLFCLADLTGIKWKKYVNGGTSAPILFYTEEDPILSSES CKLKADVIG/WRRODGFRRER\LTPHERDPILSSES CKLKADVIG/WRRODGFRRER\LTPHERDENVCTSVERIDGIDVY LLSERHITJAQQSNSPFQVILCPFGLMSTLTTQAPKWSDBATKK LIGEWKQPYPISCLKEMSBEKQEMMWEDDSLAAVEVLVAGVR MIPPACPYLVPQSDIPTPSPVGSTHCSGLAVHQVPASTRDPA MSSVTLTPPTPPBRSVQTVDPQSVQKWWKPSSVSDGPNSDSTSHH GGKIPRKLANHVVDRVWQSCMNRRAQNKRYSASSGLCEERATA AKVASWPVERTQRTICSCLSHKNILKSRRAGQGGAPSIGOOQQ ILPHKKTMKQEKSEKPQREPLTPPHHRVSVSDDWHNSDSSHSHSHSH AKVASWPVERTQRTICSCLSHKNILKSRRAGQGGAPSIGOOQQ ILPHKKTMKQEKSEKPQREPLTPPHHRVSVSDDWHNDSCHAD\ADS\A SQRLV\LSAP\DSQ\VRYSHIR\TYDDHTVPDLVPSKOM EBRIBLSLGSPPPQVQRAWTETSTTQSGHPYQMPTDPLVPSKOM EBRIBLSLGSPPPQVQRAWTETVSTTDASHPYVAPFEDERF PKKKDVEPLPPQLPSDRPKNDTVGPFGQESVTSVTISHWQCCK PLKVSDELVQQYQIKNQCLSALISDARQERKDDPYAVEGDEF LFPBKKDRGNSERAGKHKWBCGTSSVTVLSHEEDAMSLFSPS IKQDAPRTSEARPPSTSLIVDSDLAVSTUDLHEDBANIAWTYK PSKRSANGSDRSAGKSKRYNNLDPSVTVLSHEEDAMSLFSPS IKQDAPRTSEARPPSTSLIVDSDLAVSTUDLHEBDSNDELT PGSKRSANGSDRSAGKSKRYNNLDPSFYRIEGGGSNMOQE VUBGPCSPKPSBIKDPSVYKPRNCQILVGGMPEPSPEREDGSSMOQE VOTGATTPQTTTSGGMPSSAPPSNGGAGILPSPSTPFFTPFFF RTFTFRGAGGGASAGGSWKENSDLYSTSTLANSTLTNSVEP ATVPSIPERASLYVALILSSSVMILFKDCNSCCICVCNMIK GADVGVYIPDTQERQYKCTGGFSAVMRKKGRNSSRSKGSDLILL LQQCTHLFSPFCAADQDPPPKSGVISNWKRRNDVSMCSODIL LEGRGXPDMSGGKVERSDLYJASSCLIPDPSTTPFFTPFTP RTPSTFRAGGGASAGGSPAKPSSOLIANSSCLIPMERNDSWCOSODIL RMLSLQPVLQDAIQKRTVRPWGQGPLTNQGFHKMAGRGSTG TDESPEPLPIPTLIGTUDYDTLUSEFALPWRENLMERYGSQD ILTAVVLCPPRNEALINGRSFPFFCARPINGRNDSPCSQDIL LEGRGXPORMSGRSFPFCARPINGRNDSWCOSODIL RMLSLQPVLQDAIQKRTVRPWGQGRBSKKLINKTVYGGLIANSSCLIPMTORNA NTESATLASASSTMVTSGVALSSCLIPMTORNATIVGGGLAGQ CXYSLLGFTALSLEPPPDRFTPTCDASS SNAMSGVSNIKLSFPFPGSMMNAAGSMSTQANTYGGGLAGQ CYSALQTAGISGGRSSSLIPPPFFTPTORS	}			
ETVRTAKLIPVSAGLODIECKIDRPILIPRETALIZALGVVLLODD MYDESPEKPDDRPDRIDLIAMETESPSTORCEPELRPAYMYT TVLLSVLVKRIHLLSVRGQVIETKYELVYSSRERAMITVSKRY TVLLSVLVKRIHLLSVRGQVIETKYELVYSSRERAMITVSKRY PRSLCPSIMARAAVLADGGIRRRRRLLAGTMSASFVPNGASLED CHCHLSCLADLIGIKKKRYVMQCDPALIPPYTEEDPILISSSS RCLKADVIG/WRRDGRPRRRRLL*IFWGEDPVLLTLFPTMY OKKOMECGRMDPPMNAVLCPSKAVHNLLERCLMMRNFVRIGKMF VKPYEKDERPINKSHLSCSFTYFHIGDSNVCTSVEINGBQDVY LLSERHITLAQGSNSPPQVILCPFGLMSTLTGQAFKMSDSATKK LIGEMGYPTISCLKRMSBEKGMUNDEDSLAAVEVLVAGVR MIYPACFVLVPQSDIPPTSFVGSTHGSSSCLGWQVPASTRDPA MSSVTLTPTTSPESVQTVDPQSVQKWVKPSSVSDGFNSDSTSHH GGKIPRKLANHVVDRVWQCCMNNRAQNGRKYSSSGLCEBEATA AKVASMDEVBATQRTNCSCLRHRNLKSRNAGQGQAPSLGQQQQ ILPHKITNKKQKSKSEKPQKRPLIPPKHSVSDDVCMDVADAS \A SQRLV\ISAP\DSQ\VEFSNIR\TNDVAK\TPQMHCTBMANSPQ PPPLSP\HCDVVDEGVTKTPSTPQSHFYQMPTDPLVPSKDM EDRIDSLGQSPPPKYQBAVEPTVYVGTAVNLBBDBANIAMKYK FFRKKUNEFLEPQLPSDRKKDDPVQPFGGBSVTSVTELMVQCKK PFRKNDVEFLEPQLPSDRKKDDPVQPFGGBSVTSVTELMVQCK PFLKSDBELVQQYQYKNQCLSAATABAGERFIDFYAPFVGDEP LFPDKDRONSERRAGKKHKVBGGTSSVTVLSHEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSTTDLINLFNDEDELT PGSKRSANGSDBKSCKEKNTGNLDPLSCISTADLIKMYPTPPS LEQHIMGFSHMMNNKEYGSMDTTGGTVLEGSMSSIGAQFKIE VDSGFCSFKPBSKINGFVYVKFROCILVGCSMFPBLTKTPSPCF RTPRTTPRGAGGPASAGGSWKYENSIGLIPSSTTRTFFTFRTP RTPRTTPRGAGGPASAGGSWKYENSIGLIPSSTTRFFTPFTPT RTPRTTPRGAGGPASAGGSWKYENSIGLIPSSTTRFFTPFTPT RTPRTTPRGAGGPASAGGSWKYENSIGLIPSSTTRFFTPFTPT RTPRTTPRGAGGPASAGGSWKYENSIGLIPSSTRSCCCICCVONNIK GADVGVYIPDTTGGAPKGTCGFGSAVNNRKEGNNSCICCVONNIK GADVGVYIPDTTGGAPKGTCGFGSAVNNRKEGNNSCICCVONNIK GADVGVYIPDTTGGAPKGTCGFGSAVNNRKEGNNSCICCNCCTILA LEHGRQFWINNSGGKWCENSILSPROSCCICCVONNIK GADVGVYIPDTTGGAPKGTCGFGSAVNNRKEGNNSCICCNCCTILA LEHGRQFWINNSGGKVENSTLYPGGTLFFGSGTFFTPFTPT RTPRTTPRGAGGPASAGGSWKYENSTLYPGGTLFFDSCCICCVONNIK GADVGVYIPDTTGGAPKGTCGFGSAVNNRKEGNNSCICCNCCTILA LEHGRQFWINNSGGKCESLIVPRGSCLTPFDEDDFTRFTPGTPT RTPTTTRGAGGGAPAGGRAFFGALTATASGCTCCCMCTILA LEHGRQFWINNSGGKGSLELYGPFTPTPTPTGGLITTPOPMTYGNA NTPSATLASAASSTMTVTSGVALSTSVATANSTLTTAGTSSSSS SNINSGVSSNKLPSFFFFFFFFGSRNSRAAGGSMTATVGGGLGGG QYSALQVAGGTGAGGSKSLLYPGFTPDVSSSSTATUTGGGGGG				
MTTPSPHKEDTORIDUKUNTSILIGISTIGCTELRRAYMT TULSUVURKIHLIGSTIGGUTETKYRLYTSGRERANTTYSKRY  5369  1 6622  PRSLCFSLMAEAAVLADGGIRRRRRLIRGTINSASFVENGASLED CHCNLECLADLIGIKWKKYWOGPTSAPILIPYTEEDPILSSES RCLKADVIG/WRRDORPERRE L+ FYMGGEDPYULLTIFTTYT QKKKMGCGRMDPPMRAVLCYSKAVIRILLERGLMORNEVRIGKWF VKPYEKDEKPINKSEHLISCSFTFFHLIGSDSNCTSVEINOHOPVY LISERHITLAQQSNSPFQVILCPFGLNGTLIGQAFKNSDSATKK LIGEWGPYPISCCLKRMSBEKQEDMDMEDDSLAVEVIVAGGR MIPPACPVLVPQSDIPTPSFUSGSSCGUNQHQVBASTROPA MSSYTLTPPTSPESVQTVDPQSVQKWVKPSSVSDGFNSDSTSHH GGKIPRKLANHVVDRWQECMNNRAQNGKRYASSSGLCEERATA AKVASMDVENATORTNCSCLRHKNIKSRNAGOGGAPSIGGOGO ILPHKLANHVVDRWQECMNNRAQNGKRYASSSGLCEERATA AKVASMDVENATORTNCSCLRHKNIKSRNAGOGGAPSIGGOGO ILPHKLANHVVDRWQECMNNRAQNGKRYASSSGLCEERATA AKVASMDVENATORTNCSCLRHKNIKSRNAGOGGAPSIGGOGO ILPHKLANHVVDRWQECMNNRAQNGKAYASSSGLCEERATA AKVASMDVENATORTSCLRHKNIKSRNAGOGGAPSIGGOGO ILPHKLANHVVDRWQECMNNRAGNGKGYASSGCLEERATA AKVASMDVENATORTSCLRHKNIKSRNAGOGGAPSIGGOGO ILPHKLANHVVDRWQECMNNRAGNGKYTAPSTPOLHGTHRANSPO PPPLSP\LECOVODEGVTXTPSTPQSQHYQMFTGHENANSPO EBRIDSLSGSPPQYQGAVEPTVYGTAVNLEBBRANIAWKYYK PPRKUDVYELPPQLIPSORKPDDPVGPFGGESVTSVTRAMSPO EBRIDSLSGSPPQYQGAVEPTVYGTAVNLEBBRANIAWKYYK PPRKUDVEPLPPQLIPSORKPDDFOLGFGGSVTSVTIKIBEDANSLYSPS ILGDAPRTTSGRAPPTSILATDSLAVSYTILDINLENSEDELIT PGSKRSANGSIDKASCKESKTONLDPLSCTSTADLHKMYPTPPS LEGHMENGSPHANNIKEYGSMDTTSHAVSTLINDLESEDANSLPSPS ILGDHAFFTGHTSGANDPSSAPPSINGAGLIPSSTFERFTPRTP RTPTTPTGTTTSGAMPSSAPPSINGAGLIPSSTFTRFTPRTP RTPTTPTGTTTSGAMPSSAPPSINGAGLIPSSTFTRFTPRTP RTPTTPTGTTTSGAMPSSAPPSINGAGLIPSSTFTRFTPTRTP RTPTTPTGTTSGAMPSSAPPSINGAGLIPSSTFTRFTPTRTP RTPTTPTGAGGAPASAGGSVUKKENSDLYSPASTFSTCRPLNSVEP ATVPSIPEAHSLYVNLLISSSVMNLFKGCNSSCLTGCONNIK GADUVYIPDTTQEAQYRCTCGFSAVNRKKGNSSCLTCOCNNIKI CADUCYYTPOTTGCARARKPPRALARASARHVNGGLRESKLSDDLILL LOQCTINLESPYPARAATSARHVNGGLRESKLSDDLILL LOQCTINLESPYPARAATSARHVNGGLRESKLSDDLILL LOQCTINLESPYPARAMSARHVANGGLRESKLSDDLILL LOQCTINLESPYDDLYDTALLYAPTSGSLTPDWNTGNAGGSYG TDESPEPLPTFTLLIGTVYDDTVLVLAPHYMERLIHLEPYGGG TDESPEPLPTFTILLGTVYDDTVLVLAPHYMERMLHERPYGGG CKHULGSPLASHLOSBLILGQPNLVAPTSGSLTTPAGTSSSS SNINSGVSNKL	1			
TVLISVILVERILLEVBROUTETKYELVTSSRERMITTYSKRY  PRISCEPLIMARANJAROGIGERERALERTMASFVPNRASLED  CHCNLFCLADLTGIKWKKYVWQGPTSAPILEPYTEEDPILSEPS RCLKADVIG/WRRDGRPRRRE L+ TFWGEEDPYLLTIFTTMY QRKCWRGCRMPPPRNAVLCSYRKYMILERCLMMRRYBYRIGKMP VRPYEKDREPINKSEHLSCSFTFFLHGDSNVCTSVEINGROPVY LLSEBHITLAQQASPPOYILCFFGLNRGTLTQAPKWSTSTERTM LIGEWKQPYPISCCLKEMSERKGEMDMEDDSLAAVEVLVAGVR MIYPACFVLVPQSDIPTPSFVGSTTICSSSCLGVWQVPASTRDPA MSSVTLTFPTSPBERVQTVDPQSVGWKSSVSGGRNSDSTSHH GGKIPRKLANHVVDRVWQBCMMRAQNKRXYSASSGCLGERATA ARVASWDPVEATQRTDVDQSVGWKSSVSGGRNSDSTSHH GGKIPRKLANHVVDRVWQBCMMRAQNKRXYSASSGCLGERATA ARVASWDPVEATQRTDVSCLRKNILKSRAACQGQAPSIGOQQ ILPHIKTNEKQBKSEKPQRPLITPFHHRVSVSDDVCMD\ADS\A SQRLV\1SAP\DSQ\VEFSNIR\TDDVAK\7PQHHGTEMANSPQ PPLLSF\HECOVUDEGVTTPFSTPGFYVKPMTQCGC PPLLSF\HECOVUDEGVTTPFSTPGFYVGFTEMANSPQ PPLLSF\HECOVUDEGVTTPFSTPGFYVFYGFDEFY EDRIDSLGGBPPQYQBAYBPTVYVGTAWNLERDEBANIAWKYYK PPKKKDVEPLPPQLPSDKPKDDPVGPFGGDFYOMPTPDFUPSKPM EDRIDSLGGBPPQYGRAYBPTVYVGTAWNLERDEBANIAWKYYK PPKKKDVEPLPPQLPSDKPKDDPVGPFGGDFYOMFTPDFNSDDELT LFDDKKDRQNSERRAGKKHKVSDGTSSTVLSHEDAMSLFSPS LKODAPRTSEARPPSTSLIYPSGTSTTVLSHEDAMSLFSPS LKODAPRTSEARPPSTSLIYPSGTSVTLDLNCGCK PLIKLPSGTYRGSHTVGKLELLSGGPSMPTYKEGGSNMDQDE VGTATYTPGTTTSGGWPSSAPPSNGSTSLISPSSTTRFFPTPFTPT RGSKRSANGSDDKASCKESKTCNLDPLSCISTADLHKMYPTPPS LEQHIMGPSWMSNNNNKEYGSMDTTGGTVLEGMSSSLGQFKIE VDEGFCSSFKDSELINPSSAYPSNGSLLSPSSTSTTCRPINSVEP ATVPSIPPAHSLIVNILLSESVMNLFRCONSDCCICCVONNNIK GADVOVYIPPOTTGGGAPSSAPSARFKFGNNSCLIFPDBLD LIGNATDGGKRARRPPBALRARSARHVWGGLKESKKLSDDLILL LQQCTNLFSPFCAADQDFFFKGGVISNWREDCCCNCCYLA LEBERGPMDMNSGGKVDEALWKSSCLIFPWSKRMDSWGCSQDIL LEBERGPMDMNSGGKVDEALWKSSCLIFPWSKRMLERYGGSR TDESSPEDJPTFTILLGYDDTLALFYGGLTFFGSLTFPOMTYGNA NTPSATLASAASSTMTVTGGVALSTSGRATUTGGGLGGQ CKNLUGPVLASPLIDSSLIJQPNLTATSGSLITTPOMTYGGGLGGQ CYSALQYAGTSGRSSSLFFRYDFRSSSSLFTARDRKGGIFTGGGGQ	1			ETVKTAKLTPVSAQLQD1EGKIDRFIIPRETLVLYALGVVLQDP
PRILCPILMEANUADGGLERRERLAGTWSASFVPNGASLED CHCNLFCLADLTGIKWKYVWQGFTSAPILFPYTEEDPILSSFS RCLKADVLG/WRRDGRERRE\L*IFWGGEDP\VLLITLFTMTY OKKKMECGRMDPPMANULCSKAVINLIBERCLMRRHFVBIGKWF VRPYEROREPINKSHLSCSSFTFFIHGGSBVCTSVEINOHOPVY LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK LIGEWGYPISCCLKRHSBEKQRDMWENDSLAAVEULVAGVR MIPPACPVLPVQSDTPTSPVGSTHCSSSCLGVHQVPASTRDPA MSSVTLTPPTSPERVQTVDPQSVQKWVKPSSVSDGRNSDSTSHH GGKIPRKLANHVVDRVWQCCMMRAQNKRKYSASSGLCBEATA AKVASWDFVBATQRTNCSCLEHKNLKSRNAGQGQAPSLGOQQ ILLPHKTNKKQEKSEKPQKRPLTFPHHRVSVSDDVCMD\ADS\A SGRLV\1SAP\DSQ\VRFSNIF\TYNDVAK\TYQMHTTEMANSPQ PPPLSP\HPCDVVDBGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EBRIBSLSGSPPPQYGRAVBTVVGTAVALBEDBANTAMKYYK FPKKLENVELPPDLPSDRYKDDFVGPFGGSSVTSVTLEMVQCTK PLKVSDELVQQYQIKNQCLSALASDABGPEKIDPVAFVEGDESP LFPDKKDVGNSERRAGKKHKVENGTSSVTVLSHEDAMSLPSPS ILGDAPRFTSSLARPSTSLITYDSDLAVSYTDLDNLFNSDRDELT PGSKRSANGSDDKASCKRSKTGRLDPLSCTSTADLSKMYTPPPS LEGHTMGFSPHNMNKSYGSUDTTPGGTVLEGNSSSIGAQPKIE VDEGPCSPKPSBIKDFSVYVKPRNCQILVGCSMFAPLKTLPSQY LFILILPBECIYRGSWTVGKRELLSSGPSPFIKEGDGSNMDQE VTGATTPQTHTSCGMPPSSAPPSDSGGLLPBSSTPRFFPTPTP RTFRTFRGAGGPASAGGSVKYENSDLYSPASTSTCRELNSVEP ATVPSIPBAHSLYNNLLILSSVMNLPKGNNSGLFFEDELD IGRNTDGGKBARRFFRALBATSARHVNGGGCLRVILASUFFEDELD IGRNTDGGKBARRFFRALBATSARHVNGGCCQDILL LEGGQPMDNMSGGKVDEALVKSSCLHPMSRRDCCNDCYLA LEGGQPMDNMSGGKVDEALVKSSCLHPMSRRDCCNDCYLA LEGGQPMDNMSGGKVDEALVKSSCLHPMSRRDVSMQCSQDIL RMLLSLQPVLQDAIQKRGTVTRPMGVGGPLINGGFIKMARGGSYG TDESSEPLPJFIFTLIGGSDSLAGPNSRLLKLAFAQV CKYDLGFYLASLPLBGSLLSGNUAPTSGSLTGAPRTRENL TTGSIRWGSTASKKLSEKLVABKYSQAADANBAFSKLKLYAQV CKYDLGFYLASLPLBGSLLSGNUAPTSGSLTAPTTGNANTLTTASTSSSS SNINSGVSSNKLPSFPPFFSMMSNAAGSMSTQANTVGSGQLGQ GYSALQTAGISGSSSSLPTQPHPDVSSTMDRRWGGTLTDGDER	1 1			NTWPSPHKFDPDRFDDELVMKTPSSLGPSGTQECPBLRPAYMVT
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OKKMEGGROPPMRAVLCTSKAVIRILLERCEMNINFYRIGKRY VKYEKOEKPINKSBHLSCSTFYFLHGDSNYCTSVEINQHQPVY LLSEBHITLAQQSNSFFQVILCTFGLNGTLITQAFKMSDSATKK LIGEWQFYFISCCLKEMSBEKQEDMDWEDGLAAVEVLVAGVR MIYPACFVLIVPGDST PTSPSVGTHGSSSCLGVHQVPASTROPA MSSVTLTPFTSPESVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH GGKIPRKLANHVVDRWWGECNNNRAQNKRKYSASSGLCEBATA AKVASHDFWASTQFTNCSCLSHKNLKSRNAGQGQAPSLGOQQ ILPKHKINKKQEKSEKPQERPLTPPHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRENIR\TDQNAK\TTQHHGTEMAMSPQ PPLES\HPCDVDGSVTHTPGGSHFYQHFTDFLYBFKPM EDRIDSLSQSPPPQVQRAVEPTVYVGTAVNLEEDBANIAWKYYK FPKKLDVZELPPQLFSDKKNDDPVGPFGGSSTTSVTEMWQCKK PKKLSVSELPQQVJQ KNQCLSATASDABOEPKIDPYAFVEGDEF LFPDKSDGRONSERRAGKHKVEDGTSSVTVLSHEEDAMSLPSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDDLFHSDERDELT PGSKRSANSSDDKASCKEKKTONLDPLSCTSTADLEMWFYPPS LEQLIMGFSPMMNNKEYGSMDTTGGTVLEGNSSJCAQPKIE VDEGPCSPKPSEIKDFSVYVKPRNCQILVGCSMPAPLKTLFSQY LELIKLPEGCTYRGSWTYGKLELLSGGFSMPFTKEGDGSNMDQE YGTAYTPQTFTSCMPPSSAPPSNSGAGILPSPSTCRPHPTRTP RTPRTFRGAGGPASAQGSVKYENSDLYSPASTPSTCRPINSVEP ATVPSIPBAHSLYVMLLISSSVMNLFKDCNSDSCCICCCNNIK GADVGVTPDFTQBAQVRCTCGFSAVMRKFGNNSGLFFEDELD IIGRNTDCGKEBKRPRALRATSAEHVNGGLKESKLSDLILL LQQCTNLFSIPGAADQDPPKSGVISMWVRVBERDCCNDCYLA LEBGRQPHDNMSGGKVDEALVKSSCLHPMSKRNDVSMQCSQDIL RMLSLQPVLQDAIQKKRTVRPMGVQGFIKMAGRGSTG TDESSEPLPIFIFILGYDYDTVLVLSPFALPTWERLMLEPGOSQR DLAYVVLCPRWEALINGAKSPFROLTA TYSSCRLGORFPVSRLL TDGIMRVGSTASKLSEKLVABWPSQAADGNNEAPSKLKLYAQV CRYDLGPTLASLPLDSSLLSQPNLVAPTSQSLTTPPQMTTGGNA NTPSATLASASSTMTVTSGVATSSTAVTNNSTLTTASTSSSSS SNLNSGVSNKLPSPPPFGSMMSNAAGSMSTQANTVQGQLGQQ CYSALQTAGISGSSSSLPTQPHDVDXSSTTHDROKVGIPTDGDSH				
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RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSI PEAHSLYVNLILSESVMNLPKDCNSDSCCICVCNMNIK GADVGYYIPDPTQEAQYRCTCGFSAVWNRKFGNNSGLFFEDEI.D IIGRNTDCGKEBEKRPRALRATSAEHVNGGLKBSEKLSDDLILL LQDQCTNLPSPFGAADQDPPPKSGVISNWVVBERDCCNDCYLA LEHGRQPMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALINGAKSPFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNBEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSQQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH	)	j		
ATVPSIPEAHSLYVNLILSESVMNLPKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDBLD IIGRNTDCGKEABKRFRALKATSAEHUNGGLKESEKLSDDLILL LQDQCTNLPSIPFGAADQDPPPKSGVISNWVRVBERDCNDCYLA LEHGRQFWDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGFIKMAGRGSYG TDESPBPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSPFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMINTGNA NTPSATLASASSTMTVTSGVAISTSVATANSTLTTASTSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH		1		
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IIGRNTDCGKEABKRPRALRATSAEHVNGGLKBSBKLSDDLILL LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVBBRDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGFLTWQDFHKMAGRGSYG TDESPBPLPIPTHILGYDYDYLVLSPFALPYMERIMLEPYGSQR DIAYVVLCPENEALLINGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGFYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTAETSSSSS SNLNSGVSSNKLPSFPFFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSBSTMDRDKVGIPTDGDSH		1		
LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVBERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGFLTWQQFHKMAGRGSYG TDESPEPLPIPTFILLGYDDYLVLSFFALPYWRRLMLEPYGSQR DIAYVVLCPENEALLMGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGFYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTAETESSSS SNLNSGVSSNKLPSFPFFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH	'	1		
Lehgrofmonnsgkvdealvkssclhpwskrndvsmocsodil Rmllslopvlodaiokkrtvrpwgvogfliwoofhkmagrgsyg Tdesperplpitfilgydydylvlspfalpywerlmlepygsor Diayvvlcpeneallingarspfroltaiyescrlgohrevsrll Tdgimrogstaskklseklvaewpsoadgonrepsklklyaov Crydlgyllaslpldssilsopnlvaptsoglitppownthgna ntpsatlaslasstmtvtsgvaistsvatanstilttaetssss Snlnsgvssnklpspppgsmnsnaagsmstoantvoggolggo Otsalotagisgessslptophpdvsestmdrokvgiptdgdsh		1	-	
RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTFILGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALI.NGAKSPFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWPSQAADGNBAFSKLKLYAQV CRYDLGPYLASLPLDSSILSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTAGTSSSSS SNLNSGVSSNKLPSPPPFGSMNSNAAGSMSTQANTVQSQQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH		}		
TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLINGAKSPPROLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMINTGNA NTPSATLASSSTMTVTSGVAISTSVATANSTLTTASTSSSS SNLNSGVSSNKLPSPPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH		i		
DIAYVVLCPENEALLINGAKSFFRDLTATYESCRLGQHRPVSRLL TDGIMBVGSTASKKLSEKLVABWFSQAADGNNBAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLTTPPQMINTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSBSTMDRVKYGIPTDGDSH		į	i	
TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH			I	
CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSHSTMDRDKVGIPTDGDSH		i		
ntpsatlasaasstmtvtsgvaistsvatanstiltastssss sninsgvssnkipspppgsmnsnaagsmstqantvqsgqiggq qtsalqtagisgesssiptqphpdvsestmdrdkvgiptdgdsh		Í	·	
SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH		ì	ľ	
QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH	}	1		
	. ]	]		
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		<del>L</del>		THE TAXABLE TENT DESTROSS ANTIONING LIEUAN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion.
L	sequence		\=possible nucleotide insertion)
			TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAPSAP
ļ			TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPBCIRLYAPP
1	(		FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC
ł			TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV
Į.			QMSSLPWRVVIGRIGRIGHGELKDWSCLLSRRNLQSLSKRLKDM
1			CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS
i			TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
1			APNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP
			GSHYPHGGDAGXGQSTDRLLSTEPHERVPNILQQPLALGYFVST
l			AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS
1			KHSHPLDSNOTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIH
5370	1226	716	PVVLNQLYNFIMNML  DWCDYLWLODAAOARSCHDDOCOFMUDDIWARCHELL WOLDDON
/ 0	2200	,10	RWSRKLIELRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL
] .			DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR
	İ		AGRTPLHLAKSKINIIQEGHAQCLKAVR/HGGEADHPYAEGVSG
			APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR
	1		AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLYRACTSLPVG
1 .			GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKQS
			SKENTRTVEKLYKCSVDIRKIRR\*KDGYF*RMKPMLKKLRI/F
1 .			LQELGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE
	ļ		ELIKLIEQFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT
1 1	0.0		AAPNVFHNPVEKNKQMVRILQESYLDVGGSEANMKVWLLKLLSQ
i i	i .		NPFILLINSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC
1			PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLBERM
			QGLLREGISIAQIRBTPMVLELTPQIVQYRIRKLNSSGYRIKDG HLANLNGSKKEFRANFGKIQAKKVRPLFNPVAPLNVEB
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME
ļ :			PLRLLILLFVTBLSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR
j			RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG
} ]		•	GTLTITLRNLQPHDAGLYQCQSLHGSBADTLRKVLVEVLADPLD
1 1			HRDAGDLWFPG\DLRASRM?MWSTASPGASWKEKSPSHPLPSFS
1			SWPASFSSRF*QPAPSGLQPCMDRSQGHIHPVNWTVAMTQGISS
			KLCOG
5373	2814	346	VKKTKSIPNSAMQEMEVYVENIRRKFGVPNYSPPRTPYTPNSQY
	,		QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
1 1	]		TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDVLDKSTASDASTKTCOAGGLGGEDVDVEDOLGARATTTTT
1	)		ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLNLDRSKAEMDLKBLSESVQQQSTPVPLISPKRQ
	ļ		IRSPPQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
] ]			DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
			TNPVEIKERLKSTSPASEKADPGAVKDKASPEPEKDPSGKAKPS
	1		PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
	1		GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPKTPVLTRSSAQ
}			TSAAGATATTSTSSTVTVTAPAPAATGSPVKKORPLLPKE\TAP
	ļ		AVQRSCGTSSTVQQKRITQSPSTSTITLVTSTQSSPLVTSSGSM
	1		STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TRI
100			YNDLSKN/TTWKAQLAKDSQGLRIBIEKLQWLHQQEL/SEMKHN
1	ļ		LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
	l		ANFKKBAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ
	1		\QBADAE\VNTETLNKSSQGSSSSTQSAPSKTASA\SKEKETSA
	i		EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
5374	2814	345	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
3374	2014	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
	1		QMLLDPTNPSAGTAKIDKQEKVKLNPDMTASPKILMSKPVLSGG
	1	ļ	TGRRISLSDMPRSPMSTNSSVATGSDVEQDABKKATSSHPSASE ESMDPLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
j l	ļ	1	KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
	j		IRSRFQLNLDKTIBSCKAQLGINBISEDVYTAVEHSDSBDSEKS
]	j		DSSDSRYISDDEQKS*GTSQEDTEDKEGCOMDKEPSAVKKKPKP

Do beginning nucleotide location corresponding to first mino acid amino acid amino acid amino acid sequence of residue of amino acid sequence seque	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No: location corresponding to first mains acid residue of mains acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue resi	_			(A=Alanine, C=Cysteine, D=Assartic Acid R=
location   corresponding   to first   amino acid   residue of amino acid   residue of amino acid   sequence			L .	Glutamic Acid. F=Phenylalanine G=Glycine.
corresponding to first amino acid amino acid amino acid sequence should be sequence.   10.116.  10.116.  10.116.  10.116.  10.116.  10.116.  10.11				
to first amino acid residue of amino acid amino acid amino acid amino acid sequence    S-Setine, T-Threonine, X-Unknown, *=Stop codon, /=possible nucleotide deletion, \( \) \   Codon,				L-Leucine, M-Methionine, N-Asparagine,
residue of amino acid sequence (Codon, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide insertion)  TREVET KERKENSTERSE KERMINGERSE PERFORMENCE AND AND AND AND AND AND AND AND AND AND	1		1	
antino acid sequence  Codon, /=possible nucleotide insertion)  TRPPETREELASTERASERADRAYGNASERREBORSCARRES  PREVENCIA CONTROLL STATEMENT OF THE CONTR	ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Sequence	i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
TRIPPER INSELLASTISMAS PRADPECAYMON SPERIOP SCHARGE  HPP KNOKLAGASD TOUR TYVELIGAD BOSS   MENUTISAS   GRINKER PERPS PKODVOKIT PSTTVOSHS P PSTVITUSS   GRINKER PERPS PKODVOKIT PSTTVOSHS P PSTVITUSS   GRINKER PERPS PKODVOKIT PSTTVOSHS P PSTVITUS   AVORSOSTISTVOKER TOSS PSTSTITLATETOS PELVITS SCISH STUVS SVANGULE INTELASIVA AND ANTAKAS P KANGE PLANE   TVINLS KIN YTWINGLASD SCILL I ELEKALOMINOSI I, SEMISH LEITAMBARG SHOEGERIL ALIVAKOLISLE KOON ANTEKTEN   TVINLS KIN YTWINGLASD SCILL I ELEKALOMINOSI I, SEMISH   LEITAMBARG SHOEGERIR LIAVAKOLISLE KOON ANTEKTEKOM   ANTEKER T PTYCCHTES YCDYTOO \( \) OAMPEH \( \) MINGCITS AT ANTEKER PTYCH CONTROL \( \) OAMPEH \( \) MINGCITS ANTEKER PTO \( \) OAMPEH \( \) MINGCITS ANTEKER PTO \( \) OAMPEH \( \) MINGCITS ANTEKER PTO \( \) OAMPEH \( \) MINGCITS ANTEKER PTO \( \) OAMPEH \( \) MINGCITS ANTEKER PTO \( \) OAMPEH \( \) MINGCITS ANTEKER PTO \( \) OAMPEH \( \) MINGCITS ANTEKER PTO \( \) OAMPEH \( \) OAMPEH \( \) MINGCITS ANTEKER PTO \( \) OAMPEH \( \		amino acid	sequence	Codon, /=possible nucleotide deletion,
FIRE PLONGER (KENDETTS PLYVELIGLDEDES) PRINTINGENS PER GRANKER PREPER (MOUVERER PER THY TURS SHANGATATITS STANGATATITS THE STAY OF THE ANALOGO STANGATATITS THE STAY OF THE ANALOGO STANGATATITS THE STAY OF THE S	ŀ	sequence	-	\=possible nucleotide insertion)
GRNKKEFERPSPERDVVGKTPSTTVGSRISPFRTPVLTRSSAS  13AAGATATTSTSTVVTVARAPATATSFAKSPERVGSPLTFSCSTAF  AVORSGTISSTVORKTTOSPSTSTITLATSTGSSPLVTSSGSS  STLVSSVAGDLETGSADAVADILAKTSSLVANSLETAT VTSTAFAT  14DLSKONTYTWROLARDOGGLETETETETTUTSTGSSPLVTSSGSS  LELTWARDRGSRISGSREDLLATAVKTSSLVANSLETAKOR  ANEKERA FYVCORTS YCCDYCON (AMEPRILAGORILASSMYSS)  LELTWARDRGSRISGSREDLLATAVKTSCLEEKQOVETSKKORC  ANEKERA FYVCORTS YCCDYCON (AMEPRILAGORILASSMYSSTAFATSKAR)  LELTWARDRGSRISGSREDLLATAVKTSCLEEKGOVETSKKORC  ANEKERA FYVCORTS YCCDYCON (AMEPRILAGORILASSMYSTEKTSAR  LEGKESGSTLDLAGGREFPSSTILLGONGGSDERSTRAANSFEKTSTSA  SEKKESGSTLDLAGGREFPSSTILLGONGGSDERSTAANSFEKTSAR  LEGKESGSTLDLAGGREFPSSTILLGONGGSDERSTAANSFEKTSTAS  EKSKESGSTLDLAGGREFPSSTILLGONGGSDERSTAANSFEKTSTAS  BERRST YRSORD ANGENSALLASSMYSTATSGTSGSRESSYTTGTTSTAK  ROAN FRAILE PROPERTY ANGENDALAGGREFPSSTATTSTATSK  ROAN FRAILE PROPERTY ANGENDALAGGREFPSSTATTSTATSK  ROAN FRAILE PROPERTY ANGENDALAGGREFPT (ANGENDALAR PROVANCH LICTORS P	<b> </b>			TNPVEIKEBLKSTSPASEKADPGAVKOKASPRPEKOPSGKAKPS
### SAAGATATTSTSSTYTVTARARATASSPYKKOPELIPKS Typessions of the state of the sta	ŀ			PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRB
AVORSOGTSSTVOORETTOSPETSTITLIVISTOSSENJYTSEN STEUSSVROEDER (ETERASADVARDIA YNTYSKI, ADMINISTRY) TYTE VROLSEN / TYTE (VROLSEN / TYTE VROLSEN / TYTE VROLSEN / TYTE VROLSEN / TYTE VROLSEN / TYTE VROLSEN / TYTE VROUDER /	Į.	1	· ·	GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
STUVSSVINGLEPIGTASAUVADITAKTIKI, MIDALKETIT YINDLSKIN\TYTIKAQLAEDSGGLIRE ITEKI, MIDALKETIT YINDLSKIN\TYTIKAQLAEDSGGLIRE ITEKI, MIDALKETIT YINDLSKIN\TYTIKAQLAEDSGGLIRE ITEKI, MIDALKETIT YINDLSKIN\TYTIKAQLAEDSGGLIRE ITEKI, MIDALKETIGANDAN LEETIMAANGANGRIRORETISALLAEVKUOLELEKKOOLUDETKIKOOLUDETKIKOOLUDETKIKOOLUDETKIKOOLUDETKIKOOLUDETKIKOOLUDETKIKOOLUDETKIKOOLUDETKIKOOLUDETKIKOOLUDETKISA LEEKERSGOTTUJA OLORICETKISA LEEKERSGOTTUJA SEVALIKA LEEKERSTA LEEKERSGOTTUJA SEVALIKA LEEKERSGOTTUJA OLORICETKISA LEEKERSGOTTUJA SEVALIKA LEEKERSTA LEEKERSGOTTUJA OLORICETKISA LEEKERSGOTTUJA SEVALIKA LEEKERSTA LEEKERSGOTTUJA SEVALIKA LEEKERSGOTTUJA SEVALIKA LEEKERSTA LEEKERSGOTTUJA SEVALIKA LEEKERSGOTTUJA OLORICETKISA LEEKERSGOTTUJA OLORICETKISA LEEKERSGOTTUJA OLORICETKISA LEEKERSGOTTUJA OLORICETKISA LEEKERSGOTTUJA LEEKERSGOTTUJA LEEKERSGOTTUJA LEEKERSGOTTUJA LEEKERSGOTTUJA LEEKE	1	ì	1	TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
NNIJ.SKN\TYMKAQLAEDSGLRIETEKIQMINGGE\\ SAMPONTEKTKOMC     APPEREAT PYCCHYTSYCOPPO\\ QAHIPBEI\\ MESCTYSATAGA     APPEREAT PYCCHYTSYCOPPO\\ QAHIPBEI\\ MESCTYSATAGA     APPEREAT PYCCHYTSYCOPPO\\ QAHIPBEI\\ MESCTYSATAGA     APPEREAT PYCCHYTSYCOPPO\\ QAHIPBEI\\ MESCTYSATAGA     APPEREAT PYCCHYTSYCOPPO\\ QAHIPBEI\\ MESCTYSATAGA     APPEREAT PYCCHYTSYCOPPO\\ QAHIPBEI\\ MESCTYSATAGA     APPEREAT PYCCHYTSYCOPPO\\ APPEREATION     APPEREAT PYCCHYTSYCOPPORT     APPEREATION     APPERE	1		ì	AVQRSCGTSSTVQQREITQSPSTSTITLVTSTQSSPLVTSSGSM
LETTMABRIGSHOGERORLIANVEKCLELEKOONUTETIKKOON  NEKERATEVICKINTS COUPCO, ONHIPERI (MISCTIGARDAD  QEADAE\WITETINKSSQGSSSTQSAFSETASA\SKEKETSA  KOKEGGSTIDLIGGSRETTSGI LIGGNIQGSDHAR, SINKSWSSS  DRIRGS\TRISINH\TPSTURKSSLIDHGKSSAGATFICTSK  HIPLAGEKEMILERKICKGFLANGTAQPELLISGSPGGSSEQTIGES  RGROQGTISVA\GGAQAARGHARHARHARHARHARHARHARHARHARHARHARHARHARH	1			STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
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DERRIGS VIRSDIM/TPS TORICRS LIAPGRES RACTPPICTISK  1116 HIFLARKERWIERCROGIPANG PAGRILISCOSPOPTIGIESE RGLRQQGTSVA\QSCAQAPGRAHRCAHCRHPPCWVA\LWI.HTR RQQA/RGILPLOPESCERFRIRD PIGALIRQVIRAAATDQWFACH LCOSPIROWALVILAILARIBEARACGPPACKHARDAFWRKAAS SSILRRCHPSRPRGPPPICONGGRSILPTWOQ/LWVAHKRVHV SRRPY-RGGPPAKVVMOPPPRGOESPOPTOTPFOFORDWOPPY\CQC CCGRFFRIK\PWILSRHACTSGERPHO/CSRGCS\RFPINDY LTS\HRRTHTITAROPYPCKEGGRFRHKPULSHSKHKRSEGS AQAAPGGSPQLPACHQGSAABUTPAVPLKPAQEPPCAP PEHP ODPIRAPPSLYSCDDCORSTRLERPLARARQRHTGRPTCARC GRWFRKTHLIVAISRWHGSRPFILARKCREPLFRASGSGSRN SAEWARPROGPVCPDCOKAFRIKEYILAAHRPIATPARKPYCP DCKAFSQKSRILVSHRRITUTERPYACTPACKC GRWFRKTHLIVAISRWHGSRPFILARKCREPLFRASGSGSRN SAEWARPROGPVCPDCOKAFRIKEYILAAHRPIATPARKPYCP DCKAFSQKSRILVSHRRITUTERPYACTPACKC GRWFGKTHLIVAISRWHGSRPFILARKCREPLFRASGSGSRN SAEWAFSKORGORGVENGGSRQAWANDGSKRIVSTRYGSGRWIANA ARPIARVGGRVEVIGKGHRGTVAAVGATLFATCKWOUILDRAKG ROGTVOGRKYPTCDEGGICTPURGSQIQVPEDATTSPBTPDS SASKVLKRBGTDTTAKTSKLRGLKPKKAPTARKTTTRRPPTRP ASTIGVAGASSSLAPSGSASAGELSSSESTPAQTFLAARITIFT VLITSPAAVPPIDSPSRKBESGLRAQVROLISRKESTRAGTLARATIFT ASTIGVAGASSSLAPSGSASAGELSSSESTPAQTFLAARITIFT VLITSPAAVPPIDSPSRKBESGLRAQVROLISRKESTRAGTLARATIFT ASTIGVAGASSSLAPSGSASAGELSSESTPAQTFLAARITIFT VLITSPAAVPPIDSPSRKBESGLRAQVROLISRKESTRAGTLARATIFT ASTIGVAGASSSLAPSGSASAGELSSESTPAQTFLAARITIFT VLITSPAAVPPIDSPSRKBESGLRAQVROLISRKESTRAGTLETTOR KLIKELEKRITQLEQVOKAGERWEGQADLQRRIKKRABAL ASKIPKBERMAPTADAIAHATDAIAFRAKTROGERTARKABAL GRAKFIKERRAGAGGGRVAGAGGGGRASSYOLMOLISRGRAKRAL DARSTIDBLIKGVODAALGREMVEMILTDENINILERVERLEFTVG DLEANNEMNDELQRARBTELELRGCDMAARARMISHILLAMPD SETAPKIKTICLKARALIRGAGGRASVERAQRAVENAA QETVADVQQTITKKYRQLITABLIQUMREHTMQGREFLEMOCS REGIGLAGAGGGAGGGRASSYOLMOLISRGRAGGRAGGGAGGRAGGGAGGGAGGGAGGGAGGGAGGG	1		]	
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AESTIDELKEQVDAALGAEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMDRIQENARETELELREQLDMAGGAVERAQRYERA QETVADYQQTIKKYRQLTAHLQDVREELITNQQBASVERQQQPPP BTFDFKIKFABTKAHAKAIEMELRQMEVAQARMEMSILITAFMPD SFLRPGGDHDCVVLILIMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSPAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELHKDQLDETVNVEPLT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFQQVSDTLLDCRRHLTWVVAVLQEVAAAAAQLI APLABNEGLLVAALEKLAFKASEQIYGTPSSSPYECLRQSCNIL 1STMNK\LVTAMQEGSYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRBTVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADER IEKVQTRLESTQALLRKKEKEFETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAITGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITTTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLAKEEQQDDTVYMG KVTFSCAAGFGQRRRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WEGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGCQYIFIFRGMRWEBQP  5378 2009 664 QASGTTLRPIPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL		·		VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKBRYMEEMADTADAIEMATLDKEMAEKRAESLQQEVEALKER
DLBAMNEMNDELQENARETELELREQLDMAGARVREAQRRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP BTFDFKIKFAETKAHAKAIEMEIRQMEVAQANREMSILITAFMPD SFLRPGGDHDCVLVLLIMPRALICKAELIRKQAQEKFELSENCSE RPGIBRAAGEQLSFAATGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RIKAFLQGGGATDIALLIRDLETSCS\DIRQFCKXIRRMPGT DAPGIPAALAFGPQVSDTLLLCRKHLTWVAVLQEVAAAAAQLI APLAENEGLLVAALEKLAFKABEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGIGLKLEDRETVIKBLKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADER IEKVQTRLEETQALLRKKEKSFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPSGIATLVSGIAGEEQQR GAIPQQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEEFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESGEGG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGGQYTFIFRCMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRIVIMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLKEQNARLKDALV
QETVADYQQTIKKYRQLTAHLQDVNRELITNQQESVERQQQPPP BTFDFKIKFABTKAHARAIEMEIRQMEVAQANRIMSILITAFMPD SFLRFGGDHDCVLVLLLMPRLICKAELIRQAQEKHELSENCSS RPGLRGAAGEQLSFAAIGLVY\SIMPAAGHRYHRY*CHALSQCR RPGLRGAAGEQLSFAAIGLVY\SIMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSIDFLIELHKQDLDRTVNVEPLIT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLIRDLETSCS\DIRQFCKXIRRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQBVAAAAAQLI APLABNEGLLVAALERLAFKASBQIYGTPSSSPYBCLRQSCNIL ISTMNK\LVTAMQEGRYDABRPPSKPPP\VELRAAALRAEITDA EGLGLKLBDRETVIKBLKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIBKVQTRLEETQALLRKKEKBFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEBQOR GAIPGQAPGSVPGPGLVKDSPLLIQQISAMRLHISQLQHENSIL KGAQNKASILASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEBQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESGEGG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGGQYTFIFRCMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVIMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKBRYMEEMADTADAIEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ
BTFDFKIKFABTKAHAKAIEMBIRQMEVAQANRHMSILITATMPD  SFLRPGGDHDCVLVILIMPRLICKABLIRKQAQBKFELSENCSB  RPGLBGAAGEQLSFAATGLVY\SIMPAAGHRYHRX*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIBLIHKDQLDBTVUVBPLIT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGGATDIALLIRDLETSCS\DIRQFCKXIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLABNEGLLVAALEBLAFKASBQIYGTPSSSPYBCLRQSCNIL ISTMNK\LVTAMQEGBYDABRPPSKPPP\VELRAAALRAEITDA EGLGLKLBDRBTVIKBLKKSLKIKGBELSEANVRLITLLEKKLDS AAKDADER IEKVQTRLEETQALLRKKEKEFRETMDALQADIDQL EARRAELKQRLINSQSKRTIEGLRGPPPSGIATLVSGIAGEBQOR GAIPCQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET INQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVIKBTVSQRPGATVPTDFATFPSSAFLRAKEBQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESGEEG\F*YHBVRQAEGES* /WRGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGQQYIPIFRGMRWEBQP  5378 2009 664 QASGTTLRPLPDDLPQLKRREATSRNRALKPRGRIVIMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMKSKMQBQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLBEKVRELRETVG
SPLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSPAAIGLVY\SIMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDPLIELLHKDQLDRTVNVEPLIT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAPLQGGQRATDIALLLRDLETSCS\DIRQPCKKIRRRMPGT DAPGIPAALAPGPQVSDTLLDCRRHLTMVVAVLQBVAAAAAQLI APLAENEGLLVAALEBLAPKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGIGLKLEPRETVIKELKKSLKIKGBELSEANVRITILEKKILDS AAKDADER IEKVQTRLEETQALLRKKEKEFRETMDALQADIDQL EARKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GATPCQAPGSVPGPGLVKDSPLLLQUISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVIKBTVSQRPGATVPTDPATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGSEGEEG\F*YHEVRQAEGES* /WRGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIPIFRGMRWEBQP  5378 2009 664 QASGTTLRPLPDDLPQLKRREATSRNRALKPRGRIVIMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKRRYMEEMADTADA I EMATLDKEMAEERARSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLEQDARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLMLEEKVRELRETVG DLEAMNEMNDRLQENARETELELREQLDMAGARVREAQKRVEAA
RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKXIRRRMPGT DAPGIPAALAFDQPUSDTLLDCRRHLTNVVAVLQEVAAAAQLI APLAENEGLLVAALEKLAPKABEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEPRETVIKELKKSLKIKGEELSEANVRITILEKKILDS AAKDADER IEKVQTRLEETQALLKKREKEFETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRKREKEFETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRKREKEFETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GATPGQAPGSVPGPGLVVGSPLLLQOISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET INQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVIKETVSQRPGATVPTDPATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGSEGEG\F*YHEVRQAEGES* /WEGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIPIFRGMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRIVIMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL EAKRRYMEEMADTADA I EMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLECQNARLKDALV RMRDLSSSKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLMLBEKVRELRETVG DLEAMNEMNDRLQENARETELELREQLDMAGARVREAQKRVRAA QETVADYQQTIKKYRQLTAHLQDVNRELINQQEASVERQQQPPP
KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLIRDLETSCS\DIRQFCKXIRRMPGT DAPGIPAALAFGPQVSDTLLLDCRKHLTWVVAVLQEVAAAAAQLI APLABNEGLLVAALEKLAFKASBQIYGTPSSSPYBCLRQSCHIL ISIMNK\LVTAMQEGRYDABRPPSKPPP\VELRAAALRAEITDA EGLGLKLBDRETVIKBLKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADER IBKVQTRLEETQALLRKKEKBFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEBQOR GAIPGQAPGSVPGPGLVKDSPLLIQQISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEBQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESGEGG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRCMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKBAKEAL EAKRRYMEEMADTADA IEMATLOKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQIBEQNARLKDALV RMRDLSSSEKQEHVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLBEKVRELRETVG DLRAMNEMNDRLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQBASVERQQQPPP BTFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD
RIRAFIQGQRATDIALLIRDLETSCS\DIRQFCKXIRRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVAVIQEVAAAAAQLI APLARNEGLIVAALERILAFKABBQIYGTESSEYYRCIRQSCNIL ISTMIK\LVTAMQBGBYDAERPPSKPPP\VELRAALRAEITDA EGIGLKLEDRETVIKBLKKSLKIKGEELSEANVRLITLEKKLDS AAKDADER IEKVQTRLEETQALLRKEKBEFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET INQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPARAQEKGQITLSCGESGEEG\F*YHBVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEBQP 5378 2009 664 QASGTTLRPLPDLPQLKRRATSRNRALKPRGRIVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL EAKERYMBEMADTADAIEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQIBEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAZEMVEMLTDRNLNLBEKVRELRETVG DLEAMNEMNDRLQENARETELELREQLDMAGARVREAGKRVEAA QBTVADYQQTIKKYRQLTAHLQDVNREITNQQEASVERQQQPPP BTFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKABLIRKQAQSKFELSENCSB
DAPGIPAALAFGPQVSDTLLDCRKHLTWVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGSYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLITLEKKLDS AAKDADERIEKVQTRIEETQALLRKKEKEFRETMDALQADIDQL EARKAELKQRLNSQSKRTIEGLRGPPPSGTATLVSGTAGEEQQR GAIPCQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET INQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVIKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQITLSCGESGEEG\F*YHBVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGQQYIPIPRGMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRIVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMKSKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEEKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRELRETVG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASFUSEQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELLRKQAQEKFELSENCSE RPGLEGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR
APLAENEGLLVAALEBLAPKASEQIYGTPSSSPYBCLRQSCNIL  ISTMNK\LVTAMQEGBYDABRPPPKPPP\VELRAAALRAEITDA  EGIGLKLEPRETVIKBLKKSLKIKGBELSEANVRITILEKKILDS  AAKDADER IEKVQTRLEETQALLRKKBKEFFETMDALQADIDQL EARKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GATPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET INQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVIKBTVSQRPGATVPTDPATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSSLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESGEGG\F*YHEVRQAEGES* /WRGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIPIFRGMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRIVIMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMKSKMQBQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSEKQEHVK\CQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAKEMVEMLTDRNLNLEKVRELRETVG DLEAMNEMNDRLQENARETELELREQLDMAGARVREAQKRVEAA QBTVADYQQTIKKYRQLTAHLQDVARELITNQQEASVERQQQPPP ETFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSILTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSB RPGLBGAAGEQLSPAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDRTVNVEPLT
ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGIGIKLEPRETVIKELKKSLKIKGEELSEANVRLTILEKKILDS AAKDADERIEKVQTRIEETQALIRKKEREFRETMDALQADIDQL EAEKAELKQRINSQSKRTIEGIRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVVRDSPILIQQISAMRIHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEEPGSELPAGALYRKTSQILET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVIKETVSQRPGATVPTDPATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQQLQHQLHSRLIS  5377 762 1106 DVPCKRVLPAKAQEKGQITLSCGESGEGG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIPIFRCMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRIVIMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKRYMEEMADTADA I EMATLDKEMAERRARSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLEQDRACKDALV RMRDLSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLMLEKVRELRETVG DLEAMNEMNDRLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQBASVERQQQPPP BTFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSB RPGLIEGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFILELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG
EGIGLKLEDRETVI KELKKSLKIKGEELSEANVRLITLEKKLDS AAKDADER IEKVOTRLEETQALLRKKEKEFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSEIDATLVSGIAGEEQOR GAIPGQAPGSVPGPGLVKDSPLLIQQISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDPATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESEGG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFTLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRCMRWEEQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMESKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLKEQDARLKDALV RMRDLSSSEKQEHVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAZEMVEMLTDRNLNLSEKVRELRETVG DLERAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQBASVERQQQPPP ETFDFKIKFAETKAHAKALEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLBGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKQQLDETUNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKTRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI
AAKDADERIEKVQTRLEETQALLRKKEKEFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLIQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDPATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS*WPGYDGWWGGQYIFIFRGMRWEBQP 5378 2009 664 QASGTTLRPLPDLPQLKRRFATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMESKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEEKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRELRETVG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELINQQBASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELLRKQAQEKFELSENCSE RPGLEGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\YYKKVGSLYPEMSAHERSLDFLIELLHKQQLDETUNVEPLT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAFGIPAALAFGPQVSDTILDCRKHLTWVAVLQEVARAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYBCLRQSCNIL
EARKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET INQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDPATFPSSAPLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKRYMEEMADTADA IEMATLDKEMAEERABSLQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\CQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRELRETVG DLEAMNEMNDRLQENARETELELREQLDMAGARVREAQKRVEAA QBTVADYQQTIKKYRQLTAHLQDVARELITNQQEASVERQQQPPP BTFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSILTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSB RPGLBGAAGEQLSPAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYGHLYSIHLARQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLLRDLETSCS\DIRQFCKXIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLABNEGLLVAALEKLAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA
GAIPCQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET INQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGSESGEGKF*YHBVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIPIPRGMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL EAKRYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSKQEHVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMITDRNLINLBEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVWRELITNQQEASVERQQQPPP BTFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSLITAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSB RPGLBGAAGEQLSFAAIGLYY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKITRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYBCLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS
KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQILET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDIVEKL KDEVIKBTVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSSRLIS  5377 762 1106 DVPCKFVLPARAQEKGQLTLSCGESGEEG\F*YHBVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIPIFRGMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL		•		VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKRYMEEMADTADA IEMATLDKEMAERRABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLEQNARLKDALV RMRDLSSSEKQEPVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMITDRNINLEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVRRELTNQQEASVERQQQPPP BTFDFKIKFAETKAHAKAIEMELRQMEVAQARRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSB RPGLBGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFILELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTILDCRRHLTWVVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMIK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRBTVIKKLKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFETMDALQADIDQL
LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHGSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYLFIFRCMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKRRYMEEMADTADA I EMATLDKEMAERRARSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLEQDRALKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNIMLEKVRELETVG DLEAMNEMNDRLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQBASVERQQQPPP BTFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSB RPGLBGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFILELHKDQLDETUNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTILDCRKHLTWVVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRGSCNIL LISTMIK\LVTAMQEGYDAERPPSKPPP\VELRAALRAEITDA EGIGLKLEPRETVIKBLKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR
KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHIGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRRFATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMESKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEEKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRELRETVG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQRRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQBASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRFGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLEGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETUNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKTRRMPGT DAPGIPAALAFGPQVSDTILDCRRHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTILEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFETMDALQADIDQL EAEKAELKQRLMSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPCQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL
KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESGEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHIGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMESKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEEKGSDGAASSYQLKQLBEQDARLKDALV RMRDLSSSEKQEHVK\CQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRELRETVG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAQ QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP BTFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLEGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKQQLDETUNVEPLT KAIKYYQHLYSIHLABQPEDCTMQLADHIKTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTILDCRKHLTMVVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGIGLKLEPRETVIKELKKSLKIKGEELSEANVRLITLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPCQAPGSVPGPGLVKDSPLLIQQISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET
5377 762 1106 DVPCKRVLPARAQEKGQLTLSCGESGEKG\F*YHEVRQAEGES* /WFGPNVRLVHTQLRTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEBQP 5378 2009 664 QASGTTLRPLPDLPQLKRRPATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKRYMEEMADTADA IEMATLDKEMAERRABSLQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSKQEHVK\CQKIMEKKNQELEVVRQORERLQEELSQ AESTIDELKEQVDAALGAEEMVEMITDRNLNLBEKVRELRETVG DLEAMNEMNDRLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVWRELITNQQEASVERQQQPPP ETFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSILTAFMPD SFLRPGGDHDCVLVLLLMPRLICKABLIRKQAQEKFELSENCSE RPGLBGAAGEQLSPAAIGLYY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYGHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKXTRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAQLI APLABNEGLLVAALBEILAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGKYDAERPPSKPPP\VELRAAALRAEITDA EGIGLKLEDRETVIKBLKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIBKVQTRLEETQALLRKKEKEFRETMDACQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKISHEGFGSELPAGALYRKTSQLLET
/WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS+WPGYDGWWGGQYIFIFRGMRWEBQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL EAKRYMEEMADTADAIEMATLDKEMAERRAESLQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLKEQNARLKDALV RMRDLSSSKQEHVK\LQKIMEKKMQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMITDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVWRELITNQQEASVERQQQPPP BTFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLBGAAGEQLSFAAIGLYY\SIMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RIRAPLQGGRATDIALLLRDLETSCS\DIRGFCKXTRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALBELAFKASEQIYGTPSSSPYBCLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEXEFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL
SS+WPCYDGWWGGQYIFIFRGMRWEBQP  5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKRAKEAL EAKRYMEEMADTADA IEMATLDKEMAERRABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLEQNARLKDALV RMRDLSSSKQENVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAREMVEMITDRNLMLEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVWRELITNQQEASVERQQQPPP BTFDFKIKFAETKAHAKAIEMELRQMEVAQARREMSLITAFMPD SFLRPGGDHDCVLVLLLMPRLICKABLIRKQAQKFELSENCSB RPGLBGAAGEQLSFAAIGLYY\SLMPAAGHRYHRY*CHALSQCR RLNYYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKTRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI ISTMKK\LVTAMQEGBYDAERPPSKPPVVELRAAARREITDA EGLGLKLEDRBTVIKBLKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKBKEFFETMDALQADIDQL EARRAELKQRINSQSKRTIEGLRGPPPSGTATLVSGLAGEEQQR GAIPCQAPGSVPGPGLVKDSPLLLQLISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET INQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS
5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	5377	762	1106	VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMESKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\LQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAZEMVEMLTDRNLNLSEKVRELRETVG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQRRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQBASVERQQQPPP ETFDFKIKFAETKAHAKALEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELLIRKQAQEKFELSENCSE RPGLBGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKQQLDETTNVEPLT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVVG RLRAFLQGGQRATDIALLIRDLETSCS\DIRQFCKKTRRMPGT DAPGIPAALAFGPQVSDTILDCRKHLTWVVAVLQEVAAAAAQLI ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALREITDA EGLGLKLEDRETVIKBLKKSLKIKGBELSEANVRLTILEKKLDS AAKDADER IEKVQTRLEETQALLRKKEKEFEFTMDALQADIDQL EAEKAELKQRLMSQSKRTIEGLRGPPPSGTATLVSGTAGEEQQR GAIPCQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLS DVPCKRVLPAEAQEKGQITLSCGESGEEG\F*YHEVRQAEGES*
When the state of	5377	762	1106	VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMESKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\CQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRELRETVG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQRRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELINQQBASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLEGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETUNVEPLT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTILDCRKHLTWVAVUQEVARAAAQLI ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLEKKLDG EARRAELKQRLMSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPCQAPGSVPGPGLVKDSPLLLQUISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET INQLSTHTHVVDITTSTSPAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVTDPATFPSSAPLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS  DVPCKRVLPAEAQEKGGUTISCGESGEEGF*YHEVRQAEGES* /WPGPNVRLVHTQLKTKKPSGTLKAKFYLHYGSTKFAARISCTX
RELATIVILISAMPHILDNDVKIDEKDVLLIKERKSSTLKSKSSVULTR				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMESKMQEQQADLQRRLKEARKRAKEAL EAKERYMEEMADTADA IEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEEKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\CQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRELRETVG DLEAMNEMNDRLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELINQQEASVERQQQPPP BTFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKQQLDETVNVEPLT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKXIRRMPGT DAPGIPAALAFGPQVSDTLLDCREHLTWVVAVLQEVAAAAAQLI ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGIGLKLEPRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFRETMDALQADIDQL EAEKAELKQRLWSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GATPGQAPGSVPGPGLVKDSPLLIQQISAMRLHISQLQHENSIL KGAQNKASLASLPPLHVAKLSHEFGSELPAGALYRKTSQLLET INQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVIKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQUTLSCGESGEEG\F*YHEVRQAEGES* /WEGPDVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS*WPGYDGWWGGQYIPIFRGMRWEBQP
				VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEMKSKMQBQQADLQRRLKEARKRAKEAL EAKBRYMEEMADTADA IEMATLDKEMAEERABSLQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLBEQNARLKDALV RMRDLSSSEKQEHVK\CQKIMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGABEMVEMLTDRNLNLEKVRELRETVG DLRAMNEMNDRLQENARBTELELREQLDMAGARVREAQKRVEAA QBTVADYQQTIKKYRQLTAHLQDVARELITNQQEASVERQQQPPP BTFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSILTAFMPD SFLRPGGDHDCVLVLLLMPRLICKABLIRKQAQEKFELSENCSB RPGLBGAAGEQLSPAAIGLVY\SLMPAAGHRYHRY*CHALSQCR RLAKYYGHLYSIHLARQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLLRDLETSCS\DIRQFCKXIRRMPGT TDAPGIPAALAFGPQVSDTLLDCRKHLTWVAVLQEVAAAAAQLI APLABNEGLLVAALBEKLAFKABEQIYGTPSSSPYBCLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKBLKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFRETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIFGQAPGSVGGGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKBTVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVUTQEQHHQLHSRLIS DVPCKRVLPAEAQEKGQITISCGESGEEG\F*YHEVRQAEGGS* /WEGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS*WPGYDGWWGGQYIFIFRGMRWEBQP QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
] ;			Codon, /=possible nucleotide deletion,
(	amiro acid	sequence	
	sequence	1	\=possible nucleotide insertion)
		1	SFSFRNSKQTYSGVPIIAANMDTVGTFBMAKVLCKS*VPGSFWD
}		i .	VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
1	1	Į.	KHYSLVOWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
)	i	i	OVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
1		l.	BRLILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
		ľ	1
			RGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
	ſ	1	BLIERDGKKYKLFYGMSS*I\AM\KKYAGGVABYRASEGKTVEV
		ł	PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
ì		1	VNPIFSEAC
5379	2009	664	QASGTTLRPLPDLPQLKRRKATSRNRALKPRGRLVLMTSCLPAL
		1	RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR
		1	SPSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
I		1	
j i	]	J	VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
l i		I	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
1		ì	QVKYICLDVANGYSEHFVBFVKDVRKRFPQHTIMAGNVVTGEMV
1		Į.	ERLILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
[		Į.	HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
1		1	RLIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
1		i	PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTOO
1 :	[		VNPIFSEAC
5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
( ·	i	1	SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
1	1	]	SPIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
j	[	į.	SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
1		i .	RLPRRPTVESHHVSITGMODCVQLNQYTLKDEIGKGSYGVVKLA
}	1	}	YNBNDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
i	-	ŀ	RGPI/EQVYQEIA/ILKKLDHPNVV/KLVEVL/DDPNBDHLYMV
! .		ł	F\BLVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
1	•	Ì	
[	[	<b>!</b>	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1	}	1	FMAPBSLSETRKIPSGKALDVWAMGVTLYCFVFG*CPFMDERIM
1		ł	CLHSKIKSQALEFPDQPDIARDLKDLITRMLDKNPESRIVVPBI
1	Ì	<b>!</b>	KLHPWVTRHGARPLPSRDENCTLVEVTEREVENSVKHIPSLATV
		)	ILVKIMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
1			SELKT*KISPLPACCKVT*EPPHPSGCRPSCWQPPFLHTHSQPR
ì		i .	*PEPPRTDRALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
	!	j	PDLVGAPGSHFCFLNIALLRYNSHTM
53B1		2050	PSRAGGARRGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
2287	2	A 050	
1	1	5	SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSTHLGME
		J	SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
1		<b>!</b>	SGRKLSIQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
l		j	RLPRRPTVBSHHVSITGMQDCVQLNQYTLKDBIGKGSYGVVKLA
[		<b>!</b>	YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
1	1	1	RGPI\EQVYQETA\ILKKLDHPNVV\KLVEVL\DDPNBDHLYMV
		l	F\BLVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIBYLHYQKII
1		1	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
<b>,</b>		į	
] '		1	FMAPESLSBTRKIFSGKALDVWAMGVTLYCFVFG*CPFMDBRIM
		Í	CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPBSRIVVPEI
}		ŀ	KLHPWVTRHGABPLPSBDENCTLVEVTEERVENSVKHIPSLATV
ļ		1	ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
Į l		ł	SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
		1	*PEPPRTDRALCPYETGRTCWAPLLOVLWWVGTPLPFPLSTSWL
i i		Í	
			PDLVGAPGSHFCFLNIALLRYNSHTM.
5382	1536	203	GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS
		{	VFMILLIIVYWDSAGAAHFYLHTSPSRPHTGPPLPTPGPDRDRE
		1	LTADSDVDBFLDKFLSAGVKQSDLPRKETEQPPAPGSMBESVRG
			YDWSPRDARRSPDOGROOAERRSVLRGFCANSSLAFPTKERPFD
		ł .	DIPNSELSHLIVDDRHGAIYCYVPKVACINWKRVMIVLSGSLLH
		}	RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL
		j	KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV
j l		1	RQPHQPARLGARGLPRWPQ\VSPANFIQYLLDPHT3KLAPFNEH
l i		j	WRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalarine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	
ł	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P-Proline, Q=Glutamine, R=Arginine,
1		L .	S=Serine, T=Threonine, V=Valine,
Į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
	Bequence		\=possible nucleotide insertion)
			PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYRADFVLFGYPKP
		}	KNLLRD
5383	45	5250	VERLLGCRNSKRTWRMLISKNMPWRRLOGISFGMYSAEELKKLS
			VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCVODFSN
1 .		l	CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI
1		}	
			HLLLCQLRVLEVGALQAVYELERILSRFLEENADPSASEIREEL
Į			BQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC
1			PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIBEAQ
í			IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMEGRFN
l		l	PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVMKDVVL
j	j.		IRKLLALMAQEQKLPREVATPTTDEEKDSLIAIDRSPLSTLPGQ
1	1	i e	SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIRQILEKKR
1	{	[	GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVFATKLTYP
1	}		QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT
1	ŀ		QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNRQPTLH
1			RPSIQAHRARILPERKVLRLHYANCKAYNADPDGDEMNAHFPQS
1			KIGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG
1 :			CPFTREHYMELVYRGLTDKVGRVKLLSPS1LKPPPLWTGKQVVS
	<b>[</b>		
ŀ			TLLINIIPEDHIPLNLSGKAKITGKAMVKETPRSVPGFNPDSMC
1	Į į		ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV
)			LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRQRIIBESTH
1			CGPQAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNMIDLKF
1			KEEVNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT
1	ļ		MQISCI-IGQIELEGRSTPLMASGESLPCFEPYEFTPRAGGFVTG
{			RFLTGIKPPEFFHCMAGREGLVDTAVKTSRSGYLQRCIIKHLB
<b>1</b> .			GLVVQYDLTVRDSDGSVVQFLYGBDGLDIPKTQFLQPKQFPFLA
			SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHPNTLLR
			RGAPLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMWY
			BLDEESRRKYOKKAAACPDPSLSVWRPDTYFASVSETFETKVDD
1 1			YSQBWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG
1			LLAAQSIGEPSTOMTLNTFHFAGRGEMNVTLGIPRLREILMVAS
1			ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVO
			ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRPMET
1			
1 1			RPFKLLMESIKKKNNKASAFRNVNTRRATORDLDNAGELGRERG
]			EQECDEERECHIVDAEAREGDADASDAKRKEKQBEEVDYESEER
1			BEREGRENDDEDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV
]			PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD
1			TERSLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC
; 1			LINETTNNKNEKELVLNTEGINLPELFKYABVLDLRRLYSNDIH
1 1	[	-A-	Alantygiraalrvirkrikdvfavygiavdprhlslvadymcf
1 1			egvykplnrfgirsnssplqqmtfbtsfqflkqatmlgshdblr
L	·		SPSACLVVGKVVRGGTGLPKLKQPLR
5384	196	886	QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPRIRPYINI
[ ]			TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG
, I			APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT
}			GOPAAPLRGIYFFSLNVHSWNYKETYVHIMHNOKEAVILYAOPS
1 . 1			-
1 1			ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF
			SGHLIKAEDD
5385	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVESHKKNKIHM
			SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
1 1			VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
<u> </u>			SDGERKAYVRLAPDYDALVVATKIGIT
5386	326	799	LMVPRTKKEAPAPPKARAKAKAL\KAKKAVLKDVHSHKKNKIHM
	Ì		SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLITE*A
1 1	1	Ì	VKKIENNSLLVPTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
į <b>i</b>	ſ		
5387			SDGERKAYVRLAPDYDALVVATKIGIT
238/	2	2117	FVVAASGGCNFVLGERRAGSLLSASYGTFAMPGMVLFGRRWATA
) l	1		SDDLVFPGPFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY
, ,	1	-	LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL
į į	j		ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA
		ļ	TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT
			<del></del>

Do beginning nucleotide location corresponding to first amino acid sequence or session of residue of amino acid sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation   Corresponding				(A-Alanine C-Cycleine D-Assorbie Acid P
Cocrasponding to first and octid residue of antion actid amino actid amino actid amino actid amino actid amino actid amino actid amino actid amino actid sequence   Perciame of amino actid amino actid sequence   Perciame of amino actid sequence   Perciame of amino actid sequence   Perciame of amino actid sequence   Security of the control of the co	NO:			Glutamic Acid. F=Phonylalarine G-Glumino
to first amino acid residue of amino acid residue of amino acid sequence  se				Halistidine Targolaucing Valuming
bo first main acid amino acid amino acid amino acid amino acid sequence squenc	1	1		LaLeucine Mamethionine Management
### amino acid	J		l .	P=Proline, O=Glutamine P-Arminine
residue of anino acid sequence (Codon, 'possible nucleotide deletion, 'vpossible nucleotide deletion, 'vpossible nucleotide deletion, 'vpossible nucleotide insertion)  SWENTRIKLICCCTGENDIFTWARSSTRAEHFSTYFSDTDLVFSD LAGLALLHOQUINTENNESSEQWINTENSEQUENCECOPTIC 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOL'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGEDOLOC'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGETOLOC'CTSAPILATTRENAVGENEROLOCTESSING-PTM', 'v VGETOLOC'CTSAPILATTRENAVGENEROLOC'CT	1			S=Serine, T=Threenine, V=V=14me
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TADIGAGIGERGAROAURHYLYPFTGYRRRAACQAERPARS KITDLAAYQKINLGVQLINMAQETHISQUIRLCTGGGYRYGHER TNOMGSVCYKRELQRQMSENGRISPVQCTTGSVP ZAQGALDST SSSMQFSFVSNQSLLSBSVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEQSKSLE,KNRKKRIAVASCAGRKWALLGLINAGVEWF TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK ILEHLQTKN  5390  217  1332  EDERKLMEDKHWSECEGPEMSLVCIJDFQAHAREQLSKSTRDDI GGADDSTTRIDDNIAAPKETRLAPRYLRDVSSVDTRTTIQGESI SAPICLAPTGFUGLUWPDGEMSTARAAQAN\GICYITSTFASCS LEDIVIAAPEGLRWFQLYVEPDLQLKKQLLQRVESLGFKALVIT LDTPVGGNRRIDIRNQLRRRLTITDLQSPKRGNAIPFFQMTFIS TSICMNDLSWFQSITRIPJILKSILJKBDAKLAVKHVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVILDGGVRTGNDVLK ALALGAKCIFILGDAILMALASKGEHGVKEVINILTHEFHTSMA\ LTGCRSVARINKMLVQFSRL  5391  1 1292  VKRAAGERGEPTAGGGRCERAGTVMRRILGVRAWKKNRGGF OPEVCKKMIGGOLKWAPVGGNTGRDVLHERGERVYPOLBGDM VLRVLEQGKHRDVVIRQOEIFLLPARVPHSPQRFANTVGLVER RRLETELDGLRYYVGDTMVLFEKMFYCKDLGTQLAPIIQBFFS SSQYTRIGFFIDIOLINISMPSSTLEMFMSLJOHLBGEBVYPOLBGDM VLRVLEQGKHRDVVIRQOESIFLERMFYCKDLGTQLAPIIQBFFFS SSQYTRIGFPIDIOLINISMPSSTLEMFMSLJOHLBGHREIL QAATPISLFGFTYSTQVIAYGGSSKGLRQNVUVUMJULGGSSV VTMGGREILGLPWBDSLJVISMGPSY\AM\ERTGGSVATIONT TROVTREAINCHPPSCESGPRCTBAGRAABHLIMQTQPTAL PULGGGLPPAPLLIP IPLSLDTQCTSTTFRRPSIKAS  FIHKPAHGWILIPDARVLGGVSYVUYMGGCTEVLGSMRRILDPTT RTQVTRRAINCHERVGGWGSWKKKAPNKALASVLGKSNILRPA GMS1SHITSTGGLSLSVPARGGYTANTMSLOKSSTLRPA GMS1SHITSTGGLSLSVPARGGYTANTMYNSIPCKEPP1 GGGVVGADARGPPDHBEHLTVNTTGLDAPEPEDSPKKDLFDMR PPEDALKLHECSVAAGVTAABILEECGBLAGSLESPRWONTSTGTAP PGGGVVQADARGPPDHBEHLTVNTTGLDAPEPEDSPKKDLFDMR PPEDALKLHECSVAAGVTAABILDEGEPSPRRAPGAPTTERQ LLRQEFWYHGRMSRRAAGRRILARGDETJVRDSVINTGGVAVATRTERQ LLRQEFWYHGRMSRRAAGRRILARGPELTARDQCSPTRRAPGAPTTERQ LLRQEFWYHGRMSRRAAGRRILARGDETJVRDSVINTGGVAPAPPPEDALKLHECCSGVAGARGRANGSGOTDMTD AQQPHILLLUDPERGVARGVUTTAMH AQQPHILLLUDPERGVROVFROVLFFSISHLIGHHLQNGQPIVARK SELHLRGWSREP GGSSGGRAFGROVFROVLFROVINTGGCPAPAPAPPTERQ				
KOTDLAATQKSRIGVQLERMAQSTRISQVIPMLCSTGGSFYGNSR TROMCSVCYKERLORQNESERGISPVQCTDSVPAQASALBJT SSEMOPSPVSNOSLISESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKHDLLGINAGVEMF TVVYTVTOMYTIALITIXQBLKHFVFQQEFKSFGSFHQQLLEKK LLEHLQTKN  5390 217 1332 EDPRKLMEDRMWSEGEPEMSLVCI.TDFQAHAERQLSKSTRDFI EGGADDSITRDDNIAAPKRIRLPREYRIVDVSRVDTRTTIQGEEI SAPICIAFTGFHICLVWEDGEMSTARAAQAA\GLICYITSTFASCS LEDIVLAAPEGLRWFQLYVURDLQUKVGLIQQVSSLGFKALUVI LDTPVCGKRRHIDIRONJCRRNLTUTDLQSPKKGNAIPYFQMTPIS TSLCWMDLSWPQSITRLPIILKGILTKEDAKLAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKLEVVILDGGVRCTNDDVLK ALALGAKCIFHGDALIMALASKGEKVEVLNILTINFEFTISMA\ LTGCRSVABINRNLVQPSRL  VKKAAGRGGPFTAGGQRCERAFGTVMERRLUVRANVKRNRGSF QPPVCNKLMIGGGLKVMFVGGDNTRKDTHIBGEBEVFYQLBGDM VLRVLEQGKHRDVIRGGBIFLLPARVPHSPQRPANTVGLVVBR RRLSTERLGLRYYVQDTDMVLEKEMPYCKDLGTQLABILGRFKALUV QAGTPISLFGGTYTTSTUIAYGGSSEGLRQNUTVMIMQLEGSSV VYMGGRELSLGPWMGSLLUVSNGSFYMYCKGUTGTQLABILGRFKALUV PULPGGLEPAPLLDIPIPLSRYDLKFFYCKDLGTQLABILGVKYQ DPACKKSPNGBPSCHGLKAANTGVBTLEVPSLENNSFBHYLGV YCRCVPRPAHCCHPPSCPSQPRCHAPGRAAPHLLWQTQPTAL PVLPGGLEPAPLLDIPIPLSCTGCSTSTTRRPSIKAS  1623 IRGSNAQKVVGSGSGGAGGPQPPAGFGGVPALABAVLGACEPR CAAPCPLPALTSCRGAGSGSGSGGAGPQDPAGFGGVPALABAVLGACEPR CAAPCPLPALTSCRGAGSGSGSGGFGVPALABAVLGACEPR CAAPCPLPALTSCRGAGSGSGSGGFGVPAABAVLGACEPR GKISIHISTOGISLSVPATRGVIANHBMPSISPAGGGTDTMTD YVAYVAKDPINGRACHILECCEGL\AQSIISTVGQAFELRPKQY LHSPPKVALEPPRLAGPESSAKGDBEDSLERNYNSIFERGEPL GGLUDSRLALTOPCALTALDQGPSSFKINGSSFFRRAPVARPTERQ PGGGVQADARGPPDHEBILTVNTGGLDAPSPBCSFKKNLEPDMR PPEDALKLHECSVAAGVTAAPLPLEDGWSPPTRRAPVAPTERQ LLRGPEWYHGRNSRRABERNLRADGFFLVRDSVTNGQVYLTGMH AQQPKHLLLVDPBGVVRTKDVLFESISHLIDHHLQNGQPIVAAR SEHLHRGVWSREP  GGSSAGNTMETONSQNVCTRNUMLLQPLTVLLLLASADSQAAAP	5389	1569	753	
TNOMCSYCKKRILQRONSSNORLISETYPRACYTIGSYPPAGALDST SSMQPPPVSNQSLLSESVASQLDSTSVDKAVPPTEDVQASVS DTAQQPSREQSKSLE\NRNKRKIAVSCAGRKWDLLGLINGCVENF TVYYTYTYMYTTALTITIQMLKNFVFQQEFKSFGSFHQQLLEYK LLEHLQTKN  5390 217 1332 EDPRKLMEDKMSECEGPPMSLVCLTDFQAHAREQLSKSTRDFT RGCADDSITRDDNIAPFKIRLRPRYLRDVSVDTRTTIQGEEI SAPICLAPTGHICLWPPGUMSTARAAQAA\GCYTTSTFASCS LEDIVIAPEGLRWPQLSVHFDLQLNKQLLQRVSSLGFFALWIT LDTPPVCGNRRHDIRQLRKNITUTQLGSPKKGNAIPYFQMTPIS TSLCWNDLSWPQSITRLPIILKGILITKEDAKLAVKINVQGIIVS NHGGRQLDBYLASIDALTEVVARVKGKIRSTBYLDGGGFRTGNDVLK ALALGAKCIFIGDALIMADAKSKEHGVKEVINILTNEFHTSMA\ LTGCRSVARINKNLVQPSRL  1 1292 VKENAGRERGPPTAGGGRCEEAPGTVMERRLGVRANVKRNGSF OPPVCNKLMIGBGLKVMPVGGFNTRKDYHLBEGEKVFYQLRGDM VLRVLBQGKHRDVVIRQGRIFLLPARVPHSPQRPANTVSLAVER RRIEFTELDGLRYYVGDTMDULPERMFYCRDLGROLDALDSHRREL QAGTIFLSLEGDTYRTQVIARGQCSSEGLARQNUTVUMDQLEGSSV VTMGGRELGLGFWHDSLLVILKGEFSY\AW\EBTGGSVALSVY\Q DPACKKSPWGEPSCIGLKANTGVPSTLEVPSLPNNSPSPHYLGV YCRCVPRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWGYQPTAL PVLPGGLPFAPLLPIPSLGTGCSTSTPRRPSIKAS  5392 1 1623 IRGSNAQKVVGRSGSGGRGGPDPDFAGGGAAGSGDAAAAPENIRKGS FIHKPAHGWLBPDARVLGFCVSYVVRYMGCIBVLASKURLFFA GKISHIHSTGGLSLSVPATRQVHRHMPSISPAGGGDTUMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVQAFELRFKQY LISPFKVALPPERLAGPEESAGDBEDSSLEHYYNSIPAGKSPT PFEDALKHLEGVSREP PGGGVQADARGPPDHERH,VVNTQGLDAPPEDSPKNLPPIRR PGGGVQADARGPPDHERH,VVNTQGLDAPPEDSPKNLPPIRR PGGGVQADARGPPDHERH,VVNTQGLDAPPEDSPKNLPPIRR PGGGFWGRRRARRAARSMLERADGPLVRDSTSTAP PGGGFWGRRRARRAARSMLERADGPLVRDSTSTAP PGGGFWGRRARRRAARSMLERADGPTVRDSYTTRAPPTERQ LLGCFWYNGRRRRRAARSMLERADGPTVRDSYTTRAPPTERQ PGGFWGRRRRRAARSRRAARSMCHEDSPFTRRAPVAPTERQ LLGCFWYNGRRRRRAARSRRAARSMCHEDSPFTRRAPVAPTERQ PGGGVQADARGPPDHERH,VVNTQGLDAPPBPDSPKNLPPIRR PFEDALKLHECSVAACVTARAPLPLEDGDPTVRDSYTTTAPPTERQ LLGCFWYNGRRRRRAARSRMLERADGPTVRDSYTTTAPPTERQ PGGBVGRRRRRAARRRAARSMLERADGPTVRDSYTTAPPTERQ PGGGSGAGMTMSTOMSQNVCPRNLMLLGGFTVLLLLLASADSQAAAP	3303	1305	/53	
SSSMOPSPUNOSILISESVASOGLOSTSVIKAVPETEDVQASVS DTAQOPSEDSKSL NRNKKRIAVSCAGRKUDLIGINAGVEMF TOVYTTUCMYTIALITITQMIKNEVFOQEFKSFGSPHOQLLEYK ILEHLQTKN  5390 217 1332 EDPRKLMEDKMASECGGFEMSLVCLTDFQAHAREGLSKSTEDFT EGGADDSITRDDNIAAPKEIRLRPRYLRDVSKUDTRTTIQGEEI SAPICIAPTGFHICLWEPDGHSTARAAQAAGICTYTTSTFASCS LEDIVIAAPEGIRMPDLVHEPLOLINKQLIQRVSIGFFALVIT LDTPVCGNRRHDIRMQLRRNLTLTDLQSPKKGNAIPYFQMTPIS TSLCWNDLSWFQSITRLFIILKGHLTKENBAKLAVKINVQGIIVS NHGGRQLDEVIASIDAITEVAAVKGRIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILMALASKGENGVKEVLNILTNEFHTSMA\ LTGCRSVABINRNLVQFSRL  1 292 VKKNAGRERGPPTAGGGRCEBAPGTVMERRLGUHANVKENRGSF OPPVCNKLMIGBGLKVHFVGGPNTRKDYHTBGGEKYPYQLBGOM VLRVLEQCKHRDVVATRQGEIFLLEWFYLCKDLGTQLAPLIGBFTS SSRYKTGKPIPDOLLKEPPPPLSTRSIMBERGLDAHLDSHIRRL VARVLEQCKHRDVATRQUEIFLLSGENGVEYDLWROLGSSKU VTMGGRELSLGPWMDSLLVLSMGPSY\AW\KRTQGSVALSVT\Q DPACKKSPNGBPSCHGLKARATGVPSTLEVPSLPNNSPSPHYLSV VTMGGRELSLGPWMDSLLVLSMGPSY\AW\KRTQGSVALSVT\Q DPACKKSPNGBPSCHGLKARATGVPSTLEVPSLPNNSPSPHYLSV VTMGGRELSLGPWADSLLVLSMGPSY\AW\KRTQGSVALSVT\Q DPACKKSPNGBPSCHGLKARATGVPSTLEVPSLPNNSPSPHYLSV VTMGGRELSLGPWADSLLVLSMGPSY\AW\KRTQGSVALSVT\Q DPACKKSPNGBPSCHGLKARATGVPSTLEVPSLPNNSPSPHYLSV VTMGGRELSLGPWADSLLVLSMGPSY\AW\KRTQGSVALSVT\Q DPACKKSPNGBPSCHGLKARATGVPSTLEVPSLPRNSPSPHYLSV VTMGGRELSLGPWADSLLVLSWGPSY\AW\KRTQGSVALSVT\Q DPACKKSPNGBPSCHGLKARATGVPSTLEVPSLPRNSPSPHYLSV VTMGGRELSLGPWADSLLVLSWGPSYVANKAGLASVLIGGEPR CAAPCPLPALSTCRGAGSGGRAGGGRAAAABKWIRKGS FYHKPAHGWILDDARVLGPGVSYVURYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSNKKKARALASVLIGGENREFA GKISIHISTGGLSLSVPATTQVTANHEMPSISPASGGDTTMTD YVAYAKOPINGRACHILLCCGGLAQSIISTVGQAFELREKQY LHSPPKVALPPERLAGPESAWGDESDSLEHNYNSIPGKEPPL GGGVVGADARGPPDHREHLJVWTYGGLADPEPEDSPKKDLFPMR PEDDALKHLESVBARGP PEDDALKHLESVBARGPTHREGOFTLVEDSVTNNFGQVVLTGMH AGQPWHILLUDPGGVVERSKRAARBRMLRADGDFLVEDSPTRADVAPTERQ LRQEPWYHGRMSRRRAARBRMLRADGDFLVEDSPTRADVAPTERQ SCHLILLGVSSREP GGGSÄGMTMETQMSQNVCFRNILMLLQFLTVLLLLASADSQAAAP	ł			
DTAQQPSEEQSKSLE\NINKKRIAVSCAGERMIDLIGIANGVEMF TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK ILEHLQTKN  5390 217 1332 EDFRKIMEDKMASECGFEMSLVCITDFQAHAREQLSKSTEDFI EGGADDSITRDDNIAAPKRIRLRPRYIRDVSEVDTRTTIQGEEI SAPICTAPTGRICLWPROEMSTARAQAA\GICYITSTFASCS LEDIVIAAPEGLRNFQLVVHPDLQIANQLLQRVSSIGFKALVIT LDTPVCGNRRHDIRNQLRRNITLTDLQSPKKGNAIPYFQMTPIS TSLCWNDLSWPQSITREPIILKGLITKEDAKLAVKINVQGIIVS NHGGRQLDBVLASIDALTEVVAAVKGIIBVYLDGGWRTGNDVLK ALALGAKCIFLGDALIAMAS KGEHGVKEVLNILTNEPHTSMA\ LTGCRSVABINRNLVQFSRL LTGCRSVABINRNLVQFSRL VKRÄAGERERFPTAGGARGERAPGTVWBRRIGWRAWVKENRGSF OPPVCNKLMIGDGLKWPWGGBYNTRNYHIBBGBEVPYQLBGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVGR RRLETTELDGLRYYVGDTMDVLFERWFYCKDLGTQLAPIIQBFFS SBOYRTGRFIPPOLLKEPPPPLSTRSIMEPMSLDABALDSHRREL QAGTPLSLEGDTYBTQVIAYGQGSSBGLRQNVDVULMQLEGSSV VIMGGRISLGPWMDSILVISWGFSY\AW,BETQGSVALSVY\Q DPACKKSPMGBPSCFIGIKAANTCDYSTLEVPSLENDSPSHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPALLDIPLSCTQCSTTETRPSIKAS CAAPCPLPALSRCRGAGSGGGROPOPDBAGFGGVPALAAVLGACEPR CAAPCPLPALSRCRGAGSGGRGPOPDBAGFGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSGGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLIPDARVLGPGVSYVURYMGCIEVLBSMRSLDFNT YNAVYAKDPINQRACHILECCECI\AQSIISTVGQAFELRRQY VYAYVAKDPINQRACHILECCECI\AQSIISTVGQAFELRRQY VYAYVAKDPINQRACHILECCECI\AQSIISTVGQAFELRRQY VYAYVAKDPINQRACHILECCECI\AQSIISTVGQAFELRRQY LISPPEVALIKHEGSVAAGVTAAPLEDEDQWPSPPETRRAPVAPTEBQ EGGVUGADARGPPDHBEHLYWTQGLIBAPPEDSPKKULFDMLEDHA PPEDALKHLEGVSKEP LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNFGQYVLTGMH AQQPKHILLIVDPEGVVETROVLFESISHLIDHHLQNGQPIVAAE SSLHLIGWVSKEP SCHLIKGVSSEP SSLHLIGWVSKEP GGDSAGMTMETOMSQNVCPRNLMLLQFELTVLLLLASADSQAAAP	1			
TVYTTYOMTIALTITKOMLKNFVFQQEFKSFGSFHQQLLEYK ILEHLQTKN  5390  217  1332  EUDRKLMEDRWSECEGPEMSLVCI.TDFQAHAREQLSKSTRDFI EGGADDSITRDDNIAAPKEIRLRPRYLRDVSKYDTRTITQGEEI SAPICLAPTGSUFHCLVMPDGMSTARAAQAA\GICYITSFRASCS LEDIVLAAPEGLRWFQLYVHPDLQLWKQLLQKVESIGFKALVIT LDTPVCGNRRHDIRNQLRRNLTI.TDLQSFKKGNAIPYFQMTFIS TSLCWHDLSWFQSITHLPIILGLIJFKEDRALLAVHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLEDALLWALASKGEHGVKSVJLNILTINEFHTSMA\ LTGCRSVABINRNLVGFSRL  1  1292  VKKAAGRERGPPTAGGQRCEEAPGTVMERRLQVRANVKENRGSF QPPVCNKLMIGSBCLKVMPVGGFNTRRDVHILEGBESVFYQLBGDM VLRVLLEQGKHRDVVIRQGBIPTLIPARVPHSFGQFANTVGLVVBR RRIGETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPILGBFFS SBQYRTGKPPPDOLLKEPFFPLSTRS; INEPMSLDAWLDSHHREL QAATELSLEGDTYRTQVIAYGGGSSGGLRQAVDVVBLOUGHSSV VTMGGRRLSLGPWMSSLLVLSMGPSY\AM\RETQGSVALSVF\Q DPACKKSPWGEPSCHGLKANTGVPSTLEVPSLFNNSPSHYLSV YCRCVPHRPAHCCHPPSCPSQPRCTBAPGRAAPHILLWGTQFTAL PVLPGGLPPAPLLPIPLSLGANTGVPSTLEVPSLFNNSPSHYLSV YCRCVPHRPAHCCHPPSCPSQPRCTBAPGRAAPHLLWGTQFTAL PVLPGGLPPAPLLPIPLSLGANTGVPSTLEVPSLFNNSPSHYLSV YCRCVPHRPAHCCHPPSCPSQPRCTBAPGRAAPHILLWGTQFTAL PVLPGGLPPAPLLPIPLSLGANTGVPSTLEVPSLFNNSPSHYLSV YCRCVPHRPAHCCHPPSCPSQPRCTBAPGRAAPHLLWGTQFTAL PVLPGGLPAPLLPIPLSLGANTGVPSTLEVPSLFNNSPSHYLSV YCRCVPHRPAHCCHPPSCPSQPRCTBAPGRAAPHLLWGTQFTAL PVLPGGLPAPLLPIPLGANTGCSSTGGRGAAGSGDAAAAARMIRKGS FIHKPAHGGLHPDARVLGFCVSYVVRYMGCTEVLRSMRSLDPNT RTQVTREAINRLHEAVPGVGRSWKKAPMKALPAKVLGKSNLRFA GKSISHHISTGGLSLSVPATRQVINNHMPSISFASGGDTMTDT YVAYVAKDPINQRACHILECCEGL\AQSISTVGGAPELRFKQY LHSPPKVALPPPERLAGPEESAWGDEBDSLENNYNSIPGKEPPL GGLVDSRALTQPCALITALDGGPSFSLENACSLFWDVSTTTAP PGGGTVQADARGPPDHERILVTNTGLDAPBPEDSPKKOLEDMR PPEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTERQ LLQEPWHGRMSRRAABRADGGPFVPRDSVTNPGQYVUTGHH AGQPRHLLLJVDPEGVWRTKDVLFESISHLIDHHLQNGQPIVARE SELHLRGWVSRPP  5393  2  982  GGDSAGMTWETQMSQNVCPRNLMLLQPLTVLLLLASADSQAAAP	1	,		
ILEHLOTKN  5390  217  1332  EDPRKLMEDKMWSECEGFEMSLVCI.TDFQAHAREQLSKSTEDFT EGGADDSITRDDNIAAPKRIRLRPRYIRDVSEVDTRTTIQGEEI SAPICTAPTGYHCLVWPDGEMSTARAADA\GICYITSTPASCS LEDIVIAAPEGLRWFQLYVHPDLGLIKQGLIQKVESLGYKADVIT LDTPVCGNRRHDIRNQLRRNITITDLQSPKKGNATPYFGYMTPIS TSLCWHDLSWFQSITRLPIILKGILTKEDAKLAVKHNVQGIIVS NHGGRQLDEVIASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILMALASKGHIGVKEVINILTINEFHTSMA\ LTGCRSVABINRNIVQFSRL  1  1292  VKKAAGRERGFPTAGGGRCEAPGTVMERLGVKANVKKRRGGF OPPVCNKLMIGSGLKVMFVGGSTTRRDYHIESGESVFYQLRGDM VLRVLEQGHRDVINGGRIPLLPARVPHSPQRPANTVGLVVER RRLETELDGLRYTVGDIMDVLFEKWFYCKDLGTOLAPIQBFYS SSQYRTGREIPPOLLKEPPFPJSTRSIMEPMSLDAWLDSHIRBL QASTPISLEGDTYFTYQUINVGGSSEGLRQNVDVVLNQLEGSSV VTMGGRLSLGFWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCIGLKAATGVPSTLRVPGLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCTAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS  5392  1  1623  IRGSNAQKVCASGSGGAGGGRGAAGSGDAAAAEWIRKGS FIHKPAHGWLHPDAKVCAFGGSYGYRALAAAVLGACEPR CAAPCPLPALSRCRGAGSGGAGGGGAAAAAEWIRKGS FIHKPAHGWLHPDAKVCAFGGSYGYVRALAASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVTANHHMPSISPASGGDTDMTD YVAYVAKNDFINGRACHLLECCGGL\AQSIISTVGQAFELRFRQI GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGTVQADARGPPDHREHLVNNTQGLDAPSPENSPKKDLEPDMR PFEDALKLHEGSVAAGVTAALPLILEDQWFSPBTRRAPVAPTERQ LKGPWYHGRMSRRAABMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLIVDPEGYVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSRPP  5393  2  982  GGDSAGMTWETOMSQNVCPRNLMLLQPLTVLLLLASADSQAAAP	ł	ì		
S390   217   1332   EDPRKIMEDKMWSECEGPEMSLVCI.TDFQAHAREQLSKSTRDFT   EGGADDS 17RDDNIAAPKRIRLRPRYRIPUSEWDTRTTIQGEEI   SAPICLAPTGSHCLVWPDGEMSTARAADAA)GICYITSFASCS   LEDIVIAAPEGLRNFQLYVHPDLQLNKQLLQRVESIGFKALVIT   LDTPVCGNRRHDIRNQLRRNLTI.TDLQSPKKGNAIPTFQMTFIS   TSLCMDLSWPGS 17RLPIILKGILLTKEDAKLAVKHNVQGIIVS   NHGGRQLDEVLAS IDALITEVVAAVKGKLEVYLDGGVRTGNDVLK   ALALGAKCIFLGDAILMALASKGSHGVKEVLNILTINEFHTSMA   LTCCRYARINRRINGSPKKGNAIPTFQMTVIS   OPPVCNKKINGQGLKVMFVGGPNTRRDVHIEGGERYFYQLBGDM   VIKVLEQGKHRDVVIRQESIL   OPPVCNKKINGGGLKVMFVGGPNTRRDVHIEGGERYFYQLBGDM   VIKVLEQGKHRDVVIRQEEIFLLPARVPHSPQRFANTVGLVVER   RRLETTELDGLRYIVGDIMDVJEKWFYCGLIGTQLAPIIQBEFS   SBQYRTGRPIPDOLLKEPPPDLSTRSIMSPMSLDAHLDSHHREL   QAGTPLSLFGDTYSTQLIVASKGSTGVKEVNUVMLWQLEGSSV   VIMGGRELSLGFWMDSLJULSKGSTVAW RRTQGSVALSVT\Q DPACKKSPRGEPSCHGLKAATGVDSTLRVPGLIPNNSPSPHVLSV   VCRCVPHRPHCCHPSCGSPGLKAATGVDSTLRVPGLIPNNSPSPHVLSV   VCRCVPHRPHCCHPSCGSPGLKAATGVDSTLRVPGSVALSVT\Q DPACKKSPRGEPSCHGLKAATGVDSTLRVPGSIKAS   VCRCVPHRPHLIPIPLPIPLSCHGRAAAPHLLMQTQPTAL   PVLPGGLPPAPLIP PLSLGVTQCSTSTPRRPSIKAS   CAAPCPLPALSRCRGAGSGGSRGGRAGAGGDAAAAAPHLMQTQPTAL   PVLPGGLPPAPLIP PLSLGVTQCSTSTPRRPSIKAS   FIHKPAHGKILBDARVLGFGVSVVVYMGCEVLRSMRSLDFNT   RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSMLRFA   GKSISHHISTDGLSLSVPATRQVTANHHMPSISPASGGDTDMTD   VVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRPKQY   LHSPPKVALPPERLAGPEESAMGDERDSLEHNYNSIFGKSPPL   GGIVDSRLALTQPCALTALDQGPSSLKDACSLPPDVSSTGTAP   PGDGYVQADARGPPDHEELLVVNTTQLLDAPSPEDSPKKDLPDMR   PPEDALKLHCSVAAGVTAAPLPLEDQWSSTGTAP   PGDGYVQADARGPPDHEELLVVNTTQLLDAPSPEDSPKKDLPDMR   PPEDALKLHCSVAAGVTAAPLPLEDQWSPTRRAPVAPTEQ   LRQEPWYHGRMSRRAABRMLRADGDFLVRDSVTNPGQYVLTGMH   AGQPRHLLLVDPEGVRTKDVLFESISHLIDHHLQNGQPIVAAE   SELHLRGVVSRSC   GGDSAGMTWETQMSQNVCPRNLMLLQPLTVLLLLASADSQAAAP   SGBLHLRGVSRSC   GGDSAGMTWETQMSQNVCPRNLMLLQPLTVLLLASADSQAAAP   SGBLHLRGVSRSC   GGDSAGMTWETQMSQNVCPRNLMLLQPLTVLLLASADSQAAAP   SGBLHLRGVSRSC   GGDSAGMTWETQMSQNVCPRNLMLLQPLTVLLLASADSQAAAP   SGBLHLRGVSRSC   GGDSAGMTWETQMSQNVCPRNLMLLQPLTVLLLASADSQAAAP   SGBLHLRGVSRSC   GGDSAGMTWETQMSQNVCPRNLMLLQPL	1		- 17	
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QVPSMGSSSPMGLIVAVVIATAVAAIVAAVVALIYCRKKR STDPVKAQPEPPGRQMIAIRKRQLEETRIDYETADXSYM RAPTDDDKNIYLTLEPRIDHUSSIN  5395  3135  531  RASDAKNQGGLINTRRKSTDEVPISKSTLERSLS-QASDS SSGNPEAVALAPDAYSTGSSASSTLKRTKKPRPPSILKKK KPTETPPVKBTQQSPDERSLIVPSGERILASEKTRTGSKATEG LLEETPLEBPAGPKAACPLDSESVEGVVPPASGGGRUDNS RKTLPLTTAPEAGBYPPSDSGGGEVEDSPAKGHSVPLERPDYS SWDNQQENPPPTKKIGKKPVAKMPLERPKHKKTPEKLDNT PREPARPHDIPIAKSTYTYDIDKHDDDWINPFSSTSKMGE PQGSYMFDDWTCDSSVDPFTTSSSKPPSBYBSSPASSFSIDA ANGVDGDGLNKPAKKKKTPLCTDTFRVKKSPKRSPLSDPP TPAATTPETPPVISAVVRATDREKLAVVNQKNTCMTVDLEA ANGVDGDGLNKPAKKKRTPLCTDTFRVKKSPKRSPLSDPP TPAATTPETPPVISAVVRATDREKLAVVNQKNTCMTVDLEA ANGVDGDGLNKPAKKKRTPLCTDTFRVKKSPKRSPLSDPP TPAATTPETPPVISAVVRATDREKLAVVNQKNTCMTVDLEA SARIEITAPEGSFASADALLSRLAHVVSLCGALDVISPDL PPLFAQKLQRRAHPTDVSISKTALYSRIGTABVEKPAGAL PPLDSALQIARAEIITKEREVSEWKNYKESSGKELEAMG SRAIEITAPEGSFASADALLSRLAHVVSLCGALDVISPDL PPLFAQKLQRRAHPTDVSISKTALYSRIGTABVEKPAGAL VSEKTIAQNIEDBQREKSVS\NGTVQQLVLEKGQA\LADIAN \SLADLFRRYBMKSVLEGFRKNEKVLKRCAGSYLSTVKX VQALKVHA\RBKLDRANB\LAQVRGAQQEQAAHQASLA CRV\DALARTLEQOKNETIBELTKICDELIANGKS  5396  3135  531  RASDARNOBGLIMTERKSTDSVPISKSTLSFSISIJQASDP CRV\DALARTLEQOKNETIBELTKICDELIANGKS  SCHPEPPVKETQQBPDBBSLVPSGERLASETTESBACTGG LLEETTPPVKETQOBPDBBSLVPSGERLASETTESBACTGG LLEETTPPVKETQOBPDBBSLVPSGRALASETTESBACTGG LLEETTPPVKETQDBPPTKKIGKKPVAKMPLRRPKMKKTPBKLDNT PRSPABRHDIP ILAGGTTTDD DKNDDPHTNENFPSSTSKOQER PQGSVMPPDPTCRESVPFFVTSSTPSKSBPSHSPBAFETAA ANGVOGDGLNRPAKKKTPLKTDTPRVKKSPKRSPLSDDPP TPAATTPSTPPVISAVVHATDBERLAVTNOKMTCMTVOLKB PROPADLSTAFVNETKFSSPTEBLDVNNSWETISTMRKKIGSS DDAPKKQALYLMPDTSGSEVKSVPWRMSSPTPCSGSSFI ALVNTAAKNOHPVPRGLAFNOSHICUVBKSSQKELLANGER SSAIBITAPESSFASADALLSRLAHPUSLCGALDVLERDL PPLEAQKLQRRAHPTDVSISKTALYSRIGTAEVERPAGAL SSAIBITAPESSFASADALLSRLAHPUSLCGALDVLERDL PPLEAQKLQRRAHPTDVSISKTALYSRIGTAEVERPAGAL PPLEAQKLQRRAHPTDVSISKTALLYSRIGTAEVERPAGAL PPLEAQKLQRRAHPTDVSISKTALLYSRIGTAEVERPAGAL PPLEAQKLQRRAHPTDVSISKTALLYSRIGTAEVERPAGAL PPLEAQKLQRRAHPTDVSISKTALLYSRIGTAEVERPAGAL			ì		] '
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LLBETPLEPARAGEKARCPLDSESVEGVVPPASGGGRVQNS RKTLPLITAPEAGEVTPSOSGGESPAKGHSVELEPDYS SUDNOQENPPTKKIGKKPVAKMPLREPKMKKTPEKLONT PRSPABPNDIPIAKGTYTPDIDKMDDPNPPFSSTSKMQB PQQSYNFDPDTCDSSVDPFKTSSKTPSSPSKSPASFETPA ANGVDGGLMKPAKKKTPTLTDTFRVKKSPKRSPLSDPP TPAATPETPPVISAVVHATDEEKLAVTNQKNTCMTVDLRA YPQPSDLSTFVNRTKFSSPTELDYRNSYEISYMSKIGSS DDAPKKQALYLMPDTSQSSPVKSSPVRMSESPTPCSGSSF, ALWNTAAKNQHPVPRGLAPRQESHLQVPEKSSQKELEMMG SEAIELTAPEGSFASADALLSRLAHPVSLCGALDYLEPDLA PPLFAQRLQREAAHPTDVSISKTLYSRIGTABVEKPAGLI PPLFAQRLQREAAHPTDVSISKTLYSRIGTABVEKPAGLI VEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADING \SLADLFRRYENKINGRVLKRCAQBYLSRVKK VEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADING \SLADLFRRYENKINGRVLKRCAQBYLSRVKK VQALKVHA\BRILDRANBE\LADWRSKAQDQAAHQASLAV CRV\DALERTLEQKNKEIBELTKICDELIARMGKS  5396 3135 531 RASDAKNQBELLAHTRRGTDSVPTSKSTLSSELSJQASDFF SSCNPBAVALAPDAYSTGSSASSTLKRTKKPRPPSLKKK KPPETPPVKSTQQEPDRESSLVPSGENLASBTKTRSBAXTGG LLBETPLEPAAGPKAACPLDSESVBGVVPPASGGRVQNSI RKTLPLTTAPRAGEVTTSDSGGGBEAKGHSVALBETDYSI SMUNQQENPPTTKLTGKVPAKMEHERPKKKTPSKLDNTT PRSPABPNDIPIAKGTYFDIDKWDDPNFNPSSTSKMQES PQQSYMFDPTTCDESVDPFKTSSKTPSSPSRSPASFELPA ANGVDGDGLNKPAKKKTPLKTDTFRVKKSPKRSLSPLSDFP TPAATPETPPV ISAVVHATDEKLAVTNQKNTCMTVDLRAI YPQPSDLSTFVNETKFSSPTBELDYRNSYEIESYMKKIGSSI DDAPKKQALYLMPDTSQBSFVKSSPVRMSESPTPCSGSSFT ALVNTAAKNQHPVPRGLAPMOBSHLAVTNQKNTCMTVDLRAI YPQPSDLSTFVNETKFSSPTBELDYRNSYEIESYMKIGSSI DDAPKKQALYLMPDTSGSFRADALLSRLAHPVSLCGALDYLBPDLI SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLBPDLI PPLFAQKLQRPAAHPTDVSISKTALYSEIGTABVEKPERBLI PPLFAQKLQRPAAHPTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHPTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHPTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHPTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHPTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHPTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHPTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHPTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHPTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHSTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHSTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLQRPARHSTDVSISKTALYSEIGTABVEKPERBLI PPLEAGKLALAURABIITTARERBRIBBRIAMPERBLI PPLEAG					J .
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Deginning nucleotide location corresponding to first amino acid residue of amino acid sequence code	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation   Cortesponding	_			(A=Alanine, C=Cvsteine, D=Aspartic Acid, R=
Cocresponding	NO:	,		Glutamic Acid. F=Phenylalanine. G=Glycine.
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LKEELSASSARTQN\LINADLQRKEEDYADLKEKLTDAKKQIKQV QKEVSVWRDEDKILIRIKINELEKKKNQCSQELDMKOR\TIQQIK EQLINQKVEEAIQOYERACKDLNVKEKI IEDWRMTLEEQEQTQV EQDQVL\BAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE NNTDVLGKLTNLQDELQESEQKYNNADRKKHLEERMMLITQAKEA ENIRNKEMKKYAEDRERPFKQQNEMETLTAQLTEKDSDLQKWRE ERDQLVAALEIQLKALISSNVQKDMEIEQLKRI ISETSKIETQI MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV STENDQSTRFPKPELBIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKEYSLRSQASIIGUNLATKKKEGTLQKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVBASKENVSQPKRAKKKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK  5399 705 230 GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRILQTHGIDGNGELDFSTFITIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPMSKVKVDEFIHKITSYLDGTY  5400 931 248 SHCSSGMEIPPTNYPASGRALVXQNYINYQGTPHRVFBVQKVK QASMEDIPGRGHKYRLKFAVEBIIQKQVKVNCTASVLYPSTGQE				
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EQLINQKVEEAIQQYBRACKDLNVKBKIIBDMRMTLKEQBQTQV BQDQVL\BAKLEBVBRLATELDRRVVKCNDLETKNNQRSNKBHB NNTDVLGKLTNLQDEQESBQKYNADRKKWLEEKMHLTQAKBEA ENIRNKBMKKYABDRBRPFKQQNBMBILTAQLTEKDSDLQKWRB ERDQLVAALEIQLKALISSNVQKDMBIBQLKRIISETSKIETQI MDIKPKRISSADPDKLQTEPLSTSFBISRNKIBDGSVVLDSCEV STENDQSTRPPKPELBIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKRKSNEMBEDLVKCHNKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKETYSLRSQASIIGVNLATKKKBGTLQKFGDFLQHS PSILQSKAKKIIBTMSSSKLSNVBASKENVSQPKRAKRKLYTSB ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK SSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK ASPTFGBVQRHLQTHGIDGNGBLDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGERLTHKEV\DDLFRB \ADIEPNGKVKYDEFIHKITSYLDGTY SHCSGMBIPFTNYPASGRALVXQNYINYQGGTPHRVFBVQKVK QASMBDIPGRGHKYRLKFAVBBIIQKQVKVNCTAEVLYPSTGQE				
NNTDVLGKLTNLQDBLQESBQKYNADRKKWLEEKMMLITQAKBA ENIRNKEMKKYABDRERFFKQQNEMEILTAQLTEKDSDLQKWRE ERDQLVAALEIQLKALISSNVQKOMEIBQLKRIISETSKIETQI MDIKPKRISSADPDKQTEPLSTSFEISRNKIEDGSVVLDSCEV STENDQSTRPPKPELBIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKRKSNEMEBBDLVKCRNKKNATPETNLKFPISDDRNSSVKKEQ KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK  5399 705 230 GPRMAKFLSQDQINEYRECFSLTOKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKWYDEFIHKITSYLDGTY  5400 931 248 SHCSSGMEIPFTNYPASRAALVNQNYINYQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEBIIQKQVKVNCTASVLYPSTGQE	1 1	[		EQLINQKVEEAIQQYBRACKDLNVKEKIIEDMRMTLEEQEQTQV
ENIRNKEMKKYABDRERFFKQQNEME'LTAQLTEKDSDLQKWRE ERDQLVAALEIQLKALISSNVQKDNEIBQLKRIISETSKIETQI MDIKPKRISSADPDKLQTEPLSTBFEISRNKIEDGSVVLDSCEV STENDQSTRPPKPELBIQFTPLQPNKNAVKHPGCTTPVTVKIPK ARKRSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKKEYSLRSQASIIGUNLATKKKEGTLQKFGDFLQBS PSILQSKAKKIIETMSSSKLSNVBASKENVSQPKRAKKKLYTSB ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK  5399 705 230 GPRMAKFLSQDQINEYEECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRILQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRB \ADIEPMSKVKYDEFIHKITSYLDGTY  5400 931 248 SHCSSGMEIPTTNYPASGRALVXQNYINYQGGTPHRVFBVQKVK QASMEDIPGRGHKYRLKFAVEBIIQKQVKVNCTASVLYPSTGQE			•	EQDQVL\BAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE
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KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLETKTAK  5399 705 230 GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVEYDEFIHEITSYLDGTY  5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTASVLYPSTGQE				
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ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK  5399 705 230 GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGBVQRILQTHGIDGNGELDFSTFLTIMHMQIKQBDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRB \ADLEPMSKVKYDEFIHKITSYLDGTY  5400 931 248 SHCSSGMBIPFTNYPASGRALVXQNYINYQGGTPHRVFBVQKVK QASMBDIPGRGHKYRLKFAVEBIIQKQVKVNCTASVLYPSTGQE			0	
5399 705 230 GPRMAKFLSQDQINBYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGBVQRHLQTHGIDGNGBLDFSTFLTIMHMQIKQBDPKKE ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRB \ADIBPNGKVKYDEFIHKITSYLDGTY 5400 931 248 SHCSSGMBIPPTNYPASRAALVAQNYINYQQGTPHRVFBVQKVK QASMBDIPGRGHKYRLKFAVBBIIQKQVKVNCTASVLYPSTGQB	ļ			
ASPTPGBVQRHLQTHGIDGNGBLDFSTFLTIMHMQIKQBDPKKE ILLAMI.MVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIBPNGKVKYDEFIHKITSYLDGTY  5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFBVQKVK QASMEDIPGRGHKYRLKFAVBBIIQKQVKVNCTAEVLYPSTGQE	5300	700	224	
ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIBPNGKVKYDEFIHKITSYLDGTY  5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVRBIIQKQVKVNCTAEVLYPSTGQE	2228	705	230	
\adibprgkvkydefihkitsyldgty 5400 931 248 SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFBVQKVK QASMEDIPGRGHKYRLKFAVBBIIQKQVKVNCTAEVLYPSTGQE	1 1	1		
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QASMEDIPGRGHKYRLKFAVEBIIQKQVKVNCTAEVLYPSTGQE	5400	931	240	
	3400	221	248	
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	<u> </u>			THE TENETOWN TENDETOWN TENETOWN TOWN TOWN TOWN

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T-Threonine, V-Valine,
	residue of	amino acid	NeTryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1 •	\=possible nucleotide insertion)
			FGNVSPEMTLVLHLAWVACGY I I WONSTEDTWYKMVKIOTVKOV
	İ	ł	QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS
1	ļ		RLPKEVQLE
5401	3	1360	TGWSYGPTTSLAFLAPRDFPFPPKLLIHPQAVVRLSCGAGSMGS
			QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME
ľ	i		KWAPRODDMLFYVRRKLAYSGSESGADGRKAAEPEVEVRVYRRD
1	Ì		SKKLPGLGDPDIDWEESVCLNLILOKLDYMVTCAVCTRADGGDI
1			HIHKKKSQQVFASPSKHPMDSKGERSKISYPNIFFMIDSF\BE\
1			VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYKALKKVY
	,		DNRVSVAARMAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHABMA
			VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA
1			FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT
1			NLRSRSLSGTGRSLVGSWLKLNRADGNPLLYAHLTYVTLPLHRI
1			LTDILEVRQKPILMT
5402	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
			PGADILNSYAGLACVERPNDMITESSLDVAREBIIDDDDDDDTL
Į I			TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
1			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
			ALLQDKATCPKYIKWTQRBKGIFKLVDSKPVSRLWRKHKNKP\D
			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
1			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
	•		PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
			PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
1			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
-	+		MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
	.0		VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
1			ETKTLTQEVBKKESEDHLKENTEKTEQQFQPYVMVVSSSNGFTS
5403	3445	1563	QVAMKQNELLEPNSF
3403	2442	1363	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV PGADILNSYAGLACVEEPNDMITESSLDVAKERIIDDDDDDITL
			TVEASCHDGDETIETIBAAEALLNMDSPGPMLDEKRINNNIFSS
1 1			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
1 1			ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
1 .			MNYEPMGRALRYYYORGILAKVEGORLVYOKKEMPKOLIYINDE
1			DPSSSIESSDPSLSSSATSNRNOTSRSRVSSSPGVKGGATTVLK
			PCNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
			PVQAVPEGRAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
	ĺ	•	RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKPILQAIPSSQP
			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
1 1			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
			QVAMKQNBLLEPNSP
5404	187	1111	LPVILIFAKMKTLQSTLLLLLLVPLIKPAPPTQQDSRIIYDYGT
			DNFERSIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDEAI
			TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY
1 1			LYARPNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL
1			SLVEELSLABNQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK
1			KLNNLTFLYLDHNALESVPLNLPBSLRVIHLQFNNIASITDDTF
أحجيا		<del></del>	CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
5405	2199	1220	QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYBREIQPTA
			ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII
} I			PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS
1 1			nssasseqgligrspptrpvpghrserairtqpkqlivddlkgs
]			LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE
			SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR
	Ì	,	YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS
			ntvycklrscpsrcogkps
5406	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQQNLYRNVMLENY

SEQ ID No:	Predicted beginning nucleotide location corresponding to first	Predicted end nucleotide location corresponding to first amino acid	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, P=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid residue of amino acid	residue of amino acid sequence	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence		-possible nucleotide insertion  RILVPLG/IIAVSKPDLITCLEQEKEPWEPMRHEMVAKPPVMC SHPTQDFWPEQHIKDPFQXATLRRYKNCEHKNVHLKKDHKSVDR CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS HTEKKLFKCKECJKSFCMLSHLAQHKIIHTRVNFCKCEKCGKAF NCPSIITKHKRINTGEKPYTCEBCGKVFNWSSRLTTHKKNYTRY KLYKCEBCGKAFMKSSILTTHKIIRTGEKFYKCKECAKAFNQSS NLTEHKKIHPGEKPYKCEECGKAFWWPSTLTKHKRIHTGEKPYT CEBCGKAFNQPSNLITHKRIHTA\EKPYKCTECGEAFSRS\SNL TKHKEIHTEKFPYKCRECKAFKWSSKLITEHKLIHTGEKPYKCR KCGKAFNCPSIITKHNRINTGEKPYTCEBCGKVFNWSSRLITHK KNYTRYKLYKCEBCGKAFNKSSILTTHKKIHIEKKFYKCEBCGK AFKWSSKLITEHKITHTGEKPYKCBCGKAFNHFSILTKHKRIHT GRXPYKCEBCGKAFTQSSNLITHKLHTGBKYYKCECGKAFTQ SSNLTTHKKIHTGKPYKCBCGKAFNQFSTLTKHKIHTEKP YKCEBCGKAFKWSSTLTHKKIHTGKFYKCBCGK
			L9THKIIHTGEKPYKCBKCGKAFNRPSNLIBHKKIHTGBQPYKC ERCGKAFNYSSHLNTHKRIHTKBQPYKCKECGKAFNQYSNLTTH NKIHTGEKLYKPRDVTV1LTTPQTFSNIK
5407	3	659	RPRRRQSSCCTGWLAGWLLRAAPRFCRRTETDMEQGKGLAVLIL AIILLQGTLAQSIKGNHLVKVYDYQEDGSVLLTCDAEAKNITWF KDGKNIGFLTEDKKKWNLGSNAKDPRGWYQCKGSQNKSKPLQVY YRMCQNCIELNAATISGFLFABIVSIFDLAVGVYFIAGTGMEFR QS\RASDKQTLLP\NDPAPTQPLKDPEKMTQYSHLQGN\QLRRN
5408	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSBPWGQSQEPPTMPQR:.P
			HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRP STPCFGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHWAKCYGD LVQRLWSGTQKWVAPLKLRWTIAKYAPRFNGFQQQDSQEILLAFL
		·	LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEANDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL BITVIKLDGTTPVRYGLRLNMDBKYTGLKKQLSDLCGLNSBQIL LAEVHGSNIKNFPQDNQKVRLSVSGFLCAPBIPVPVSPISASSP
5409	2745	6128	TOTDESSSPSTMEMETELTINGDLPRPIFIPINGMPNT-VVPCGTEX NFTWOMVNGHMPSLPDSPPTGYIIAVHRKMMRTBLYPISSQKNR PSLEGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPOBASNH AQDCDDSMGYQYPPTLRVVQKDGNSCAMCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPTALHIRYQTSQERVVDEHRSVEQSRRAQ VEPINLDSCLRAFTSBEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRRQFVNGRWIKSQKTVKFPRSSFDPSAFLVPRDP ALCOHKPLTPQGDELSEPRILARRVKKVDAQSAGEEDVLLSKS PSSLSANIISSPRGSPSSSRKSGTSCPSSKMSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPBLVTPQDHEVALANGFLYEHRACGNGCGNGYSNGQLG NHBEBDSTDDQRBDTRIKPIYNLYAISCHSGILGGGNYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\BKYCVLQ QGSKGTCHPQAQQDWDEGVWQEAPSQSBPPWGQSQEPPTMPQRLP
3.02	3,13	V120	HARCHTPLPLCSADYRRVVSVRPQCPHRDPKDSRDAARREQGSL APREVPASRGCKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRPLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYBLNRTNPIGMKGHMAKCYGD LVQBLWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLJEDLNRVHEKPYVELKDSDGRPDWKVAAEAMUNHLRRNRS IVVDLFHGQLREQVKCKTCGHISVRPDPPNPLSLPLPMDSYMHL BITVIKLDGTTPVRYGLRLNMDBKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKNPPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

SEQ	Predicted	T Base 34 - 1 - 3 - 1 - 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
ı	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine,
1	amine acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1 .			TOTOFSSSPSTNEMPTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
1	1		NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
1	l	] .	PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
J	]	}	AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGR
1		į	DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
1		}	VBPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
1	ł	1	LPPILIIHLKRFQFVNGRWIKSQKIVKFPRBSFDPSAFLVPRDP
1	ļ		ALCOHKPLTPQGDELSBPRILARBVKKVDAQSSAGEEDVLLSKS
			PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
1			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICKLADALSRGH
1	ł		VLGGSQPELVTPQDHEVALANGPLYEHEACGNGCGNGYSNGQLG
ł			NHSBEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
i			PNCKWYCYNDSSCKELHPDBIDTDSAYILFYBQQGIDYAQFLPK
<u> </u>			TDGKKMADTSSMDEDFESDY\EKYCVLQ
5410	2	710	LRPPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY
1			VHQNPSSHYRATIGVDFALKVLHWDPETVVRLQLNDIAGQERFG
i			NMTRVYYREAMGAPIVFDVTRPATFEAVAKWKNDLDSKLSLPNG
I .			KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK
			ENINIDEASRCLVKHILANECDLMBSIEPDVVKPHLTSTKVASC
-			SG\CAKILVGTPAGVW
5411	1302	289	TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC
i :			GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLQNHQQ⊇N
1			GGEFFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS
i · ·			QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNKLILKTLKEITEG
1 1	Ψ.		KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR
	*		DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV
			KPA/FBBFCLPPK/KYADVIIPR/GADN/RVPINLIVQHIQ/DI
5412			LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
2412	3180	313	QGISNFFHKEANFWFEVSGYLISPLRSPFVDPALEWSLMASPWN
1	'		KMEGESSRFEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
1 1	·		NEQSQITRRKKRKKDFQHLISSPLKKSRICDETANATSTLKKRK
1 1			KRRYSALEVDEBAGVTVVLVDKBNINNTPKHFRKDVDVVCVDMS
]			IBOKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
1 1			KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA
1 /			HKNKSKKKKKSSNRBYET\LAMPEGSQAGREAGTDMQESQPTV
) )			GLDDETPOLLGPTHKKKSKKKKKKKKKNHQBPBSLAMPEGSQVGS
•			BVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKKSNHQEF
			EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK
1 1			SKKRKLTSVKRARVSGDDFSVPSKNSESTLFDSVEGDGAMMEG
			VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSBIRY
, ,	1		LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD
	[		LERPKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD
[ [	İ		KLLYTDRYPREKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA
	j		KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL
'	ļ		SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQBLK
	ļ		BVD3KLQENPESCL3IVREKLYKGISWVEVEAKVQTRNWMQCKS
į	ľ		KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDINEI
	į		DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPBIIDYL
	J		YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD
			SEGGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	RPPAGVAPRRAMANVSKKVSWSGRDRDDEBAAPLLRRTARPGGG
	1		TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP
l	ļ	į	HPFPKBIPHNEKLLSLKYESLDYDNSKNQLFLEKERRINHTAFR
	§		TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID
1	ĺ	ĺ	KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIRPVAAGSGIPQ
	1		IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH
	į.		SGSVIAAGISQGRSTSLKRDPKIPEYLRRDTEKRDFVSAGAAAG
ŀ		1	VSAAFGAPVGGVLPSLEEGASFWNQPLTWRIPPASMISTPTLNF
			VLSIYHGNMWDLSSPGLINFGRFDSBKMAYTIHEIPVFIAMGVV
ĺ	1		GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA
			FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K-Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
I	sequence	1 -	\=possible nucleotide insertion)
<b> </b>		<del></del>	SVSLEHDPPGSYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP
ļ		}	SLLIGAAWGRLFGISLSYLTGAAIWADPGKYALMGAAAOLGGIV
I		1	RMTLSLTVIMMEATSNVTYGFPIMLVLMTAKIVGDVFIEGLYDM
í	1	1	
Į.	Į.	l	HIQLQSVPFLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV
l	į	<b>(</b>	DVLSDTASNHNGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV
ł			FVERSNLGLVQRRLRLKDPRDAYPRFPP1QS1HVSQDERECTMD
l		1	LSBFMNPSPYTVPQEASLPRVPKLFRALGLRHLVVVDNRNQVVG
}		}	Lvtrkdlaryrlgkrglerlslagt
5414	2130	390	GVASAWDRALFSPLLSPTSRVFRTSPPRCVSTETGRRDRARVPS
i			OWCSVLOGKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR
ļ	1	ł	AGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGCQGPRGTRSP
1	I		RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINILINYMDRFTV
1	1	1	AGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDRYN
1	1	I	RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASY
I	I	[	STIAPTLIADLEVADORSRMLSIFYFAIPVCSGLGYIAGSKVKD
I	1	1	
ľ	1	1	MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPL
}		1	NPTSWWADLRALARNPSFV_SSLGFTAVAFVTGSLALWAPAFLL
l			RSRVVLGETPPCLPGDSCSSSDSLIPGLITCLTGVLGVGLGVEI
i	(	Í	SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYIF
}		}	IPIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD
}	]	1	AGSPYLIGLISDRLRRNWPPSFLSRFRALQFSLMLCAFVGALGG
}		İ	aaflgtahlh
5415	693	2986	IPPKTKLELQKH\LTTLT\NQEQATIFEKVQKLRPRNBQRENEL
ļ		ļ	IISPLECLPEBROKEHIHIGEMKOTSOMAAENIGSELPPSATRF
Ì		1	RLDMLKNKAKRSLTESLESILSRGNKARGLQBHSISVDLDSSLS
1	{		STLSNTSKEPSVCEKRALPISESSPKLLGSSEDLSSDSESHLPE
Į.			KPAPLSPQQAFRRRANTLSHFPIBCQE2PQPARGSPGVSQRKLM
1			RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFL
		1	RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPE
}		ì	The state of the s
ł			EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKR
l .	{	<b>!</b>	LKLDYBEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ
		-	GAL/KHHKGRIMKLTVEÖLHTKHÖLDSKÖÖLKDALAKETTKÖTT
ł	· ·		SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE
1			VGYCQGLSFVAGILLLHMSEBEAFKMLKFIMFDMGLRKQYRPDM
[	į.	· ·	IILQIQMYQLSRLLHDYHRDLYNHLBEHBIGFSLYAAPWFLTMF
Į.			asofplgfvarvfdmiflogtkvifkvalsllgshkplilohen
}	į	ł	LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH
	1	ľ	VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG
1	0	ì	RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVBELRRRS
J	ļ	l	AKPSDREPECTOPEPTGD
5416	27	4074	KSQLFCFWGGKAGDILSGDQDKRQKDPYFVBTPYGYQLDLDFLK
-1.20	1		YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES
ł	1	ł	LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
1	1	1	ENROLPPPSPOLPKHNLHVTKTLMETRRRLEGERATMOMTPGEP
	i		RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHOLONGYQGNGDYG
{	•	(	
1	1	}	SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQM
	1	]	AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
Ì	1	1	SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEBEBME
Į.	1	1	TVEQSTQRIKBFRQL\TADMOALEQKIQDSSCEASSELRENGEC
1	1	<b>[</b>	RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
[			AMLGVMTEADKEIBLQQQTIBSLKEKIYRLEVQLRETTHDREMT
1	1	i	KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
}	1	]	MDLVDTCVGTSVETNSVGISCOPECKNKVVGPELPMNWWIVKBR
1			VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
1		{	NLNLKEVRS IGCGDCSVDVTVCS PKECASRGVNTEAVSOVEAAV
		i	
1		1	MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDKQ
i	1	1	TSTQTVBTRTVAVGKGRVKDINSSTKTRSIGVGTLLSGHSGFDR
l		ł	PSAVKTKRSGVGQININDNYLVGLKMRT1ACGPPQLTVGLTASR
I		<b>{</b>	RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYTERIQELLAEQQ
[	· ·	ĺ	TLLAENYSBLARAFGEPHSQMGSLNSQLISTLSSINSVMKSAST
	1	1	EBLRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPB
			<del></del>

SEO	Predicted	Predicted end	Theiro poid
n	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Tsoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
)	1		ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
1	ł		ESSSESDDECDVIEYPLEBEEEEEDEDTRGMAEGHHAVNIEGL
1	Ĭ	Ï	KSARVEDEMQVQECEPEKVBIRERYELSEKMLSACNLLKNTIND
1	ł		PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI
i			SPDVLRYVINLADGNGNTALHYSVSHSNFRIVKLLLIDADVCNVD
1			HONKAGYTPIMLAALAAVEAEKOMRIVEELFGCGDVNAKASQAG
1			QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLLAQPGCNGHLEDNDGSTALSIALRACHRDIAVLLYA
1			HVNFAKAQSPGTPRLGRKT8PGPTHRGSPD
5417	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK
0.127	[	10/1	YVDDIQKGNTIKRLNIQKRRKPSVPCPBPRTTSGOOGIWTSTES
ì			LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
1	}		ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF
			RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
ſ	Í		SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQN
1	Į		AIALKRLKELEEQVRTIPVLQVKISVLQBBKRQLVSQLKNQRAA
1	ì		SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEKERME
	[		TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCRASSELRENGEC
	1		RSVAVGARENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTB
1			ANLGVMTRADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT
i			KIKQRIQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDIVDTCVGTSVETNSVGISCOPECKNKVVGPRLPMNWWIVKER
	ĺ . I		VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTERSVNDLTLLKT
			NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
j			MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ
i		4.	TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
1	·		PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR
}		1.0	RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ
1			TLLABNYSELABAFGRPHSQMGSLNSQLISTLSSINSVMKSAST
i			EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE
ł			QBVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
}			ESTLKSIMKKKDCNKDSNGAKKNLQPVGINGGYETTSSDDSSSD
1			ESSSSESDDECDVIEYPLEEEBBEEDEDTRGMAEGHHAVNIEGL
		•	KSARVEDEMQVQRCEPEKVETRERYELSEKMLSACVLLKNTIND
i i			PKALTSKOMRFCLNTLQHEWFRVSSQXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFRIVKLLLDADVCNVD
1		•	HONKAGYTPINIAALAAVRABKONRIVERLFGCGDVNAKASQAG
			QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
1	Ì		HVBIVKLLLAQPGCNGHLEDNDGSTALSIALBAGHKDIAVLLYA
			HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5418	24	1133	SVPRAGGDMRTGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR
			KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDBKR
			RQELEBKIRKKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL
] .			DCHQEVEKVQPPGPVKEMAHGSQRAEAPGAVAGAAEVPR\EPPI
	}		LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK
1			GKQVSVALSSSSIRVAMLBENGERVLMEGKLTHKINTESSLWSL
			BPGKCVLVNLSKVGEYWWNAILEGERPIDIDKINKERSMATVDR
			EBQAVLDRLTPDYHQKLQGKPQSHBLKVHEMLKKGWDABGSPFR
5419	1395	350	GORFDPAMENISPGAVOF
اقتدا	1333	259	GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAREG SESKACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNNKHPERADA
, ,			
			KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH
( I			BLEAIILRAKQQAVREDBESNEGDSDDTDLQIFCVSCGHPINPR
, 1			VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT
			YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFBLTGDFCRLPK
(	,		RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN
			RAGILALMIHOTIOHDPLTTDLRSSADR
5420	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
			GGFLPARPPRAQRHLGFSHARQSMEAPDYEVLSVREQLFHRRIR

Destanting medication of moticotide corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding to first asino acid amino acid sequence sequenc	SEO	Predicted	1 5 17 1 1 1	
Not	_		Predicted end	Amino acid segment containing signal peptide
Corresponding to first amin acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence   PPTOLINE, Q=Glutamine, R=Arginine, S=Gerine, T=Threonine, V=Valline, V=Typtophan, Y=Tyrosine, X=Dukkowa, *=Stop Code, (*possible mucleotide insertion)	,			
corresponding to first amino acid residue of amino acid residue of amino acid sequence sidue of amino acid sequence sequence sequence colon, "	NO:		1	
to first amino acid residue of amino acid anino acid sequence  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide deletion, V=possible mucleotide insertion)  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion)  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion)  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A-possible mucleotide insertion  ##Tryptophan, Y=Tyrosine, X=Unknown, Y=Tyroyn, X=Tyr	1			
amino acid residue of anino acid sequence sequence  sequence  sequence  sequ			to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid esidue of anino acid sequence  Sequ	1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
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YETVVMIMILITILIVICMVWWASAITOKKANDESIYDEMETYLE YINGSISPIGUILILIVITPIGIANDESVIGALVKEPILEDLER QLYCSAFERALITRI CNPTSCMLPLIMELLIRQUIAIQTQRVI. LERRRRSSAMQRAIGYPLAMICLIVITSISVILIVAHILLEILII BAMPREKAGTSIGQUSFSKLESBEAVIQVULIPTIMWSSVOGP YSSPLERSIRPRHIDTAMTQIIGNCUCILIVISSALPVPSRTLGI. TRIDLIGDGRFWHIGHNYIVPINNAAPAGITTICLVKTFTAAV RAKLIRARGERS  5422  3 1263 SCGBELPTWLAGASRPGIGRKGGAWGGRGSSSPAQVILLSPGPVF KAGCMWHILGSBQAGVGCDLGSSQPPLGFKRPSCISLESSMD YRSTVLCVSKWEADLSGFNIDAPRKDORTTIGRVHIFINITDER TVPUSERSILDARXVMUERSEMOVVP PTGTQVEQLIATAKKLIVSAP HPITGEKNNVIGRNSFQLDEGHIITGFMLQFYRTMFAVIFMQNIFMQN NQSPALIVATYNRKABAPTSVEQMALSTATTATTAVATAVGNNM LITKKAPPINGRWPPAAVAANCVNIPMERQGELKGICVKDRN RNSIGHSRRAAAIGTQVVISRITMSAPOHILLIVFYMERLEKLH PMCKVEVL/SAPLQVMISGCFLIFMVPVAGGLPPQKCELVSVIL EPHLQDTIKAKVGELBPVYFNKGI.  5423  3186  905  GVSMAIGREKKABARASEDTKADSVGRGSCERRELDIPPMGGG PPLURARGGLISPWGABGIPAPTCWIGTDPGGPSRAHQPQASD ANREPVARSEPALSGLPPATWGSCDLLLSGESQVERTKIGSSE EPPGTISLPRTTICSGHADTPEDDPSLADLPQALDLSQQPHSG GSLAKVSSSLEPVVPQEPSSVUGLIPPSPQPVFSGGDASGL GRRILSPQAKVMCVLPDSLPPSPRRISPLMMPMKYRDLLDYT YPLRRPQOLPKHLDSKYPADPVLQDSGVDLDSFSVSPASTLKSP TWESPNCPPREATALPFSGPRRPSLKQWPSRVPPRGGGMGLASW SQLASTTRABGSRDARWRRREPALRGARDELTIGRHDMGSPQL RTRDIGWSPPRPREKETRSQSARRPTTENGSWRGEBEVSEDDEY LALDRAILOVSSUSVILGSISTLVTLPTGDIRGOPLARSFVRABIDSAG EGSIGSSQALGVSVSGLLKTRPSLPARLDRNPSDPDVEGQLPRK GEGGKSSILVGLVXKTFC\QDIBELICMYNV\ADVIDHOTPAR SMLTSLK\SSLGLYNTGVKGDLDEGGGDFLRSFVRABIDSAG EGSIGSSQALGVSVSGLLKTRPSLPARLDRNPSDPDVEGQLPRK GEGGKSSILVGLVXKTFC\QDIBELICMYNV\ADVIDHOTPAR SMLTSLK\SSLGLYNTGKDDDFSLTFSVLQKGETLLGCLLE NTPULEDVIGRIAKGGERISBIADRIJDSILASESQUETKILSSE EPPGTILSIPRTTICSGHADMTEDDPSLADLPQALDLSQQDHSGG PRERBREGGLISPWMABERIPERGFTRSVLGSSLCHORDRRAREPGG GSLAKVSSSLEPVVPQEPSSVUGLIPPPPSSGLLDSGESQUETKILSSES EPPGTILSIPRTTICSGHADMTEDDPSLADLPQALDLSQQDHSGG GRREFVARESPELSGELPPATMGGGLLLISGESQUETKILSSES EPPGTILSIPRTTICSGHADMTEDDPSLADLPQALDLSQQDHSGG GSLAKUSSSLEPVVQEPSSVUGLEPPROPSDPLDDPSLADLPQALDLSQQDHSGG GSLAKUSSSLEPVVPQEPSSVUGLSPSPLANDRYBEPGG GSLAKVSSLEPVPQEPSSVUGLSPSPLANDRYBERGERG GSLAKVSSLEPVPQEPSSVUGLSPSPLAND	I	·		
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NTPVLBDVIGRTAKQSGELESHADRLYDSILASLDMLAGCTLIP DKKPMAAMEHPCEGV  5424  3186  905  GVSMALGEEKAEARASEDTKAQSYGRGSCRERELDIPGPMSGEQ PPRLBABGGLISPVWGABGIPAPTCMIGTDPGGPSRAHQPQASD ANREPVABRSEBPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAQPSSCSIBASSTGSSLQCHQBRAEPRG GSLAKVESSLEPPVPQEPSSVVGLGFPPQWSPQPVFSGGDASGL GRRRLSPQARYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP				
DKKPMAAMEHPCEGV  5424  3186  905  GVSMALGEEKAEARASEDTKAQSYGRGSCRERELDIPGPMSGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVERTKLSSSE EFPQTLSLPRTTICSGLPPATMGSGDLLLSGESQVERTKLSSGE EFPQTLSLPRTTICSGLPDADDPSLADLPQALDLSQDPHSSG LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQCHQBRAEPRG GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL GRRRLSPQARYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP		į		
5424 3186 905 GVSMALGEEKAEARASEDTKAQSYGRGSCRERELDIPGPMSGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE EFPOTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQCHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL GRRRLSPQARVWACVLPDSLPPSPDRHSPLNNPNKEVEDLLDVT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP				-
PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE EPPOTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAQPSSCSIEASSTGSSLQGHQBRAEPRG GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL GRRRLSPQARVWACVLPDSLPPSPDRHSPLNNPNKEVEDLLDVT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP	5424	2106	000	
ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE EFPOTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAQPSSCS I EASSTGSSLQGHOBRAEPRG GSLAKVSSSLEPVVPQEPSSVYGLGPRPQWSPQPVFSGGDASGL GRRILSFQARYWACVLPDSLPPSPDRHSPLNNPNKEYEDLLDVT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP	2444	2790	305	
EFPOTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQCHQBRARPRG GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQFVFSGGDASGL GRRRLSPQARYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP	1	ì	i	
LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQCHQBRARPRG GSLAKVSSSLBPVVPQEPSSVVGLGPRPQWSPQFVFSGGDASGL GRRRLSPQARYWACVLPDSLPPSPDRHSPLWNPNKBYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP		1	!	
GSLAKVSSSLBFVVPQEDSSVVGLGPRPQWSPQFVFSGGDASGL GRRRLSFQARYWACVLPDSLPPSPDRHSPLWNPNKBYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP		İ		EFPOTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
GRRRLS PQARYWACVLPDSLPPS PDRHS PLWNPNKBYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVS PASTLKSP	į	į		LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQRRARPRG
GRRRLS PQARYWACVLPDSLPPS PDRHS PLWNPNKBYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVS PASTLKSP		j	j	
YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP	i	Į		
	' 1	ł		
TOTAL OF THE PROPERTY OF THE P	I	ł		
		<u>.                              </u>		The state of the s

SEQ	Predicted	I beed and	Lamina mila managaran da lamana
	beginning	Predicted end	Amino acid segment containing signal peptide
ID		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G-Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
<del> </del>		<del></del>	SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPOL
l	i	1	RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEREVESDDEY
ŀ	1	•	· ·
Į			LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
i		[	PASPPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
į.	<b>[</b>	•	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
ł	ì		GGBQGKBSLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
l	1		SNLTSLK\SSLQLYRQFKXDIDEHQSLTESVLQKGEILLQCLLE
i	1		NTPVLEDVLGRIAKQSGELRSHADRLYDSILASLDMLAGCTLIP
		ł	DKKPMAAMEHPCEGV
5425	1086	115	GPCPSPSLGHQPPRVLHPTMSMAVETFGPFMATVGLLMLGVTLP
1		1	NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML
1	1		ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK
}			AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
}	l		KYELGPALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP
1	1		YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA
1 .	•	}	
1			PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
F422			NCSWEVAYLPSEAGSLIF
5426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
	į.		PAAHAKPDPGSGGQPAGPGAAGRALAVLTSFGRRLLVLIPVYLA
Í			GAVGLSVGFVLFGLALYIGWRRVRDEKERSLRAARQLLDDEEQL
1			TAKTLYMSHRELPAWVSFPDVBKAEWLNKIVAQVWPFLGQYMEK
l			LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
i	i		KBQILLDLNISYVGDVQIDVEVKKYPCKAGVKGMQLHGVLRVIL
1			RPLIGDLPFVGAVSMFFIRRPTLDINNTGMTNLLDIPGLSSLSD
į	1		TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
	i		LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
í	:		POWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
			LOASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
	}		KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGFNSRLYM
		,	KLVMRILYLDSSRICPPTVPGCPGAWDVDSENPQRGSSVDAPPR
			PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
		8.	VKLKLAGRSFRSHVVRBDLNPRWNBVFBVIVTSVPGQBLBVBVF
			DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLRDVPSGRLHLRL
			ERLTPRPTAABLEEVLQVNSLIQTQKSARLAAALLSIYMERAED
<u> </u>	İ		LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASPLI
[			RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
			65GQCQVLLRAQLGILVSQHSGVEAHSHSYSHSS6SLSEBPBLS
			GGPPHITSSAPEV\RQRLTHVDSPLRAPAGPLGQVKLTLWYYSK
			ERKLVSIVHCCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
[			KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
.			LGKVQLDLARTDLSQGVARWYDLMDNKDKGSS
5427	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
			PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
]			GAVGLSVGFVLFGLALYLGWRRVRDBKERSLRAAROLLDDBEOL
			TAKTLYMSHRELPAWVSPPDVEKAEWLNKIVAQVWPPLGQYMEK
			LIAETVAPAVRGSNPHLQTFTFTRVBLGBKPLRIIGVKVHPGOR
			_
100			KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
	1		EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
			TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDBBLN
			POWGETYEVMVHEVPGQBIEVEVFDKDPDKDDFLGRMKLDVGKV
			LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
			MVQLSIQDVTQESKAVYSTNCPVWEKAFRFFLQDPQSQELDVQV
0.00	Ì		KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
			KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
		1	PCHTTPDSQFGTRHVLRIHVLEAODLIAKDRFLGGLVKGKSDPY
			VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
LI			DKDLDKDDPLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methicnine, N-Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	1	Sequence	\=possible nucleotide insertion)
	sequence		
		]	BRLTPRPTAAELEBVLQVNSLIQTQKSAELAAALLSIYMBRABD
1	1	ľ	LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
1	1	3	RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
ſ	1	i	SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
l	ł	ł	GGPPHITSSAPEV\RQRLTHVDSPLRAPAGPLGQVKLTLWYYSE
1		i	ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
ſ		<b>[</b>	KKRTLSPEPNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
}	<b>S</b>		LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5428	3	1839	SSRSERLSACATAPPWLVSSRPARPAQLQRPGKMVEDGAEELED
5428	} 3	1839	•
l	1	1	LVHFSVSELPSRGYGVMEBIRRQGKLCDVTLKIGDHKFSAHRIV
1			LAASIPYFHAMFINDMMECKQDRIVMQGMDPSALEALINFAYNG
1	1	1	NLAIDQQNVQSLLMGASFLQLQSIKDACCTFLRBRLHPKNCLGV
	1		ROFARTMMCAVLYDAANSFIHOHFVEVSMSEEPLALPLEDVLEL
1		1	vsrdelnvkseeqvfeaalawvrydreqrgtfl\rnlqsnirll
)	1	1	FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP
1		Ī	AFRTRPRCCTS LAGLIYAVGGLNSAGDSLNVVEVPDP LANCWER
1	{	{	CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT
ļ	}	1	WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE
1		ŀ	TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH
ì	1	}	YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI
	l	Į.	AENYSSV\ADOWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT
1	(	t	
	1	Į.	TGQSNL\SSVGDVLTPRTDCWTFM\APMACHEGGVGVGCIPLLT
<u></u>			I
5429	828	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
}			AQRERFHRFQPTYPYLQHEIDLPPTISLSDGBBPPPYQGPCTLQ
1		ł .	LRDPEQQLELNRESVRAPPNRTIPDSDLMDSARLGGPCPPSSNS
1		i	GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFQHQQSSGPPSL
			LEGTRLHHTHIAPLESAAIWSKBKDKQKGHPL
5430	441	1507	OKRRKRRKKIMKTIOPKNHNSISWAIFTGLAALCLFOGVPVRS
		1	GDATFPKAMDNVTVRQGBSATLRCTIDNRVTRVAWLNRSTILYA
1	ļ	1	GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN
i .	ĺ		HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP
1		1 .	TVTWRHISPKAVGPVSEDBYLEIQGITREQSGDYECSASNDV\A
1	1	1	APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA
l .	į	(	
i	i		BFQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSEHDYGNYT
1	ì	1	CVASNKLCHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL
L	l	L	HLLLKF
5431	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
	1		LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELBLDEQQ
1	1	1	KKRLRAFLTQKAKVGELKDDDFRRISHLGAGNGGVVTKVOHRPS
1		]	GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
1	Ī	1	SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
1		Į.	YLREKHOIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
1		1	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
1		1	DAKELEAIFGRPVVDGEEGRPHSISPRPRPPGRPVSGHGMDSRP
j .	}	)	
[			AMAIFRILDYIVNRPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
		<u> </u>	DLKMLTNHTFIKRSEVBBVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
í			LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
}	1	1	KKRLBAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
1		· ·	GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
l	į	{	SDGEISICMEHMDGGSLDOVLKEAKRIPEEILGKVSIAVLRGLA
ļ	ļ	1	YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
		ł	FYGTRSYMAPERLOGTHYSVOSDIWSMGLSLVELAVGRYPIPPP
1	}	1	,
1	Į.	1	DAKELEAI FGRPVVDGEEGEPHS I SPRPRPPGRPVSGHGMDSRP
1	1	i	AMAIFELLDYIVNEPPPKLPNGVFTPDFQBFVNKCLIKNPAERA
	<u> </u>		DLKMLTNHTFIKRSEVBEVDFAGWLCKTLRLNQPGTPTRTAV
5433	360	1885	SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV
1	1	<b>{</b>	LFGWP3LVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF
]	ļ	1	SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI
			<u></u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, R=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	1		
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
	<del>                                     </del>	<del> </del>	IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI
			ITLYNGAPDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC
	ŀ	Į.	
	ì	1	STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT
			GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL
	Į	į.	SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL
	j	j	CAPWNGLLMDRLKQKYQKBARKTGSSTLAVALCSTVPSLALTSL
	1	1	LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAFLTLAFP
	}	1	SEHPGKLPGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF
	į.	1 -	
			MLAILLTPFHPFLVYRECRTWKESPSALA
5434	66	652	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLWWLF/GSGK
	1		HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
	1		LROGREGMEIGCINYPECENTBLIDKPDETAITCPQCRTGHLVQ
Í	1		RRSRYGKTPHSCDRYPBCQFAINFKPIAGECPECHYPLLIEKKT
	1		The state of the s
		ļ	AOGURHFCASKOOGKPUSAK
5435	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPINVTLSSGPVADRGVKH
	I .		HSGGEKPFQAQKQBPHPGTSRQRQTRVNPHSLPDPEVNKQSSSK
	i	1	GMFRKKOGWKAGPEGTSQBIPKYITASTFAQARAAEISAMLKAV
	Ī		TOKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQBIAQKRAEKA
	1	1	VROKKEHSKNKCHKARRCHMNRTLBFNRROKKNIWLETHIWHAK
	1	į.	RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
	j	1	LKGKBEBILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN
	}	j	
	1		KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE
	ł	l	INAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKRKR
	{	l .	KDDGENAKPIKKIIGDGTRDPCLPYSNISPTTGIIISDLTMEMN
	I	[	RFRLIGPLSHSILTEAIKAASVHTVGEDTEETPHRWWIETCKKP
		i	DSVSLHCRQEAIFELLGGITSPABIPAGTILGLTVGDPRINLPQ
	1	1 .	KKSKALPNPEKCODNEKVROLLLEGVPVECTHSFIWNQDICKSV
		1	TRNKISDODLNRMRSELLV?GSQLILGPHESKIPILLIQQPGKV
		ŧ.	
)		}	TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKBSAVH
		I	SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
1	t	1	YVKLGTLAPFCCPWEQLTQDWESRVQAYEZPSVASSPNGKESDL
			RRSBVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG
	1 .	[	PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
	}	}	RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPR
	1	1	
	1	i	PHTMICVPAKEDPLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
	1	1	KKREKROKP\GRASEDGPAGEBPVAGQBALTLGLW9GPLPRVTL
	1	ì	HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ
		1	RGLVLLRPPASLQYRFARIAIRV
5436	1781	635	ASDS1PWSKARTTRKLAORGCOWSLPRRMPLVVFCGLPYSGKSR
5,50	1 2,02	}	RAEELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG
		1	ALRASVERRUSEHDVVILDSLNYIKGFRYELY\CLARAARTPLC
ļ	1	J	
	1	1	LVYCVRPGGPIAGPQVAGANENPGRNVSV8WRPRABEDGRAQAA
	<b>J</b>	}	GSSVLRELHTADSVVNGSAQADVPKELEREBSGAARSPALVTPD
İ	1	1	SEKSAKHGSGAFYSPELLBALTLRFEAPDSRNRWDRPLFTLVGL
	1	1	ERPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS
	]	1	QVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAKLSRLRR
	1	[	OPISYTKMHPNNBNLPQLANMFLQYLSQSLH
		ļ	
5437	739	1672	CQEAASEPGGPLHTPAMPLRRLGGWLPRPWGRRKPMRPDPPYPB
		J	PRRVDSSSENSGSDWDSAPETMBDVGHPKTKDSGALRVSRAASE
		1	PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
		1	
	<b>\</b>		WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEKPGRREKLLGWLR
			GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
			Gepgapsrylggpeeclqistnltihlellasallalcsrplr aaldtiglrgpiglwihglisflaalhglhavlslltahplhfa
			GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
			Gepgapsrylggpeeclqistnltihlellasallalcsrplr aaldtiglrgpiglwihglisflaalhglhavlslltahplhfa
5418	2443	1152	GEPGAPSRYLGGPEECIQISTNLTIHILELLASALLALCSRPLR AALDTIGLRGPLGLNLHGLLSFLAALHGLHAVLSLLTAHPLHFA CLFGLLQALVLAVSLREPNGDEAATDWRSEGLEREGEEQRGDPG KGL
5438	2443	1152	GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR AALDTIGLRGPLGLMLHGLLSFLAALHGLHAVLSLLTAHPLHFA CLFGLLQALVLAVSLREPNGDEAATDWRSEGLEREGEGRGDPG KGL TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
5438	2443	1152	GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR AALDTIGLRGPIGLMLHGLISFLAALHGLHAVLSLLTAHPLHFA CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDPG KGL TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS LAPPSLRRPMMCQSEARQGPELRAAKWLHPPQLALRRRLGQLSC
5438	2443	1152	GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR AALDTIGLRGPLGLNLHGLLSFLAALHGLHAVLSLLTAHPLHFA CLFGLLQALVLAVSLREPNGDEAATDWRSEGLEREGEEQRGDFG KGL TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS LAPPSLRRPMMCQSEARQGPRLRAARNLHFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
5438	2443	1152	GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR AALDTLGLRGPLGLNLHGLLSFLAALHGLHAVLSLLTAHPLHFA CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDFG KGL TKPKKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS LAPPSLRKPMMCQSEARQGPELRAAKNLHFPQLALRRRLGQLSC WSRPSLKLRSWPLITVLYYLLPFGALRPLSRVGWRPVSRVALYKS VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKBAAVE
5438	2443	1152	GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR AALDTIGLRGPLGLNLHGLLSFLAALHGLHAVLSLLTAHPLHFA CLFGLLQALVLAVSLREPNGDEAATDWRSEGLEREGEEQRGDFG KGL TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS LAPPSLRRPMMCQSEARQGPRLRAARNLHFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
5438	2443	1152	GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR AALDTLGLRGPLGLNLHGLLSFLAALHGLHAVLSLLTAHPLHFA CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDFG KGL TKPKKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS LAPPSLRKPMMCQSEARQGPELRAAKNLHFPQLALRRRLGQLSC WSRPSLKLRSWPLITVLYYLLPFGALRPLSRVGWRPVSRVALYKS VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKBAAVE

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	to first	to first amino acid	L-Leucine, M-Methionine, N-Asparagine, P-Proline, Q-Glutamine, R-Arginine,
	amino acid	residue of	S=Proline, Q=Glucamine, R=Arginine,   S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	sequence	\=possible nucleotide insertion)
			REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHPPGSLMSVNP
1	}	1	GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
I			FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
			FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGRALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
			LAPPSLRRPMMCQSBARQGPELRAAKWLHFPQLALRRRLGQLSC
l .	i		MSRPALKLRSWPLTVLYYL::PFGALRPLERVGWRPVSRVALYKS
	l	}	vptrllsraugrlngvblphwlrrpvyslyiwtfgvnmkraave
1	ļ		DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
1	ĺ		NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT
ł	Į.		REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
	}	ļ	GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
			FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
5440	693	253	PNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL  BPIPVTPDHRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA
340	]	ددء	MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFNTLFMNTCCLG
1			PIAPAYSVKSRDRKMVGDVTGAQAYASTAKCINIWALILGIPMT
1			ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLBIKTQCSGPRMDPKICPADPAFFSFIN
			NSDLWVANIETGEERRLTPCHQGLSNVLDDPKSAGVATFVIQEE
1			FDRYTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVPSP
]			ALEKRKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE
<b>,</b>			LVQPPSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLL
1			PPALPIPSTENEEQ\RLASARAVPRNVQPYVVYBEVTNVWINVH
}			DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW
l '		,	SEPFSPGEGEQSLINAIWVNEETKLVYFQGTKDTPLEHHIJYVVS
7	1	. •	YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY KLSGPDDDPLHKQPRFWASMMEAAKIFHFHTRSDVRLYGMIYKP
1			HALQPGKKHPTVLFVYCGPQVQLVNNSFKGIKYLRLNTLASLGY
]			AVVVIDGRGSCORGLRFEGALKNOMGOVEIEDOVEGLOFVAEKY
1		•	GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVMM
1			AYDTGYTBRYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH
			GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER
			HSIRCPESCEHYEVTLLHFLQEYL
5442	1	3474	CGQRSRRRSPDMPBAKPAAKKAPKGKDAPKGAPKBAPPKBAPAB
	·		APKEAPPEDQSPTAEEPTGVPLKKPDSVSVBTGKDAVVVAKVNG
	1		KELPDKPTIKWFKGKWLELGSKSGARPSFKESHNSASNVYTVEL
			HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRODASGOSL
			ESFKRTSEKKSDTAGELDFSGLLKKREVVEERKKKKKEDDDDLG IPPEIWELLKGAKKSEYEKTAFQYGITDLRGMLKRLKKAKVEVK
			KSAAFTKKLUPAYOVDRGNKIKLMVZISDPDLTLKWPKNGOBIK
			PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTBLFV
			KEPPVLIVTPLEDQQVFVGDRVEMAVEVSBEGAQVMWMKDGVEL
			TREDSFKARYRFKKDGKRHILIFSDVVQEDRGRYQVITNGGQCE
			AELIVEEKQLEVLQDIADLTVKASEQAVPKCEVSDEKVTGKWYK
	ľ	•	NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDYTFVPDGYAL
			GSLSAKLNFLEIKVEYVPKQ\EPPKIPLGFASGGKTSENAD/IV
1			VVAGNKLRLDV\SITGEAPSPFAT\WLKG\DEVFTTTEGRTRIE
	ł		KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIFLQVVDVP
			DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQ
	[		RWMKLNPEVPTETTYRSTKMIEGILYEMRVFAVNAIGVSQPSMN
			TKPPMPIAPTS3PLHLIVEDVTDTTTTLKWRPPNRIGAGGIDGY
			LVEYCLEGSEEWVPANTEPVBRCGFTVKNLPTGARILFRVVGVN
			IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN
			LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA
			RSDSGBYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT
			NALVEWQAPKDDGNSEIMGYFVQKADKKIMEWFNVYERNRHTSC TVSDLIVGNBYYFRVYTENICGLSDSPGVSKNTARILKTGITFK
			PPEYKEHDFRMAPKFITPLIDRVVVAGYSAALNCAVRGHPKPKV
			VWMKNKMBIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV
			NRIGEALABCRLEVRVPO
			Provide and a series of the K

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1			S=Serine, T=Threonine, V=Valine,
1	amino acid	residue of	
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSSPRRSRSAAEPA
Į.			MALSMPLNGLKEEDKBPLIELFVKAGSDGESIGNCPFSQRLFMI
ļ			LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKTDV
1	1	1	NKIEEFLEEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS
ł	ł	ł	RPEANEALERGLLKTLQKLDRYLNSPLPDBIDENSMEDIKFSTR
			KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY
l			LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHQVKSRLLKEVS
ì		ł	FMSSP
5444	2	344	SGPIGVTGAOMAKWLRDYLSFGGRRPPPOPPTPDYTESDILRAY
	_		RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL
l	ľ	1	IKVEAADMARAKALIGGPGEELEADTEYLDPFDAQPHPAPPDDG
i	ł	l	YMBPYDAQWVMSELPGRGVQLYDTPYREQDPBTADGPPSGQKPR
ļ	]	}	QSRMPQEDERPADEYDQPWEWKKDHISRAFAVQFDSPEWERTPG
		İ	SAKELRRPPPRSPOPAERVDPALPLEKOPWFHGPLNRADAESLL
			SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVV
j	l .	J	LGOHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTQTP*Q
1		1	*PDWGDRRPNGOVATGLPBLWGARAPSAAAHPGLHRBRHPEGLP
i I	ĺ		RAEKPGLRGPLLGLREPLGAGPRGPWGLOEPRRCOVWFSOAFAH
l i			QCGGCGYGQSQGPSGRPRGGAGSRH
5445	2364	486	ILSRGFLGSVEICIOLPLPASEPVLLLTWARRRWRETRSRREPT
2442	2304	400	TLRAQSVCPWWI*BTRMNRSIPVEVDESEPYPSQLLKPIPEYSP
ì			ERESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
Į į			ORPVSROVTCLRTOVLEDSEDSFCRRHPGLGKAFPSGCSAVSBP
			ASESVVGALPARHOPSPMEKRNOWLVSQLSAASPDTGHDSDKSD
[	[		
)			QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ
			DVLGIRQLERPLPLTSVCYPQDLPRPLRSREFPQFEPQRYPACA
1			QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP
1	ł		ALPGQPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSPPG
			LPRHQDQPHHQPPNRAGAPGESLECPABLRPQVPQPPSPAAVPR
			PPSNPPARGTLKTSNLPEKLRKVFITYSMDTAMEVVKFVNFLLV
{	•	·	NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKQ
l ·	}	•	DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRPIPVLF
	ļ		PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEXVAPPRGP
			LPTLQVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQ
	Ì		TLDVKCDYTLEKFASSQKANQIIRDGEMPKTLACTERPSKNSHP
		}	VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH
'			MLFDRIRLVVTKGPSGTPGSNENSTQNVYKIPPTTTKALCPLYT
(			TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA
1			GGFLSKSLVFSVLFAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA
			KGGGRR
5447	207	617	MTARTLSIMASLVAYDDSDSEAETEHAGSFNATGQQKDTSGVAR
			PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR
			GSCPSQRLQWPGKRPQVTFPIKEPSCSSLWTSHVPASHMPLAAA
			RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFQKKRCEDCVVPY
			TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF
			IQPYLNSHYKETTVPRKVLPHLRGHRGPVNTIQWCPVLSKSHML
			LSTSMDKTFKVWNAVDSGHCLQTYSLHTBAVRAARWAPCGRRIL
1		4	SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG
}	l		GFSSBMKANDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD
			ASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALHPREPV
			FLAQTNGNYLALFSTVNDYRMSRRRRYEGHKVEGYSVGCECSPG
			GDLLVTGSADGRVLMYSFRTASRACTLQGHTQACVGTTYHPVLP
			SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL
1,1			KSPSPSKSLLVLLCGRAMFOPATCPWQLPALSK
5448	194	1833	MASKVIDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
		2000	HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
			RWNLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
			GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV
			HREGDGSSTTDNTQEGAVONHGTSTSHSVGTVFRDLWHAAFFLS
			GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGKDGIQNHEPQCET
L			CONTINUED TO TO TAKE I ASTRONOM LANGUAGE MURE ACCEL

		· · · · · · · · · · · · · · · · · · ·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
!	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
ł .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			IRPEETAWNIGTLRNGPSKDTQRTITNVSDBVSSBEGPETGYSL
			RRHVDRTSEGVLRNRKSHHYKKHYPNEJAPKSGTSCSSRCSSR
		Ì	QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
(	ĺ	•	VKREYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
ì		}	VLBISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
1			TDLBQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
	ĺ	1	FFFLLCVARRTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK
			SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
			SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
ì			VWEGNDCKKADMSVLBISGMIMNRVNSHIPGIGYQIFGNAVSLI
Į.	}		LGLTPPVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
			IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5449	194	1833	MASKYTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
	[		HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
·	(		RNWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
[	<b>!</b>		GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV
1			HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLMHAAFFLS
1			GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCST
i			IRPEBTAWNTGTLRNGPSKDTQRTITNVSDBVSSBEGPBTGYSL
			RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
			QDSBSARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
			VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
	ł		VLRISGMIMNRVMSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
			TDLEQLTAHEASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
			FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDA>K
(			SGTSCSSRCSSSRQDSESARPESETEDVLWEDLIHCAECHSSCT
			SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
			VWBGNDCKKADMSVLBISGMIMNRVNSHIPGIGYQIFGNAVSLI
1			LGLTPFVFRLSQATDLEQLTAHSASBLYVIAFGSNEDVIVLSMV
			IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5450	8136	1242	GQQFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPBALLLLAAG
ĺ			PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTVV
<b>i</b>			LTVVRGWATLSVDGFLNASSAVPGAPLBVPYGLFVGGTGTLGLP
			YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD
			VALGESGPHSLAAFPANGTQDBGTLEFTLTTQSRQAPLAFQAGG
			RRGDFIXVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVSV
		,	HINAHRLRISVDQYPTHTSNRGVLSYLBPRGSLLLGGLDARASR
		•	HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMA AGCRLEEBEYEDDAYGHYEAPSTLAPEAWPAMELPEPCVPEPGL
			PPVFANFTQLLTISPLVVARGGTAWLRWRHVQPTLDLMEARLRX
			SQVLPSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD
			GSEDTSDOLVLEVSVTARVPMPSCLRRGOTYLLPIOVNPVNDPP
			HIIPPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTPQVLGT
			SSGLPVERRDOPGEPATEFSCRELEAGSLVYVHCGGPAODLTFR
			VSDGLOASPPATLKVVAIRPAIOIHRSTGLRLAOGSAMPILPAN
ľ			LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWATQ
			AFHORDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSNL SPPVTIORATVWMLRLEPLHTONTOOETLTTAHLEATLEEAGPS
	!		1
			PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDD1QAGRVTYGA TARASKAVEDTFRFRVTAPPYFSPLYTFP1H1GGDPDAPVLTNV
		•	
			LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG
			TODKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQGE
			SSGDMANEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL
			TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF
			TOEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP
			YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT
			YLRVANGSSLVVPQGGGTIDTAVLHLDTNLDIRSGDBVHYHVT AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF
			YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDBVHYHVT AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDIMAF SVBAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI
			YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDBVHYHVT AGPRWGQLVRAGQPATAPSQQDLLDGAVLYSHNGSLSPEDTMAF SVBAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS
-			YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDBVHYHVT AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF SVBAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQBAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE
			YLRVANGSSLVVPQGGQGTIDTAVIHLDINLDIRSGDEVHYHVT AGPRWGQLVRAGQPATAPSQQDLLDGAVLYSHNGSLSPEDIMAF SVBAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS

SEQ	1 5 47 3		
ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
10:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	1	corresponding	H=Ristidine, I-Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P-Proline, Q=Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV
1	İ	1	HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDOPPILT
	1	<u> </u>	TNTGLOMWEGATAPIPAEALRSTDGDSGSEDLVYTIEOPSNGRV
1			VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
l	i	ł	TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS
		ļ	SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA
i	i	} ·	CNILYEHEMPPEPFNEAHDTLELOLSSPPARDVAATLAVAVSPE
J	J		
1	ì		AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSPQ
ł	i	İ	RSEHDVLFQVTQFPSRGQLLVSEBPLHAGQPHFLQSQLAAGQLV
İ	}		YAHGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN
ł .	į.		BRPPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGRIEYEVQ
į.	J.	1	RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF
1	1		QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL
i	1	}	SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSQFQI
			DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV
1	1		WAGGPWPQGATLRLDPTVLDAGRLANRTGSVPRFRLLEGPRHGR
1	1		VVRVPRARTEPGGSQLVEQFTQQDLRDGRLGLEVGRPBGRAPGP
1	100		AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA
ł			ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV
			IIPMCLVLLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA
	•		GDTKTFRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP
			ALKNGQYWV
5451	1	2274	RDSSEQGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR
	l		KNSEPGSPHSLEALRDAAPSQGLNFLLLPTKMLFIFNFLFSPLP
1			TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK
			GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ
	1		PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW
E	<b>j</b>		IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPO
	ł		KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIRILSL
ļ			
			YDARNIGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN
	ļ		IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
i			CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE
i			AKTPLKKFILKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL
j		•	GGRVRVIVTGAAPMSTSVMTPFRAAMGCQVYEAYGQTECTGGCT
l	ĺ		FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG
1			INVPKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK
	,		KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV
	[		VVPDTDVLPSFAAKLGVKGSFEELCQNQVVRRAILEDLQKIGKE
			sclktfeqvkalflhpepfsienglltptlkakrgelskyfrtq
L			IDSTAKHIOD
5452	1833	1138	SRVPSLCLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR
]			LGSLLSLSCLALSVLLLAQLSDAAKNPEDVRCKCICPPYKENSG
1	ĺ		HIYNKNISQKDCDCLHVVBPMPVRGPDVRAYCLRCECKYRERSS
]	,		VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAOLIOS
			DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
			RKSVFDRHVVLS
5453	111	1520	I. The state of th
55		1320	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
			AGPAPSTVPSSTSKDRPVSQPSLVGSKBBPPPARSGSGGGSAKE
<b>i</b>	l		PQEERSQQQDDIEELETRAVGMSNDCRFLKFDIEIGRGSFKTVY
			KGLDTETTVEVANCELQDRKLTKSERQRFKEEAEMLKGLQHPNI
			VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKYMKIKVL
(			RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
			LGLATLKRASFAKSVIGTPBFMAPEMYEEKYDESVDVYAFGMCM
			LEMATSEYPYSECONAAQIYRRVTSGVKPASFDKVAIPEVKEII
	ŀ		EGCIRONKDERYSIKDLINHAFFQESTGVRVELABEDDGEKIAI
			KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPRDVAQEMVRSG
	· ·		YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5454	111	1520	PSIPAAVPQSAPPBPHRBETVTATATSQVAQQPPAAAAPGEQAV
	<b>_</b>	2520	
	1		AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
1	l		PORERSQQQDDIERLETKAVGMSNDGRFLKFDIEIGRGSFKTVY
L	<u> </u>		KGLDTETTVEVAWCELQDRKLTKSERQRFKREAEMLKGLQHPNI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	LaLeucine, Mamethionine, NaAsparagine,
1	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			VRFYDSWESTVKGKKCIVLVTBLMTSGTLKTYLKRFKVMKIKVL
í	Ĭ	l	RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
ì	1		LGLATLKRASFAKSVIGTPEFMAPEMYREKYDESVDVYAFGMCM
1	{	<b>[</b>	LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKBII
1	ļ	1	EGCIRONKDERYSIKDILINHAPFQEETGVRVELAERDDGEKTAI
1	}	ì	KLWLRIEDIKKLKGKYKDNEAIEFSFDLRRNYPEDVAQEMVESG
ł	ł	ľ	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLPGCLGVFGLFRIAO
1	1		WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
j	j		GALEELIRELTASHATKVQTHKPYLVTFDLTDSGATVAAAARIL
1		ł	-QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT
1	]	ł	KALLPSMIKRROGHIVAISSIQGKMSIPPRSAYAASKHATOAFF
i	]		DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT
ì	Ì		TAQGRSPVRVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG
	i		LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
}			TEVDMDPQRSPLLEVKGNIELKRPLIXAPSQLPLSGSRLKRRPD
1			QNEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
I.			QKVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG
ľ			KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR
1			DAQQQVKALGTERTTLEGHLAKVQAQABQGQQELKNLRACVLEL
)			EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLQTSEA
			ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL
}			QELKGNIRVFCRVRPVLPGBPTPPPGLLLFPSGPGGPSDPPTRL
l '	- 4		SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFEEIA
			MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPR
			ALRHLFSVAQELSGQGWTYSFVASYVEIYNBTVRDLLATGTRKG
			QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARQNR
1 :			AVARTAQNERSSR6HSVFQLQISGEHSSRGLQCGAPLSLVDLAG SERLDPGLALGPGERERLRETQAINSSLSTIGLVIMALSNKESH
			VPYRNSKLTYLLQNSLCGSAKMLMPVNISPLBENVSESLNSLRP
1			ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVCV
1			MSMYRVRGGRVAGGCFIGWRAPCPRAIK
5457	2	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA
			LLRSABRIMRKVKKLRIDKENTGSWRSFSINSEGAERMATTGTP
1 1			TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK
1			APHDFQFVQKTDESGPHSHRLYYLGNPYGSRENSLLYSEIPKKV
i i			RKBALLLLSWKOMLDHFQATPHHGVYSRBRBLLRERKRLGVPGI
i l			TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
l i			PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIRTGEER
1 1			RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW
1 1			EGSEGLKTLRILYEKVDESEVEVIHVPSPALEERKTDSYRYPRT
!!			GSKNPKIALKLARFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI
			ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA
l			ASLCQSCPQECPAVCGVRGGHQRLDQCS
5458	6642	4022	FVPGLREPQWEPAQPSATMSAPSEEEBYARLVMKAQPEWLRAEV
!!	ſ		KRLSHELAETTREKIQAAEYGLAVLEBKHQLKLQFEELEVDYEA
] ]			IRSEMEQLKEAFGQAHTNHKKVAADGBSREESLIQESASKEQYY
۱ I	1		vrkvlelqtelkqlrnvltntqsenerlasvaqblkeinqnvei
!!	ì		QRCRLRDDIKEYKFREARLLQDYSELERENISLQKQVSVLRQNQ
ļ [		ļ	VEFECLKHEIKRLBEETEYLNSQLEDAIRLKEISERQLEEALET
1 1	1	İ	LKTEREQKN9LRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
ļ l	ļ		EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
	*	İ	DLLSBLNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
		ļ	SLSEQQEKVTRLTENLSALRRLQASKERQTALDNERDRDSHEDG
1		1	DYYEVDINGPEILACKYHVAVARAGELREQLKALRSTHEAREAQ
	ł		HABEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS
]	1	1	DVAGETQGSLSVAQDELVTPSEELANLYHHVCMCNNETPNRVML
	<b>!</b>		DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA
	J		DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLIAIRDQIKHLQ
L			AAVDRITRLSRORIASQELGPAVDKDKEALMERILKLKSLLSTK

SEQ	Predicted	Predicted end	Design and design and the second seco
ID	beginning	ž –	Amino acid segment containing signal peptide
NO:	_ ~ ~	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first .	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V≈Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
<del></del>			REQITTLRTVLKANKOTAEVALANLKSKYENEKAMVTETMMKLR
1	}		NELKALKEDAATFSSLRAMFATRCDEYITQLDEMOROLAAARDE
1	ł		
l		<u> </u>	KKTLNSLLRMAIQQKLALTQRLBLLELDHBQTRRGRAKAAPKTK
	L		PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGNASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
		i	KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
1		ļ	GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGRP
İ	<b>S</b>	İ	DLLATGVEREQSERFNVYLMPSPNLGCYMGECALOITYEYICLW
J	1	1	DVQNPRVKLISWPLSALRRYGRDTTWFTFBAGRMCETGEGLF1P
1	i		QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA
1			SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
			PAYRSEH
5460	45	2097	
7400	1 73	1 2031	RPGCRAGELSTGSRARBRVRNRVSAPCGQDSRRCDPEVLRGRSP
		]	GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL
1		1	GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
1	1		ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
1	į	1	CEKCHHPFVVLSEADSKKSIIKEPESAABAVKLAFQQKPPPPPK
ł	i	}	KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAB
		ļ	VBKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ
ł	1.	ł	QQVNQQIPQKKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
ļ	1	(	AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
1	Ì	1	VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
1			TIVNVPEKNSRKLRGBTVQVDTTNILFVASGAFNGLDRIISRRK
1	i		NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHODIEEKDRL
1	9	ļ	LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR
1	1		NAVI POYOALFSMDKCELNVTEDALKALARLALERKTGARGLRS
}	ľ		IMBKLLLEPMPEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
1			SEEEYDSGVEREGWPROADAANS
5461	1481	160	
3401	1401	700	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD
1			SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD
			SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
) '			NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC
			ASTRLPPTPLLLFPEERATNGREGLLRFSSWPFSIQDVVQPLTL
l l			QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
1 1	·		EANBEFALRVQQLVAKBLGQTGTRLTPADKAEHMKRQRHPRLRP
1	<b>i</b> .	!	QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK
			TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV
1			TPOPTALTFAKSSNARQESLQERKQALYBYARRRFTERRAQEAD
5462	663	3353	KIKEROMSANNSPPSAOKSVLPTAIPAVLPAASPCSSPKTGLSA
_			RLSNGSPSAPSLTNSRGSVHTVSFLLQIGLTRRSVTIRAOELSL
			SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILQLIT
i l	[		SADEIHEGDLVEVVLSALATVEDFOIRPHTLYVÄSYKAPTFCDY
	]		
[ ]			CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
		İ	VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI
1 1			WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLPRQGMQC
j l			KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
] 1			NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDERAVKTI
] .	I I		SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGMMVHYTSRDNLRK
	1	-	Protomati mare a fortal indication and its and
1 1		9	RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS
		~	RHYWRLDSKCLTLFONESGSKYYKEIPLSEILRISSPROFTNIS
		Ÿ	RHYWRLDSKCLTLFQNBSGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
		*	RHYWRLDSKCLTLFQNBSGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE
		Ť	RHYWRLDSKCLTLFQNBSGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
		Ť	RHYWRLDSKCLTLFQNBSGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM RFPTKQBSQLRNBVAILQNLHHPGIVNLBCMFETPERVFVVMEK
		*	RHYWRLDSKCLTLFQNBSGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM RFPTKQESQLRNBVAILQNLHHPGIVNLBCMFETPERVFVVMEK LHGDMLEMILSSBKSRLPBRITKFMVTQILVALRNLHFKNIVHC
		Ť	RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK LHGDMLEMILSSEKSRLPRRITKFMVTQIIVALRNLHFKNIVHC DLKFENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY
		Ť	RHYWRLDSKCLTLFQNBSGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM RFPTKQESQLRNBVAILQNLHHPGIVNLBCMFETPERVFVVMEK LHGDMLEMILSSBKSRLPBRITKFMVTQILVALRNLHFKNIVHC
		T. C. C. C. C. C. C. C. C. C. C. C. C. C.	RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM RFPTKQESQLRNEVAILQNIHHPGIVNLECMFETPERVFVVMEK LHGDMLEMILSSEKSRLPERITKFMVTQIIVALRNLHFKNIVHC DLKFENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY
		T. C. C. C. C. C. C. C. C. C. C. C. C. C.	RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGGGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK LHGMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRESVVGTPAY LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI
		T. C. C. C. C. C. C. C. C. C. C. C. C. C.	RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM RFPTKQESQLRNEVAILQNLHHPGIVNLBCMFETPERVFVVWEK LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC DLKPENVLLASABPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI QNAAFMYPPNFWRBISGBAIDLINNLLQVKMRKRYSVDKSLSHP
5463	237	1012	RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMYYFYGENNGDSSHNPVLAATGYGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM RFPTKQESQLRUBVAILQNLHHEGIVNLECMFETPERVFVVMEK LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC DLKPENVLLASABPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY LAPEVLRSKGYNRSLDMMSVGVIIYVSLSGTFPFNEDEDINDQI QNAAFMYPPNPRBISGEAIDLINNLLQVKMRKRYSVDKSLSHP WLQDYQTWILDLREFETRIGERYITHESDDARWEIHAYTHNLVYP KHPIMAPNPDDMEEDP
5463	237	1012	RHYWRLDSKCLTLFQNBSGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFBIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQPGIVYGGKHKKTGRDVAIKVIDKM RFPTKQBSQLRNBVAILQNLHHPGIVNLECMFETPERVFVVMEK LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC DLKPENVLLASABPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY LAPBVLRSKGYNRSLDMMSVGVIIYVSLSGTFPFMEDEDINDQI QNAAFMYPPNPWRBISGEAIDLINNLLQVKMRKRYSVDKSLSHP WLQDYQTWLDLREFETRIGKRYITHESDDARWBIHAYTHNLVYF

ID beginning nucleotide (A=Alanine, C=Cystei	containing signal peptide
NO:   nucleotide   location   Glutamic Acid, F=Phe	enylalanine, G=Glycine,
location corresponding H=Histidine, I=Isole	
corresponding to first L=Leucine, M=Methion	•
to first amino acid P=Proline, Q=Glutami	
)	
	•
	sine, X=Unknown, *=Stop
amino acid sequence Codon, /=possible nu	
sequence \=possible nucleotid	
	WLSSSNTSYCELCHFRFAVERKPR
PLVEWLRNPGPQHEKRTLFG	DMVCFLFITPLATISGWLCLRGAV
DHLHFSSRLEAVGLIALTVA	LFTIYLFWTLVSFRYHCRLYNEWR
RTNQRVILLIPKSVNVPSNQ	PSLLGLHSVKRNSKETVV
5464 195 677 SPSMNPRKKVDLKLIIVGAI	GVGKTSLLHQYVHKTFYEEYOTTL
GASILSKIIILGDTTLKLOI	WDTGGOBRVRSMVSTFYKGSDGCI
_	VLAKIVPMEOSYPMVLLGNKTDLA
DRKYQSILENHLTESIKLSP	
	SAHLHEWIDLIFGYKOOGPAAVBA
1 1	PLKETATIGFINNFGQIPKQLFKK
<u> </u>	
	LPGSTSDKIFFHHLDNLRPSLTPV
	EQNKVLIPPTWNKTFAWGYADLSC
	GQILCAICPNPKLVITGGTSTVVC
	LGHTDTVTCATASLAYHIIVSGSR
	HRAPVSALCINELTGDIVSCAGTY
	SQQIICCCMSEMNEWDTQNVIVTG
,	APEPARVLEMQEDCPEAQIGQEAQ
,	TPEQPESTSHRPRAASCRATAANC
	DGFIFVNYSEGQTRAHLQGPLSHP
	RQLVFRSKLTMHTAFDRKDNAHFA
EVTALGISKDHSRILVGDSR	GRVFSWSVSDQPGRSAADHWVKDR
GGDSCSGCSVRFSLTERRHH	CRNCGQLFCQKCSRFQSEIKRLKI
SSPVRVCQNCYYNLQHERGS	EDGPRNC
5466 3 992 HACAHASAHASGRLVRWWRK	RRSVMGIQTSPVLLASLGVGLVTL
LGLAVGSYLVRRSRRPQVTL	LDPNBKYLLRLLDKTTVSHNTKRF
RFALPTAHHTLGLPVGKHIY	LSTRIDGSLVIRPYTPVTSDBDQG
YVDLVIKVYLKGVHPKFPEG	GKMSQYLDSLKVGDVVBFRGPSGL
LTYTGKGHFNIQPNKKSPPE	PRVAKKLGMIAGGTGITPMLQLIR
AILKVPEDPTQCFLLFANQT	EKDITLREDLEELQARYPNRFKLW
FTLDHPPKDWAYSKGFVTAD	MIREHLPAPGDDVLVLLCGPPPMV
QLACHPNLDKLGYSQKMRPT	,
<u></u>	RIFIQKKOLEEDESVTAAHLKSRG
,	TFRDVAIDFSQBEWECLOPDORTL
1	SKPDVITLLEQRKEPWMVVRKETS
	TSEVNLPKQVIKQISTTLGIEAFY
[ ] · · · · · · · · · · · · · · · · · ·	INOKMISYEKLPTHTPHASLICHT
,	QHQSIHTGEKPYKCKECGKAFQLH
	CGKAFNLPTQLNRHKN1HTVKKLP
	IHAGVKPYOCKECGKAFNRGSNLI
, , ,	FRYHYOLIEHCOIHTGEKPFECKE
	BKPFECRECGKAFSLENQLNRHKN
, , , , , , , , , , , , , , , , , , , ,	
	SNLVQHQSIHAGIKPYECKECGKG
	VCRECEMAFRYHCQLIEHSRIHTG
	OHQSIHTGKKPYBCKECGKAFRLY
	CGKFFRRGSNLNQHRS IHTGKKPF
	LHTGEKPFECKECGKAFRLHMQLI
RHQKLHTGBKPFBCKBCGKV	
1 1 - 1	YETTOTTTRLOAKKALVBFTNSPD
CLSKCQLLLERGSSSYSQLLI	AATCLTKLVSRTNNPLPLEQRIDI
RNYVINYLATRPKLATFVTQI	ALIQLYARITKLGWFDCQKDDYVF
RNAITDVTRFLQDSVEYCIIG	GVTILSQLTNBINQVSATAFLIBA
DTTHPLTKHRKIASSFRDSSI	LFDIFTLSCNLLKQASGKNLNLND
	DFIGTSTDESSDDLCTVQIPTSWR
	KTCALLVOLFDOSAOSYOELLOSA
	IGAVIGGRVSFASTDEQDAMDGEL
	eklelamlsppeqprkiyigdqvq
	VLSVFIGKIITNLKYWGRCRPITS
	KLSAVQFMLNNHTSEHFSFLGINN
	CARLLES CARLES OF A LANGE OF THE CARLES OF T
QSNLTDMRCRTTFYTALGRII	
AVAÇMESTNSENEQEAKRILV	VGLVRDLRGIAFAFNAKTSPMMLF DPACTTPVLKIMAELVHNRSQRLQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glucamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<del>                                     </del>	<del></del>	FDVSSPNGILLFRETSKMITMYGNRILTLGEVPKDQVYALKLKG
1		1	ISICPSMLKAALSGSYVNPGVPRLYGDDALDNALQTPIKLLLSI
1	ł	İ	PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS
1	j	j	ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSR6TKKRTTPLNQ
1		l .	ESDRFLHIMQQHPEMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG
1	ì		LILLNEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNIL
l			TKNRDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DOEFETSLVPWHLPMGWLCSGLLFPVSCLVLLQVASSGNMKVLO
	1	2055	EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYOLVFLLSEAHTC
1		1	VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGOOLLWKGSPKPS
1	}	1	EHVXPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN
i			IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ
ł	ł	ł	CYNTTWSEWSPSTKWHNSYREPFEOHLLLGVSVSCIVILAVCLL
			CYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSOWBKRSRCO
<b>!</b>			EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFOGSGK
ſ	ĺ		SAWCPVBISKTVLWPBSISVVRCVELPEAPVECERERVREEKG
}			SFCASPESSRDDFQBGREGIVARLTESLFLDLLGBENGGFCQQD
i			MGESCLLPPSGSTSAHMPWDEFPSAGPKRAPPWGKEOPLHLEPS
			PPASPTQSPDNLTCTBTPLVLAGNPAYRSPSNSLSOSPCPRBLG
ļ	}		PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNV
]			LQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG
			YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPA
			PVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP
1 .			KPPLPQEQATDPLVDSLCSGIVYSALTCHLCGHLKQCHGQEDGG
			QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLRASLCPA
			SLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNPVSVGPTYM
			RVS
5470	17	1418	TACRIRTSLNRGIAAVKKDAVEMLASYGLAYSLMKFFTGPMSDF
			KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI
			INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
1			SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA
	,		LVRCTTLCLGYYKNIHDIIPDRSGPBLGGDATIRKMLSFWWPLA
1			LILATORISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP
! !			YGNLTBIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA
1			LSLTLCFVMFWTPNVSEKILIDIIGVDFAPAELCVVPLRIFSFF
1			PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL
l i			GVHGATLGVGSLLAGFVGBSTMDALAACYVYRKQKKKMBNBSAT
			EGEDSAMTOMPPTEEVTDIVEMREENE
5471	1868	658	RSSAPPGPQRAAAATAAAAAGVEMAAAAAQGGGGGBPRRTEGV
			GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR
]			KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR
			ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR
			GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
	İ		htgflteyvatrwyrapeimlnskgytksidiwsvgcilaemls
			NRPIPPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL
			PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
1			YLEQYYDPTDEPVAREPFTPAMELDDLPKERLKELIFQETARFQ
l			PGVLRAP
5472	1469	753	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR
			DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR
	1		GSDKMPGRVVTLLEDHBGCTWGVAYQVQGEQVSKALKYLNVREA
			VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPERA
			IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA
	1		VGTMLPCPCPTEQALALV
5473	3	2119	FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPOERG
	ļ		KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLRELEKOMTS
	1		PYDSLGKINEIITVLEREAQSSALPKOKHQELLACQENCKKTLT
	1		LIEKGSQSVQKFVTLSNVLKHFDQTRLQRQIADIHVAFQSMVKK
			TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLEERGDPEE
į	i	Ì	LLRRHTEPFSQLDQRVLNAFLKACDELTDILPEQEQQGLQEAVR
: I	į		KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTBLDRET
	•		

SEO	Predicted	Predicted end	Dening and dening the second
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
<del></del>	Doguesto	<del> </del>	KLMPQEGSEKIIKKHRVFFSOKGPHHLCEKRLQLIBBLCVKLPV
			RDPVRDTPGTCHVTLKELRAAIDSTYRKLMEDPDKWKDYTSRFS
í	<u>.</u>		EFSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVTKRG
ł		ì	ETISMLKSRLKVLTEVSSENEAQKQGDBLAKLSSSFKALVTILS
l	1	ļ.	EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQARKILDTE
1		1	NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPDRG
1			HBBLRKLESTLDGLERSRERQERRIQVTLRKWERFETNKETVVR
	}	1	YLPQTGSSHERFLSPSSLESLSSELEQTKEFSKRTESIAVOAEN
1	1		LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEBEYVIDK
1		i	S S S S S S S S S S S S S S S S S S S
5474	1 2	780	TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLROSTI
	-		LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINIRTG
1	ļ		QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAWKFT
1			LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGRTLS
1			LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYGOO
	}	!	PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF
5475	2	506	ARGWLESLSLTCOTTPPPSSPCLLHSPBTFIHTMPPNLTGYYRF
1		**-	VSQKNMEDYLQALNISLAVRKIALLLKPDKEIBHQGNHMTVRTL
i			STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQK
			GEVPNRGWRHWLEGEMLYLKI.TARDAVCBOVFRKVR
5476	192	1457	SDSMSLLDCFCTSRTQVBSLRPBKQSBTSIHQYLVDEFTLSWSR
			PSTRASEVLCSTNVSHYELQVEIGRGPDNLTSVHLARHTPTGTL
1 1			VTIKITNLENCHEERLKALQKAVILSHFFRHPNITTYWTVFTVG
1 :			SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGLN
1		i	YLHQNGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQRHR
] !			AVYDFPQFSTSVQPWLSPELLRQDLHGYNVKSDIYSVGITACEL
1 '			ASGOVPFODMHRTOMLLQKLKGPPYSPLDISIFPQSESRMKNSQ
1			SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC
			LOODPEKRPSASSLLSHVPFKOMKEBSODSILSLLPPAYNKPSI
			SLPPVLPWTRPBCDFPDEKDSYWRF
5477	3	1044	RGNSRLRYSHEDELQLPRLPELFETGRQLLDEVEVATEPAGSRI
			VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEE1ASTDLKYLLV
			PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEF3
			LPKIMNNSAKNHTANSSMAYPSLVAMASQRQAKIQRYKQKKBLE
1 1			HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIBSIDQ
<b>l</b> 1			BIKILRERDSSREASTSNSSRQERPPVKPPILTRNMAQAKVFGA
, ,	j		GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE
			EQERKEEDDEQTLHRARENDDWKDTHPRGYGNRQNMG
5478	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
j	}		VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
		ı	LWDKSSRECVHSYCKHGGFVTYVDPHPSGTCIAAAGMDNTVKVW
			DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
			MEGRILLYTLHGHQGPATTVAFSRTGEYPASGGSDEQVMVWKSNP
1 1			DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLERDKLKQC
5479	2	035	LENQQLIMQRATP
] "" ]	4	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
[			VKVNATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
; !	İ		LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW
1	j		DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
[			MEGRILLYTLHGHQGPATTVAPSRTGBYFASGGSDEQVMVWKSNF
	1		DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
5480	144	1052	LENQQLIMQRATP
3200	444	1952	LSLTSRMEBABLVKGRLQAITDKRKYQEBISQKRLKIEBDKLKH
			QHLKKKALREKWLLDGISSGKBQBEMKKQNQQDQHQIQVLEQSI
	I		LRLEKEIQDLEKAELQISTKEKAILKKLKSIERTTEDIIRSVKV
			EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR
	ł		KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ
	ĺ		KSVYAVSSNHSAAYNGTDGLAPVEVERLLRQASERNSKSPTEYH
	!	ł	EPVYANPFYRPTTPQRETVTPGPNFQERIRIKTNGLGIGVNESI
L			HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
[	to first	amino acid	n-beddine, wemethionine, weapparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
ſ		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			LMTPWRESNVMQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCQE
1	<b>{</b>	ł	DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDRKFLT
1	1	1	GYDGIIHAELVVIDDEEEEDEGEABKPSYHPIAPHSQVYQPAKP
1	f	· ·	TPLPRKRSEASPHEKHKS
5481	3	1422	
	ı	1 ****	NSPGSVCLCQCVCPSLLHCLPPLLLLLLPLLLHRSPQPPALRV
1			VATSSDRNFMNKHQKPVLTGQRFKTRKRDBKEKFEPTVFRDTLV
1			QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA
i	į į		PGGTRIDDGDKTKNTNHCVFSANEDHETIRNYAQVFNKLIRRYK
1	ļ	j	YLEKAFEDEMKKLLLPLKAFSETEQTKLAMLSGILLGNGTLPAT
ŀ	!		ILTSLFTDSLVKEGIAASPAVKLFKAWMAEKDANSVTSSLRKAN
1			LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR
1			KELQKBLQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT
1	ĺ		CIMNAVEWNKKERLVAEQALKHLKQYAPLLAVFSSQGQSRLILL
1			QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSBEAILKWYKEAHV
			AKGKSVFLDQMKRFVEWLQNAREESRSEGEEN
5482	1492	528	
		JA0	THVVMTCMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL
1 1			EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS
1			CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPA
1			LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLKVSTGP
			GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALBEPANDIKEDA
1 1			IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP
1 1	i		TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP
			VNVPAQSQAGSLV
5483	1	788	PPPPKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA
1 1	ì	•	ENRIKOLETOSSEEISRYQEMIQKLQNVLESERENCGLVSEORL
1 1		,	KLQQENKQLRK3TESLRKIALEAQKKAKVKISTMEHEFSIKERG
1 1			FEVOLREMEDSNRNSIVELRHLLATOOKAANRWKEETKKLTESA
	'	*	RIRINNLKSELSROKLHTOELLSQLEMANEKVARNEKLILEHOR
1 1			KANRLORRLSOAEERAASASOOLSVITVORRKAASLMNLENI
5484	3	1997	IMADMEDLYGSDADSKAERKDSDSGSDSDSDQENAASGSNASGS
	, = .	~~~	ESDQDERGDSGQPSNKELFGDDSKDEGASHHSGSDNHSERSDNR
1 (			
1 1		•	SRASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE
1 1			AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAQGSDEDK
1 1	i		LQNSDDDEKMONTDDEERPQLSDDERQQLSEEEKANSDDERPVA
1 1			SUNDURKONSODREOPOLSDERKMONSODERPOASDREHRHSDD
( I	1		EEEQDHKSESARGSDSEDEVLRMKRKHAIASDSEADSDTEVPKD
	1		NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQERE
[. [	ľ		PIPETRIEVRIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYR
, ,	ł		DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESWAR
j	•		IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA
1 !	1		VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTOKIRILPMAGRD
į l	1	į	PECORTEMIKKEBERLRASIRRRSQORRMRBKOHORGLSASYLE
j (	i	ĺ	PDRYDREEEGKESISLAAIKNRYKGGIREERARIYSSDSDEGSE
}	1		EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEELTDQ
j <b>!</b>	1		AGTN
5485	161	1074	
	***	20/2	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG
į į	1		CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY
j J	j		RGILPPLMQKTTTLALMPGLYEDLSCLLHKHVSAPEFATSGVAA
j	1		VI.AGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI
, 1	i		GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN
[ ]	:		DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGBPQSFPKVFQKI
1			wlerdrklinlfrgahlnyhrsliswgiinatybfllkvi
5486	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR
	[	Í	PAAGKEAOKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
1	)		GSLATS I SQMVKTEGKGAKRKTSEERKNGSEKLVEKKVCKASSV
1			
	ł		IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRVSY
j	j	ļ	FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL
[	[		LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG
j J			DSRAILCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGGNVR
			DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL

	T 8 1	,	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	corresponding to first	to first	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *⇒Stop
ì	amiro acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	sequence	\=possible nucleotide insertion)
<b> </b>	sequence	ļ <del>-</del> -	ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC
	<u> </u>	ţ	NRLANKAVQRGSADNVTVMVVRIGH
5487	535	182	AVSLEOIRGLOTPAPVPLPLOPCPSNCDMERVTLALLLLAGLTA
3407	333	1 202	LEANDPFANKDDPPYYDWKNLOLSGLICGGLLAIAGIAAVLSGK
1			CKCKSSQKQHSPVPEKAIPLITPGSATTC
5488	1072	259	AMAASGEPOROWOEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH
3100	1072	1 -33	GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDYIEN
1		1	LKONDISTRFTYOTKDAATGTASIIVNNEGONIIVIVAGANLLL
j		]	NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL
ŀ	ļ		FNPAPAIADLDPQPYTLSDVFCCNESBAEILTGLTVGSAADAGE
1		f	AALVILKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVKAVD
Į.		Į.	TTVSFKI
5489	81	893	GKGPVAAFIDQSNIFLTDFKIFLGQWREEPKMPLLLLGETEPLK
	1		LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
1	}	<b>[</b>	LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
l .		1	LAGDEDNRRWMRENVPGEKKPONGIPLPPQIPNEBQYCGDFDSF
<b>(</b>		ĺ	PSAKEENI IYSFLGLAPPPDSKGSEKAREGGETEAQKEGSEDVG
1	Į.	ł	NLPEAQEKNEREGETATRETERIAMEGAEGRABEREETAEGEEP
			GEDEDS
5490	61	893	GKGPVAAFIDQSNIFLTDPKIFLGQWRBEPKMPLLLLGBTEPLK
1		ł	LERDCRSPVERWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
ļ	·		LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
1			IAGDEDNRRWMRENVPGBEEPQNGIPLPPQIFNEEQYCGDFDSF
l		}	FSAKRENIIYSFLGLAPPPDSKGSEKAEEGGETBAQKEGSEDVG
	*		NLPBAQEKNEREGETATEETEEIAMBGAEGEAEEEBETABGEEP
[			GEDEDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEGRSE
			QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEETSC
			LAKLFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCNTPKP
}		l	SFFDFEGKQKWBAWKALGDSSPSQAMQEYIAVVKKLDPGWNPQI
			PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENNIDH
		3.	ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLQHRAD
			INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDGCLP
			BEVTGCKTVSLVLQRHTTGKA
5492	3	1896	ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNIPYEATEE
1		l	QLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM
1		l	RNLNGREFSGRALRVDNAASEKNKBELKSIGPAAPIIDSPYGDP
1		}	IDPEDAPES ITRAVAS LPPEQMFELMKQMKLCVQNSHQEARNML
į			LONPOLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSQ
!		1	SVSVSGPGPGPGLCPGPNVLLNQQNPPAPQPQFLARRPVKDI
		1	PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGMPG
1	(	{	VGPVPLERGQVQMSDPRAPIPRGPVTPGGLPPRGLLGDAPNDPR
1	}	}	GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHEMRG
			GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMETE
1	ł :		VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP
j			MTCGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ
]			GTGMQGAGIQGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ
1			PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI
F422			LILKEQIQKSTGAS
5493	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL
	{		TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH
]			VQKSDVDLMRTKLRRLBEENSRKDRQIEQLLDPSRGTDFVRTLA
}			BERPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE
1			EMRIAMETYYEBVHRIQTILASSETTGKKPLGEKKTGAKRQKKM
]	]		GSALLSLSRSVQELTERNQSLKEDLDRVLSTSPTISKTQGYVEW
			SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL
1			HRQPRGDRNKDHERLRGAVRDLKBERTALQEQLLQRDLEVKQLL
}			QAKADLEKBLECAREGEEERREREEVLREEIQTLTSKLQELQEM
1			KKBEKEDCPBVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP
1	1	1	RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR

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SEQ   Predicted end   Desginning   mucleotide   location   corresponding   to first   amino acid   sequence   sequence   location   corresponding   to first   amino acid   residue of   amino acid   sequence
NO: mucleotide location corresponding to first amino acid amino acid residue of secution of the corresponding to first amino acid amino acid residue of amino acid sequence se
location   corresponding   to first   amino acid   residue of   residue of   residue of   residue of   amino acid   sequence   seq
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amino acid residue of amino acid sequence    M=Tryptophan, Y=Tyrosine, K=Unknown, *=S   Codon, /=possible mucleotide deletion,    -possible nucleotide insertion)   GHITETKILASKAHGSEPSSUFGIPGSSPVPRVPSPIAQ   FVQEEAIVIIGSALRAHLARARHSATSKRTTTAASTERES   HGBASSPPPLAALDDPSPSGPQAVAPLPGDDVNSDDDII   SLPTKNIPV   Sid
residue of amino acid sequence Codon, /-possible nuclectide deletion, /-possible nuclectide insertion) sequence Sequence Codon, /-possible nuclectide insertion, /-possible nuclection insertion, /-possible nuclectide insertion, /-possible nuclection, /-possible nuclectide insertion, /-possible nuclection insertion, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possible nuclection, /-possibl
amino acid sequence    Codon, /=possible nucleotide insertion    -possible nucleotide insertion     CRINTRYKLLASKAHGSEPSUPGEDEUGSSFVFRVPSPIAQ     PVQEEAIVIIQSALRAHLARARHSATSKRTTTASTRRRS     HCDASSPPPLAALPDPSPSGPQAVAPLEQDDVNSDDSDD1     SLPTKNPPV
-possible nucleotide insertion
GRITETKILASKAHGSEPPSVEGLPDQSSPVPRVPSPLAQ PVQEAIVIIQSALRAHLARARHSATJEKTTTAASTRRS HGBASSPPFILAALPDPSPSGPQAVAPLEGDDVNSDDSDDI SLPTKNPPV  5494 71 536 RSKAKIGTTTREVPSTDMXVRRESSSLTHRPAPSPATFR RRVILAVSSGTGCADAMELVILVPLCSLLAPMVLASAARKE PFHYDYQTIRIGGLVPAVVLPSVGILLILSRRCKCSFNQK GDERAQVERILITANATEPQKARN  5495 273 2168 DSILLIQVDTMPFTLHLESRLPSAIRSLILQKKPNIRWIS ERRPASLVVLPRSLAPAPERFCQVNTGPLPLLGQSPBERM QCAJSSTRMSHPQFWXPFSCATGSLASLEQVSEQLKDMV GCSFSLERALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPKDKLEGLVRACCSLGGGGGGVEIMGDPBLLG SKPAYGDAMVCPPGEVPVPMPSPLTSLGAVSSCETPLAFA CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSLASV KIRELSSMIG IDPCHNGIGHLLCKDELLKASLSLEHARSV GPPTHPNHBPPETTOGPGAVALVAFLQALEKEVATIVDQ LHQKIVEDAVEQGVLKTQIPLITYGGGSVEAAQAPLCKNG PRRDHLVALERAGRAADGRYYMARKMNIKHLVDPJDDLFL IPGISSTGVDGGGNEIGMGKVKRAVRRHIRHGDVIACDVE VIAGVSNNGGYALACALYILYSCAVRHQYLRKAVGPSRAP MTQALPSVIKREKMIGILVQHKVRSGVSGTVOMEVDGLEY ARMIQKIVDVTTAQV  5496 3 2408 QDTKMHEIYKGNITPQLIKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPVDSPPLSWICQPTRYARSGKRPQTCNQV SQSESSDLAGRLKRKKILKKYYSTRSEPLINGGQKPSSDD PSPSSSEADIHLLVHVHKHVSMGJUHYQYLLLLIFLSESLI NILKKDVEAVTGSPASTSICIGILLKRABLALLLHEVOQA SPVSESVSPVPDYJLPTRNDDFLSGKRKQISRDINNIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LIGKIBEDBSSGLVYKSGSGEIGSETBDKKOFYTDSSSVL DSMILSFDGSGNNILISSTLTEKRINETIRSIFKABBILIPE SRNLDISKBETPPVRTLKSQSSLEGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILERGLUESDGSDSHMFLRKGN TINYRGTARSVNAGANLQNYGETSPDAISTNSGGAQENID VVVPKITGVNGBIDIRGEDTEICLQVNQVVTPDQLGMISLR NRRVGSDQKAVHSKSSSPISLEFFSGPGGAVLHSLLALLSLR NRRVGSDQKAVHSKSSSPISLEFFSGPGGAVLHSLLALLAR TNYRGTARSVNAGANLQNYGETSPDAISTNSGGAQENID VVVPKITGVNGBIDIRGEDTEICLQVNQVVTPDQLGMISLR NRRVGSDQKAVHSKSSSPISLEFFSGPGGAVLHSLLALLAR NRRVGSDQKAVHSKSSSPISLEFFSGPGGAVLHSLLALLAR NRRVGSDQKAVHSKSSSPISLEFFSGPGAVLHSLLALLAR NRRVGSDQKAVHSKSSSPISLEFFSGPGGAVLHSLLALLAR NRRVGSDQKAVHSKSSSPISLEFFSGPGGAVLHSLLALLAR NRRVGSDQKAVHSKSSSPISLEFFSGPGGAVLHSLLALLAR NRRVGSDQKAVHSKSSSPISLEFFSGPGAVLHSLLALLAR NRRVGSDQKAVHSKSSSPISLEFFSGPGAVLHSLLALLAR NRRVGSDQKAVHSKSSSPISLEFFSGPGAVLHSLLALLAR NRRVGSDQKAVHSKSSSPISLEFFSGFGAVLHSLLALLAR NRRVGSDQKAVHSKSSPI
PVQKEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRS HEGNASSPPILAALPDBSPSEQQAVAPLEQDDVNSDDSDI SLPTKNPPV  5494  71  536  RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATFR RRVILGVSBGTGCADAMELVLVFLCSLLAPMVLASAAEKE PPHYDYQTIRIGGLVPRAVVLPSVGILLILISRRCKCSFNQK GDEEAQVENLITANATEPQKARN  5495  273  2168  DSILLIQVDTMPFTLHLESRLDSAIRESLIQKKVPNIRNTS GRAPASLAVULPSLAPHTLASGREDEATRESLIQKKVPNIRNTS GRAPASLAVULPSLAPAPREPQANTGPLPLILGGEPBRKM QCAISETRMGHPQFNKYBPGACTGSLASILGQYSEQLKDMV GCSFSLEBALEKNGLPRRDPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPRINLEGLVRACCSLAGGGGGPVHEGOPELILG SKPAYGDAMVCPPGEVPVPWPSPLTSIGAVSSCETPLAFA CTVMTDLKDAKAPPGGLTLEKTPLEVHHISQDPLHYSLASV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHLACKDELLAKSLSLEHARSV KIRELESMIG IDPGMRGIGHT LACKDELLAKSUSLEHARSV VIAGVSNMGGYALLACALYILYSCAVERGVIGVEMEVDGLEF VIAGVSNMGGYALACALYILYSCAVERGVIGVEMEVDGLEF VIAGVSNMGGYALACALYILYSCAVERGVIGVEMEVDGLEF ABMIQKLVDVTTAQV  SPESSISADIHLIVANTKKTSGASTOVANVYYSQEWI MKSGKRPLISFVDSPILSWICCPTRYARSGKRPGTCNDY SQSESSDLAGRLKRKKLLKEYYSTRSEPLTNGGQKPSSSD PSESSESDLIGGLLKKRKLLKEYYSTRSEPLTNGGGKPSSSD PSESSESDLIGGLLKRAKLALLHEVODA SPYSESVSPVPDYPLFTRNDDFLSKRKQISKDINKIRSV MSDKRSMSVOLSHIPLKGNITISSTANLKGGSTFTDSSGALE LKRKSSDGSSGVYKSGSGGIGSETDKKORSFYTDSSSVL DSMILSFDGSGGNVILISSTATEKGNBTI SSIFKABBLLER SRNLDISKBETPPVRTLKSQSSELGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILERGLEBSDGSMMFLERGN TNYRGTARSVNAGANLQNYGETSPDAI STNSEGAQENID VVVYKITGVNGBIDIRGEDTE ICLQVNQVYPDQLGMISLE NRRVGSDQKAVIHSKSSPISLEKPSGPGCVUTSDLAGLING NRRVGSDQKAVIHSKSSPISLEKPSGPGAVUTSDLAGLING NRRVGSDQKAVIHSKSSPSISLEKPSGPGAVUTSBLALLAN NRRVGSDQKAVIHSKSSPSISLEKPSGPGAVUTSBLALLAN NRRVGSDQKAVIHSKSSPSISLEKPSGPGAVUTSBLALLAN NRRVGSDQKAVIH
HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDI  SLPTKNPPV  RSKAKIGTPTREVPSTDMKVRRESSSSLTHEPAPSPATFR RRVLLGVSBGTGCADAMELVLVFLCSLLAPMVLASAAEKE PPHYDYQTTLEIGGLVFAVVLFSVGFLLILISRRCKCSFNQK GDESAQVENLITANATEPQKAEN  5495  273  2168  DSLLLIQVDTMPFTLHLESRLPSAIRSLILQKKPNIRNTS RLPFASLVVLPRSLAPAPERFCQVWTGPLPLLGGSPFREM GCSFSLEEALEKAGLPRRDFAGHSQAGYKTTVPCVTHAG LVVTMRPIPKDKLEGLVRACCSLGGGGGPVEMGDPELLG SKPAYGDAMVCPPGEVPVFMPSPLTSIGAVSSCETPLAPA CTVMTDLKDAKAPPGCLTPREIPEVHHISQDPLHYSIASV KIRELESMIGIDPCNRGIGHLLCKDELLKASLSLSHARSV GPFTHFNHEPPETTIGPPGAVALVAFLQALEKEVALIVDQ LHQKIVEDAVAGCGVLKTQIPILITYGGSVEAAQAFLCKNG PRPDHLVAIERAGRAADGNYNARKMNIKHLVDPIDDLFL 1PGISSTGVDDGGNELGMKVKEAVRRHIRHGDVIACOVE PRICHLVAIERAGRAADGNYNARKMNIKHLVDPIDDLFL 1PGISSTGVDDGGNELGMKVKEAVRRHIRHGUTACOVE VIAGVSNMGGVALACALYLLYSCAVHSQIVRAVGFSRAP WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDCLPP ARMIQKIVDVTTAQV SQESSDLAGRLKKKLLREYYSTESPLITNGGQKPSSD MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQV SQESSDLAGRLKKKLLREYYSTESPLITNGGQKPSSDI NIRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKRQISRDINRIESV MSDKRSMSVDLSHIPLKDPLLFKSASDTNAIKGGISFMDVL LKKISBDESSGLVYKSGSGEIGSETSDKKDSFYTDSSVL DSNILSFDSCNONILSSTLTSKGMRTIESIFRABDLLPE SRNLDISKEBTPPVRTLKSQSSLGKPKRCPPNLAPLCV MKRSSQMSLDTISLDSMILESQLLESBGSDSBHMPLEKGN TNYRGTABSVNAGANLANYGETSPDAISTNSEGAGENID VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGRISLE NRRVGSDQKAVIHSLLAEKN
HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDI  SLPTKNPPV  RSKAKIGTPTREVPSTDMKVRRESSSSLTHEPAPSPATFR RRVLLGVSBGTGCADAMELVLVFLCSLLAPMVLASAAEKE PPHYDYQTTLEIGGLVFAVVLFSVGFLLILISRRCKCSFNQK GDESAQVENLITANATEPQKAEN  5495  273  2168  DSLLLIQVDTMPFTLHLESRLPSAIRSLILQKKPNIRNTS RLPFASLVVLPRSLAPAPERFCQVWTGPLPLLGGSPFREM GCSFSLEEALEKAGLPRRDFAGHSQAGYKTTVPCVTHAG LVVTMRPIPKDKLEGLVRACCSLGGGGGPVEMGDPELLG SKPAYGDAMVCPPGEVPVFMPSPLTSIGAVSSCETPLAPA CTVMTDLKDAKAPPGCLTPREIPEVHHISQDPLHYSIASV KIRELESMIGIDPCNRGIGHLLCKDELLKASLSLSHARSV GPFTHFNHEPPETTIGPPGAVALVAFLQALEKEVALIVDQ LHQKIVEDAVAGCGVLKTQIPILITYGGSVEAAQAFLCKNG PRPDHLVAIERAGRAADGNYNARKMNIKHLVDPIDDLFL 1PGISSTGVDDGGNELGMKVKEAVRRHIRHGDVIACOVE PRICHLVAIERAGRAADGNYNARKMNIKHLVDPIDDLFL 1PGISSTGVDDGGNELGMKVKEAVRRHIRHGUTACOVE VIAGVSNMGGVALACALYLLYSCAVHSQIVRAVGFSRAP WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDCLPP ARMIQKIVDVTTAQV SQESSDLAGRLKKKLLREYYSTESPLITNGGQKPSSD MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQV SQESSDLAGRLKKKLLREYYSTESPLITNGGQKPSSDI NIRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKRQISRDINRIESV MSDKRSMSVDLSHIPLKDPLLFKSASDTNAIKGGISFMDVL LKKISBDESSGLVYKSGSGEIGSETSDKKDSFYTDSSVL DSNILSFDSCNONILSSTLTSKGMRTIESIFRABDLLPE SRNLDISKEBTPPVRTLKSQSSLGKPKRCPPNLAPLCV MKRSSQMSLDTISLDSMILESQLLESBGSDSBHMPLEKGN TNYRGTABSVNAGANLANYGETSPDAISTNSEGAGENID VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGRISLE NRRVGSDQKAVIHSLLAEKN
SLPTKNPPV  5494  71  536  RSKAKTOTPTREVPSTDMKVKRESSSSTHRPAPSPATPR RRVLLGVSBGTGCADAMELVLVPLCSLLAPMVLASAAEKE PPHYDYCTLRIGGLVPAVVLESVGILLILSRRCKCSPMQK GDERQUENLITANATEPOKARN  5495  273  2168  DSILLIQVDTMPFTLHLKSRLEPSAIRSLILQKKPNIRNTS RLEPASLVVLPRSLAPAPERPCQVMTGPLPLIGGSPRKW QGAISETRMGHPQFWKYEPCACTGSLASLEQYSEQLKDMV GCSFSLEEALEKAGLPRRDPAGHSGAGAYKTTVPCVTHAG LVVTMRPIPKDKLEGLVRACCSLAGGEGGPVPMMCPPELLG SKPAYGDAMVCPPGEVVPWPSPLTSIGAVSSCETPLAPA CTVMTDLKDAKAPPGCLTPBRIPEVHHTSOPPLHYSLASV KIRELESMIGIDPGNRGIGHLICKDELLKASLSLSHARSV GFPTHRNHBPPESTTGPPGAVALVAFLQALEREVALIVDQ LHQKIVEDAVEQGVLKTQIPTLTYQGGSVEAAQAPICKNG PRIPHLVAIERAGRAADGNYNAKMINKHLVDPIDDLFL IPGISSTGVGDGGMELGHKGVKEAVRRHIRHGDVIACDVE VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAP WTQALPSVIKERKMIGILVQHKVRSGVSGIVGMKVDCLPP ARMIQKIVDVTTAQV SQSSSDLAGRIKKKKLLKEYYSTESPLTNGGQKPSSD MKSGKGRPISFVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSSSDLAGRIKKKKLLKEYYSTESPLTNGGGKPSSD MKSGKGRPISFVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSSSDLAGRIKKKKLLKEYYSTESPLTNGGGKPSSD NILKRDVEAVTGSPASQTSICTGILLRSAELALLHPUDQA SPVSESVSPVVPDYLPTENDDFLSKKRKQISRDINRIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLCKGISFMDYL LGKISRDESGLVYKSGSGEIGSETSDKKDSFYTDSSVL DSNILSFDSDCMOMILSSTLTSKKRCPPNIAPLCV MKRSSSQMSLDTISLDSMILESQLIKSRCPPNIAPLCV MKRSSSQMSLDTISLDSMILESQLIKSDGSDSHMFLEKGN TINYRGTASSVNAGANLQNYGETSPDAISTNSGGQENID VVVPKITGVNGEIDIRGEDTEICLQVNQVTPDQLGRISLA
5494 71 536 RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPR RRVILIGVSBGTGCADAMELVILVPLCSILIAPMVLASARSKE PFHYDYOTLRIGGLVFAVVLPSVGILLILSRRCKCSFNQK GDEEAQVENLTTANATBPQKARN  5495 273 2168 DSILLIGVDTMPFTLHLESRLPSATRSILLQKKPNIRWTS ELRPASLVULPRSLAPAPFERPCQVNTGPLPLLGQSPBRKM QGAISETRMGHQPFMKYBEGACTGSLASLBQYSEQLKDMV GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPKDKLBGLURACCSJAGSRGSQPVHMGDPBLLG SKPAYGDAMVCPPGBVPVFWPSPLTSIGAVSSCETPLAPA CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASV KIRELESMIGIDPGNRGIGHLICKDELLKASLSLSHARSV GFPPHPNHEPPEBTGSPPGAVALVAFLQALSKEVATIVDQ LHQKIVBDAVBQGVLKTQIPILTYQGGSVEAAQAPLCKNG PREPHLVAIERAGRAADGNYVNARKMNIKHLVDPIDDLFL IPGISSTGVGDGSNELGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNMGGTALACALYILYSCAVHSQYLKKAVGPSRAP WTQALPSVIRBEKMIGILVQHKVRSGVSGIVGMEVDGLPF ABMIQKLVDVTTAQU SGSESSDLAGRLKRKKLLKEYYSTESEPLTNGGKPSSSD MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGGKPSSSD PSSSESDLAGRLKRKKLLKEYYSTESEPLTNGGGKPSSSD SPVSESVSPVVPDYLPTRROGDFISSKKKQISRDINTIKSGLIFNDYL LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSVL DSNILSFDSCNGNILSSTLTRENBTIGSIFFRABDLLPE SRNLDISERSPLOMNILSSTLTRENBTIGSIFFRABDLLPE SRNLDISERSPLOMNILSSTLTRENBTIESIFFRABDLLPE SRNLDISERSPSDVAGANLQNYGFTSPDAISTNSEGAQENHD VVVFKITGVNGBIDTREDDTBICLCUVNQVTPDQIGNISLE NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN NRFVGSDQKAVIHSKSSPISLRFFSGOFGAVIHSLAKKN
RRVILGVSBGTGCADAMELVILVFLCSLLAPMVLASAAEKE PPHYDYQTLRIGGLVFAVVILFSGILLILGRRCKCSFNQK GDBEAQVENLITANATEPQKAEN  5495  273  2168  DSILLIQVÖTMPFTIHLESRLPSAIRSLILQKKENIRNTS ELRPASLVVLPRSLAPAPERFCQVNTGPLPLLGQSEPEKM QGAISSTRMGHPQFWKYBEGACTOSLASLBQYSEGLKDMV GCSFSLEEALEKAGLPROPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPKDKLBGLVRACCSLGGEQGQPVHMGDPELLG SKPAYGDAMVCPPGRVPVPMPSPLTSIGAVSSCETPLAPA CTVMTDLKDAKAPGCLTPRIPSIGAVSSCETPLAPA CTVMTDLKDAKAPGCLTPRIPSIPPHHISQDPLHYSIASV KIRELESMIGIDPGRNGIGHLACKDELLKASLSLSHARSV GFPTHPNHEPPESTDGPPGAVALVAFLQALEKEVAIIVDQ LHQKIVEDAVSQGVLKTQIPILTYQGGSVERAQAPICKING PREDHLVAIRERAGRADGVYNARKMIKHLVDPIDDLPL LHQKIVEDAVSQGVLKTQIPILTYQGGSVERAQAPICKING PREDHLVAIRERAGRADGVYNARKMIKHLVDPIDDLPL LYIGUSSNNGGVALACALYILYSCAVHSQYLKKAVGPSRAP WTQALPSVIKBEKMIGILVQHKVRSGVSGIVGMEVDGLPP ARMIQKLVDVTTAQV SQESSDLAGKLKKRKLLKEYYSTESSPLTINGGQKPSSD MKSGKGRPISFVDSFPLSWICQPTRVAESQKRPQTTCNQ SQESSDLAGKLKKRKLLKEYYSTESSPLTINGGQKPSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLESSLI NLRRDVBAVTGSPASGTSICIGILLRSABLALLHPUDQA SPVSESVSFVVPDYLPTRRDOPLSSKRXQISRDINRIRSV MSDKRSNSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISRDESSGLVYKSGSGEIGSTSDKKDSFYTDSSSVL DSNILSFDGEDQNILSSTLTSKGNBTIRSIFKABDLLPE SRNLDISKEBPTPPVRTLKSQSSLSGRYKERCPPNLAPLCV MKRSSQMSLDTISLDSMILBEQLLBSDGSDSHMFLEKGN TINYRGTABSVNAGANLQNYGETSPDAISINSEGAQENHD VVVFKITGVNGGIDIRGETGLQVNQVTPDQLGNISLE NRPVGSDQKAVIHSKSSPISLRFRSGPGAVIHSLLAEKN NRPVGSDQKAVIHSKSSPISLRFRSGPGAVIHSLLAEKN
PFHYDYQTLRIGGLVFAVULFSVGILLILSRRCKCSFNQK GDBEAQVENLITANATEPQKARN  5495  273  2168  DSILLIQUDTMPFTLHLERSLPSATRSLILQKKPNIRNTS ERPASLVULPRSLAPAPERPCQVMTGPLPLLGGSPBRKM QGAISETRMGHPQFMKYEPGACTGSLASLEQYSEQLKDMV. GCSFSLEEALEKAGLPRRDPPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPKDKLEGLVRACCSLGGGGQPVHMGDPELLG SKPAYGDAMVCPPGEVVPWPSPLTSIGAVSSCETPLAFA CTVMTDLKDAKAPPGCLTPBRIPEVHHISQDPLHYSIASV KIRELESMIG IDPENRGIGHLLCKDELLKASLSLSHARSV GFPTHPNHSPPEBTDGPPGAVALVAFLQALEKEVAIIVDQ LHQKIVEDAVEGGVLKTQIPTLTYQGGSVEAAQAPLCKNG PRPDHLVAIERAGRAADGNYNARKMNIKHLVDPIDDLPL IPGISSTGVGDGGNELGMGKVKEAVRHHRGDVIACDVE VIAGVSNMGGYALACALYILYSCAVHSQYLKKAVGPSRAP MTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPFL ABMIQKLUDVTTAQV  5496  3  2408  QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRISFVDSFPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTRSEPLTNGGQKPSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLERSLI NLRKDVBAVTGSPASQTSICIGILLRSABLALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKKKQISRDINRIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISRDESSGLVYKSGSGETGSET3DKKDSFYTDSSSVL DSNILSFDSGONNILSSTLTSKGNBTJESIPKABDLLPE SRNLDISKEBTPPVRTLKSQSSLSGKPKERCPNHLAPLCV MKRSSSQMSLDTISLDSMILEBQLLBSDGSDSHMPLEKGN TTMYRGTABSVKAGANLQNYGKTSPDAISTNSEGAQRMHD VVVPKITGVNGBIDIRGBTREICLQVUQVTPDQLGNISLER VVPFKITGVNGBIDIRGBTREICLQVUQVTPDQLGNISLER VVPFKITGVNGBIDIRGBTREICLQVUQVTPDQLGNISLER NRPVGSDQKAVIHSLSSSPBISLRFRSGPCAVHISLLAEKM
GDBEAQVENLITANATEPQKAEN  5495  273  2168  DSILLIQVOTMPFTLHILESRIPSATESLILQKKENIRNTS ELRPASLVVLPRSLAPPERFCQVNTGPLPLLGQSEPBEKM QGAISETEMGRPOFMXVEFGACTGSLASLEQYSEQLKOMV. GCSFSLEEALEKAGLPRADPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPKDKLBGLVRACCSLGGGGGPVHMGDPBLLG SKPAYGDAMVCPPGEVPVPMPSPLTSLGAVSSCETPLAPA CTMTDLKDAKAPPGCLTPBRIPEVHHISQDPLHYSIASV. KIRELESMIG IDPENRGIGHLLCKDELLKASLSLGHARSV GFPTHPHHEPPEETDGPFGAVALVAFLQALEKEVAIIVDQ LHQKIVEDAVEGGVLKTQIPTLTYQGGSVERAQAPTCKNG PRFDHLVAIERAGRAADGNYVNARKMNIKHLVDPIDDLFL IPGIBSTTGVGGGNERLGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNMGGYALACALYILYSCAVHSQYLKRAVGPSRAD MYGALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPF AEMIQKLVDVTTAQV  5496  3  2408  QDTKMHEIYKGNITPQLNKNTLKTSAATDWAVYFSQFWI MKSGKGRPISPVDSPPLSINICQPTRYAESQKEPQTCNOV SQSESSDLAGRLKKKKLLKEYYSTBSEPLINGGCKPSSD PSPSSSPADIHLLVHVHKHVSMQINHYQYLLLLFLHESSLI NLRKDVEAVTGSPASGTSICIGILLRSAELALLLHPVDQA SPPUSEVSPVVPDYLPTENGDFLSSKKKQISFDINRIESVL MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESSGLVYKSGSGRIGSFTSDKKDSFYTDSSSVL DSNILSFDSDGNONILSSTLTSKGNETIESIPKABDLLPE SRNLDISKEBTPPVRTLKSQSSLSGKPKERCPNHAPLCV MKRSSQMSLDTISLDSMILEEQLLBSDGSDSHMPLKKGN TTMYRGTABSVARGANLQNYGETSPDAISTNSEGAQRMID VVVPKITGVNGBIDIRGETEICLQVUQVYTPDQLGNISLER VVVPKITGVNGBIDIRGETEICLQVUQVYTPDQLGNISLER VVVPKITGVNGBIDIRGETEICLQVUQVTPDQLGNISLER
273 2168 DSILLIQUOTMPFTLHLRSRLPSAIRSLILQKRPNIRNTS ELRPASLVULPRSLAPAPERFCQWITGPLPLLGQSPERKM QGAISETRMGHPQFWKYBFGACTGSLASLBQYSEQLKDMW. GCSFSELEBALBKAGIPRRDPAGHSQAGAYKTTYPCVTHAG LVVTMRPIPKDKLEGLVRACCSLGEGGGGPVHMGDPELLG SKPAYGDAMVCPPGEVPVMPSPLTSLGAVSSCETPLAPA CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASV KIRELESMIGIDPGNRGIGHILCKDELLKASLSLSHARSV GFPTHPNHEPPEETDGPPGAVALVAFLQALEKEVAITUDQ LHQKIVEDAVEQGVLKTQIPILTTQGGSVEAAQAPLCKNG PREDHLVAIERAGRAADGMYNNARKMNIKHLVDIDLIPL IPGISSTGVGGGGGRELGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNNGGYALACALYILYSCAVHSQYLRKAVGPSRAP WTQALPSYIKBEKMIGILVQHKVRSGVSGIVGMEVDGLPF ARMIQKLVDVTTAQV ARMIQKLVDVTTAQV SQSESSDLAGRLKRKKLLKEYYSTRSEPLTNGGGKPSSD MKSGKGRPISPVDSFPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTRSEPLTNGGGKPSSD FSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLESLI NIRKDVEAVTGSPASCTSICIGILLRSAELALLHPVDQA SPVSESVSPVVPDYLPTENGDFLSKRKQISRDINRIRSV MSDKRSMSVOLSHIPLKOPLLFKSASDTNLQKGISFMDYL LGKISEBESSGLYYKSGSGEIGSETSDKKDSFTYDSSVLL DSNILSFDGGRONDILSSTLTSKGNBTIRSIPKABBLLPE SRNLDISKBETPVRTLKSQSSLGGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILBEQLABSDGSBMFLKRGN TINYRGTARSVNAGANLQMYGETSPDAISTNSEGARENDO VVYFKITGVNGBIDIRGBDTBICICQVNQVTPDQLGNISLK NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVHSLLAEKN
ELRPASLVULPRSLAPAPERFCQVNTGPLPLIGQSEPEKM QGAISETRMSHPQFWKYBFGACTGSLASLBQYSEGLKIMWV GCSFSLEBALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPKDKLBGLVRACCSLGGEQGQPVHMGDPBLLG SKPAYGDAMVCPPGEVPVVMPSPLTSLGAVSSCBTPLAFA CTVMTDLKDAKAPPGCLTPBRIPEVHHISQDPLHYSIASV KIRELESHIGIDPGNRGIGHLLCKDELLKASLSLSHARSV GFPTHPHBPPEETDGPPGAVALVAFLQALEKEVAIIVDQ LHQRIVEDAVEQGVLKTQIPILTTQGGSVEAAQAPLCKNG PREPHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFL IPGISTGVGDGGNELGMGKVKEAVRRHTRHGDVIACDVE VIAGVSNMGGYALACALITLYSCAVHSQYLRKAVGPSRAP WTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPF ARMIQKLUDVTTAQV  5496 3 2408 QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYF9QFWI MKSGKGRPISPVDSPPLSIWICQPTRYABSQKEPQTCNQV SQESSDLAGRLKKKLLKEYYSTESEPLTNGGQKPSSD MKSGKGRPISPOSPPLSTWICQPTRYABSQKEPQTCNQV SQESSDLAGRLKKKKLLKEYYSTESEPLTNGGQKPSSD NIRKDVEAVTGSPASQTSICIGILLRSABLALLLHPVDQA SPVSESVSPVVPDYLPTRNGDFLSKRXQISRDINRIESV MSDKRSMSVDLSHIPLKVDPLLFKSASDTNILQKGISFMDYL LGKISEDESGLVYKSGSGBIGSETSDKKDSFYTDSSSVL DSNILSFDSGGNQNILSSTLITSKGNBTIESIFKABDLLPE SENLDISKBETPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTITSLDSNILBEQLABSDGSDSHMFLKRGN TINYRGTASVNAGANLQNYGETSPDAISTNSKEAQENHDL VVVPKITGYNGBIDIRGBDTBICICQVNQVTPDDLGNISLR VVVPKITGYNGBIDIRGBDTBICICQVNQVTPDDLGNISLR NRPVGSDQKAVHISKSSPBISLRFRSGPGAVHSLLAEKN
QGAISETRMGHPQFWKYEPGACTGSLASLEQYSEQLKDMV. GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPKDKLBGLVRACCSLGGEGGPVEMGDPELLG SKPAYGDAMVCPPGEVPVFMPSPLTSIGAVSSCETPLAFA CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASV. KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSV GFPTHPNHBPPEBTTOGPPGAVALVAFLQALEKEVAITVDQ LHQKIVEDAVEQGVLKTQIPTLTYQGGSVEAAQAPLCKNG PREPHLVAIERAGRAADGNYVNARKHMIKHLVDPIDDLFL IPGISSTGVGDGGNBLGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNMGGYALACALYILVSCAVHSQYLKRAVGPSRAP WTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPF. ABMIQKLVDDTTAQV  5496 3 2408 QDTKMHEYYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPVDSPPLSIWICQPTRVABSQKEPQTCNQV SQEBSDLAGRLKRKKLLKEYYSTESEPLINGGQKPSSSO PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLSESLI NLRKDVEAVTGSPASQTSICTGILLRSAELALLHPVDQA SPVSESVSPVVPDYLPTBNGDFLSSKRXQISRDINRIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESSGLVYKSGSGEGGSTSDKKDSFYTDSSSVL DSNILSFDGDCNQNILSSTLTSKGNBTIESIFKABDLLPE SENLDISKEBTPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLASGGSBIGSTSNSEGAGENDD VVVPKITGVNSGIDTRGEDTBICLQVWQVTPDQLGNISLR TNYRGTAESVNAGANLQNYGETSPDAISTNSEGAGENDD VVVPKITGVNSGIDTRGEDTBICLQVWQVTPDQLGNISLR NRPVGSDQKAVIHSKSSPBISLRFESGPGAVIHSLLAEKN
GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPKDKLEGLIVACCSLGGEGGGPUHMEDPELLG SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSCETPLAFA CTVMTDLKDAKAPPGCLTPBRIPEVHHISQDPLHYSLASV KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSV GFPTHPNHBPPETTGPPGAVALVAFLQALEKEVAIIVDQ LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAPLCKNG PRFPHLVAIERAGRAADGNYVNARKMIKHUVDPIDDLFL IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNNGGYALACALYILYSCAVHSQYLRRAVGPSRAP WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPP: ABMIQKLVDVTTAQV  SAMIQKLVDVTTAQV  MKSGKGRPISPVDSPPLSIWICQPTRYAESQKBPQTCNQV SQSBSSDLAGRLKRKKLLKEYYSTESPLTNGGQKPSSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI NLRKDVEAVTGSPASQTSICIGILLRSABLALLLHPUDQA SPVSESVSPVVPDVLDFTENGDFLSKKKQISRDINRIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESGILVYKSGSGBIGSETSKKOSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNBTIESIPKABDLLPE SRNLDISKBETPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILEBQLLESDGSDSHMFLEKGN TINYRGTABSVNAGANLQNYGETSPDAISTNSEGAQENHD VVVPKITGVNGGIDTRGEDTRICLQVUQVTPDQLGNISLR NRPVGSDQKAVIHSKSSPRISLRFRSGPGAVIHSLLAEKN
GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAG LVVTMRPIPKDKLEGLIVACCSLGGEGGGPUHMEDPELLG SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSCETPLAFA CTVMTDLKDAKAPPGCLTPBRIPEVHHISQDPLHYSLASV KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSV GFPTHPNHBPPETTGPPGAVALVAFLQALEKEVAIIVDQ LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAPLCKNG PRFPHLVAIERAGRAADGNYVNARKMIKHUVDPIDDLFL IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNNGGYALACALYILYSCAVHSQYLRRAVGPSRAP WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPP: ABMIQKLVDVTTAQV  SAMIQKLVDVTTAQV  MKSGKGRPISPVDSPPLSIWICQPTRYAESQKBPQTCNQV SQSBSSDLAGRLKRKKLLKEYYSTESPLTNGGQKPSSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI NLRKDVEAVTGSPASQTSICIGILLRSABLALLLHPUDQA SPVSESVSPVVPDVLDFTENGDFLSKKKQISRDINRIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESGILVYKSGSGBIGSETSKKOSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNBTIESIPKABDLLPE SRNLDISKBETPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILEBQLLESDGSDSHMFLEKGN TINYRGTABSVNAGANLQNYGETSPDAISTNSEGAQENHD VVVPKITGVNGGIDTRGEDTRICLQVUQVTPDQLGNISLR NRPVGSDQKAVIHSKSSPRISLRFRSGPGAVIHSLLAEKN
LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLG SKPAYGDAMVCPPGEVPVPMPSPLTSIGAVSCETPLAFA CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASV KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSV KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSV LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAPLCKNG PRPDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLPL IPGISTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNMGGYALACALYILYSCAVHSQYLKKAVGPSRAP MYQALPSVIKEKMLGILVQHKVRSGVSGTVGMEVDCLPP AEMIQKLVDVTTAQV  5496 3 2408 QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTRSEPLTNGGQKPSSD NERKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKKKQISRDINAIRSV MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKLSEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVL DSNILSFDSCMONILSSTLTSKGNETIESIPKAEDLLPE SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSNILEEQLLESDGSDSHMFLKKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGNHD VVVPKITGVNGBIDIRGEDTEICLQVNQVYPDQLGRISLRI NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAPA CTVMTDLKDAKAPPGCLTPERIPEVHHISODPLHYSIASV KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSV GFPTHPNHEPPESTDGPPGAVALVAFLQALEKEVAITVDQ LHQKIVEDAVACVGVLKTQIPILTYGGGSVEAAQAFLCKNG PRFDHLVAIERAGRAADGNYNARKMNIKHLVDPIDDLPL IPGISSTGVGDGGNELGMGKVKRAVRRHIRHGDVIACDVE VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAP WTQALPSVIKREKMLGILVQHKVRSGVSGIVGMEVDGLPF ARMIQKLVDVTTAQV  5496  3 2408 QDTKMHEIYKGNITPQLMKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISFVDSFPLSIWICQPTRYAESQKEPGYTCNQV SQSESDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSDD FSPSSSEADIHLLVHVHKRVSMQINHYQYLLLIFLESSIL NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKKXQISRDINRIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVL DSNILSFDSSCMONILSSTLTSKCMRTIESIFKAEDILPR SENLDISKEBTPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLOSMILEEQLLESDGSDSHMFLEKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGENDD VVVPKITGVNGBIDIRGBDTEICLQVNQVTPDQLGRISLK NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKN
CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASV  KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLGHARSV  GFPTHPHHEPPEBTDGPGAVALVAFLQALBKEVATIVDQ  LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAPLCKNG  PRPDHLVAIERAGRAADGMYYNARKMNIKHLVDPIDDLPL  IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVE  VIAGVSNMGGYALACALYILYSCAVHSQYLRKAVGPSRAP  WTQALPSVIKERKMLGILVQHKVRSGVSGIVGMEVDGLPF  ARMIQKLVDVTTAQV  SQMENQKLVDVTTAQV  SQSESDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSDD  MKSGKGRPISFVDSFPLSIWICQPTRYAESQKEPQTCNQV  SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSD  PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI  NILRDVEAVTGSPASQTSICIGITLGRABLALLLHPVDQA  SPVSESVSPVVPDYLPTENGDFLSKKKQISRDINRIRSV  MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL  LGKLSEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSVL  GKLSEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSVL  DSNILSFDGDGNQNILSSTLTSKGNETIESIPKAEDLLPE  SENLDISKEBTFPVRTLKSQSSLGGKPKERCPPNLAPLCV  MKRSSSQMSLDTISLDSMILESQLLESDGSDSHMFLEKGN  TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD  VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLK  NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
KIRELESMIGIDPCNRGIGHLLCKDELLKASLSLSHARSV GFPTHPNHEPPEBTDGPPGAVALVAFLQALEKEVAITVDQ LHQKIVEDAVEGGVLKTQIPILITYGGGSVERAQAFLCKNG PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLPL IPGISSTGVEDGGNELGMGKVKEAVREHIRHGDVIACDVE VIAGVSNMGGYALACALYILYSCAVHSQYLRKAVGPSRAP MTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPF AEMIQKIVDVTTAQV  5496 3 2408 QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGKLKRKKLLKEYYSTRSEPLTNGGQKPSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI NIRKDVEAVTGSPASCTSICIGILLRSAELALLLHPUDQA SPVSESVSPVVPDTYPENGDFLSKKKQISRDINRIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKLSEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVL DSNILSFDGGNQNILSSTLTSKGNETIESIFKAEDLLPE SENLDISKEETPPVRTLKSQSSLGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILEEQLLBSDGSDSHMFLKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLR NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
GPPTHPNHBPPEETDGPPGAVALVAFLQALEKEVAITVDQ LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAPICKNG PRPDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLPL IPGISSTGVGDGGNELGMGKVKEAVERHIRHGDVIACDVE VIAGVSNNEGSVALLACALYILYSCAVHSQYLRKAVGPSRAP WTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPP: AEMIQKLVDVTTAQV  5496 3 2408 QDTKHHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSV MSDRKSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKLEEDESSGLVYKSGGGEIGSFTSDKKDSFYTDSSSVL DSNILSFDSGGNONILSSTLTSKGNETIESIPKAEDLLPE SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLKKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGNHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLEN NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAPICKNG PRPDHIJVAIERAGRAADGNYYNARKMNIKHJVDPIDLDFL IPGISTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNMGGYALACALYILYSCAVHSQYLRKAVGPSRAP WTQALPSVIKEKMLGILVQHKVRSGVSGTVGMEVDCLPP AEMIQKLVDVTTAQV  5496  3 2408 QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPVDSPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFFESSLI NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKKXQISRDINRIRSV MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKLSEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVL DSNILSFDSDCNQNILSSTLTSKGNETIESIPKAEDILDE SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSNILEEQLLESDGSDSHMFLKKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGENHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLR NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKN
PREDHLVATERAGRAADGNYYNARKMNIKHLVDPIDDLPL  IPGISSTGVEGGGNELGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAP, WTQALPSVIKERKMLGILVQHKVRSGVSGIVGMEVDGLPF AEMIQKLVDVTTAQV  5496  3 2408 QDTKMHEIYKGNITFQLMENTLKTSAATDVWAVYFSQFWI MKSGKGRPISFVDSFPLSIWICQPTRYAESQKEPQTCNQV SQSESDLAGRLKKKKLLKEYYSTESEPLTNGGQKPSSDD PSPSSSEADIMLLVHVHKHVSMQINHYQYLLLIFLSESLI NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKKXQISRDINRIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESGLVYKSGSGEIGSETSDKKDSFYTDSSSVL DSNILSFDSDCMQNILSSTLTSKCMRTIBSIPKAEDLLPR SENLDISKEBTPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSNILEEQLLESDGSDSHMFLEKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGHDD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLRI NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKN
IPGISTGVODGGNELGMGKVKEAVRRHIRHGDVIACDVE VIAGVSNMGGYALACALYILYSCAVHSQYLRKAVGPSRAP WTQALPSVIKEKMLGILVQHKVRSGVSGTVGMEVDCLPP: AEMIQKLVDVTTAQV  5496  3 2408 QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISFVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSD PSPSSSEADIHLUHVHKHVSMQINHYQYLLLLIFLSESLI NLRKDVEAVTGSPASQTSICIGILLKSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSKRKQISRDINRIRSVL MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESSGLVYKSGSGEIGSBTSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNBTLESIPKAEDLLDE SENLDISKEBTPPVRTLKSQSSLSGKPKERCPPNLAPLCV. MKRSSSQMSLDTISLDSMILEEQLLBSDGSDSHMFLKKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLK NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKN
VIAGVSNMGGYALACALYILYSCAVHSQYLRKAVGPSRAP WTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPF ABMIQKLVDVTTAQV  5496  3 2408 QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPUDSPPLSIWICQPTRYAESQKBPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI NIRKDVEAVTGSPASQTSICIGITLGRABLALLLHPVDQA SPVSESVSPVVPDTLPTENGDFLSKRKQISRDINRIRSV MSDRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKLSEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSVL DSNILSFDSGNQNILSSTLTSKGNETIESIPKAEDLLPE SRNLDISKEETPPVRTLKSQSSLGSKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILEGLUBSDGSDSHMPLKENHD TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLR NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
WTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPF AEMIQKI.VDVTTAQV  5496  3 2408 QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPVDSPPLSIWICQPTRYAESQKBPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTRSEPLTNGGQKPSSD FSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI NLRKDVEAVTGSPASQTSICIGITLGRABELALLLHPVDQA SPVSESVSPVVPDYLPTRNGDFLSSKRXQISRDINNIRSV MSDRKSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKLSEDESSGLVYKSGSGEIGSFTSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPE SRNLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILEEQLLBSDGSDSHMFLEKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGENHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLR NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKN
ABMIQKLVDVTTAQV  5496  3  2408  QDTKMHEIYKGNITPQLNKNTLKTSAATDWAVYFSQFWI MKSGKGRPISFVDSFPLSIWICQPTRYABSQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLIFLSESLI NLRKDVEAVTGSPASQTSICIGILLRSABLALLLHPVDQA SPVSESVSPVVPDYLPTRNGDFLSSKRXQISRDINRIRSV MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESSGLVYKSGGGEIGSETSDKKDSFYTDSSSVL DSNILSFDSDCNQNILSSTLTSKGNETIESIFKAEDILDE SENLDISKEBTPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSNILEEQLLESDGSDSHMFLKKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGNHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLR NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKN
5496 3 2408 QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTRSEPLTINGGQKPSSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI NIRKDVEAVTGSPASQTSICIGILLRSABLALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINAIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESGLVYKSGSGEIGSETSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNETIBSIPKAEDLLPR SRNLDISKEBTPPVRTLKSQSSLSGKPKERCPPNLAPLCV. MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLKKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD VVVFRITGVNGBIDIRGEDIEICLQVNQVTPDQLGRISLR NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
5496 3 2408 QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWI MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTRSEPLTINGGQKPSSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI NIRKDVEAVTGSPASQTSICIGILLRSABLALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINAIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESGLVYKSGSGEIGSETSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNETIBSIPKAEDLLPR SRNLDISKEBTPPVRTLKSQSSLSGKPKERCPPNLAPLCV. MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLKKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD VVVFRITGVNGBIDIRGEDIEICLQVNQVTPDQLGRISLR NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQV SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLSESLI NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSV MSDLRSMSVDLSHIPLKOPILLFKSASDTNLQKGISFMDYL LGKISEDESSGLVYKSGSGEIGSPTSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNBTIESIFKAEDLLPB SENLDISKEPTPPVRTLKSQSSLSGKPKERCPPNLAPLCV. MKRSSSQMSLDTISLDSMILEBQLLBSDGSDSHMFLKKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD VVVFKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLE NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSD PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHSSLI NIRKDVEAVTGSPASQTSICIGITLKRSAELALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSV MSDKRSMSVDISHIPLKUPILLFKSASDTNLQKGISFMDYL LGKISEDESGLVYKSGSGEIGSETSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDILDE SENLDISKEBTPPVRTLKSQSSLSGKPKERCPPNLAPLCV. MKRSSSQMSLDTISLDSMILEEQLLBSDGSDSHMFLEKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD VVVFRITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLR NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKN
PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLI NIRKDVEAVTGSPASQTSICIGIILRSAELALLLHPVDQA SPVSESVSPVVPDYLPTRINGDFLSKRKQISRDINRIRSV MSDRRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKLSEDESSGLVYKSGGGEIGSETSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPE SRNLDISKEETPPVRTLKSQSSLGSKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILEEQLLBSDGSDSHMFLEKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGNHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLEI NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKN
NLRKDVEAVTGSPASQTSICIGILLRSABLALLLHPVDQA SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSV MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESSGLVYKSGSGBIGSETSDKKDSFYTDSSSVL DSNILSFDSDCMONILSSTLTSKGMRTIESIFKAEDLLPE SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLEKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGNHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLRI NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKN
SPVSESVSPVVPDYLPTENGDFLSKRKQISRDINRIRSV MSDRRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESSGLVYKSGSGEIGSBTSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNBTIESIPKABELLPE SENLDISKBETPPVRTLKSQSSLSGKPKERCPPNLAPLCV. MKRSSQMSLDTISLDSMILBEQLLBSDGSDSHMFLEKGN TINYRGTABSVNAGANLQNYGETSPDAISTNSEGAQENHD VVVFKITGVNGBIDIRGEDTEICLQVNQVTPDQLGNISLE NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
MSDRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYL LGKISEDESSGLVYKSGSGBIGSETSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNETISSIFKABDLLDE SRNLDISKBETPPVTLKSQSSLSGKPKERCPPNLAPLCV. MKRSSQMSLDTISLDSMILBEQLLBSDGSDSHMFLKGN TINYRGTABSVNAGANLQNYGETSPDAISTNSEGAQENHDV VVVFKITGVNGBIDIRGBDTBICLQVNQVTPDQLGNISLR: NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVL DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPR SENIDISKEETPPVRTLKSQSSLEGKPKERCPPNLAPLCV. MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLKKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD. VVVFRITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLR. NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKN
DSNILSFDSDGNQNILSSTLTSKGNETIESIPKAEDLLPE SRNLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCV MKRSSSQMSLDTISLDSMILEEQLLBSDGSDSHMFKERGHD TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAGENHD VVVPKITGVNGBIDIRGEDTEICLQVNQVTPDQLGRISLE NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKN
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MKRSSSOMSLOTISLDSMTLEEQLLESDGSDSHMFLEKGN TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHD. VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRE NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKN
Tinyrgtaesvnaganlonygetspdaistnsegaqenhd VVVFKitgvngeidirgedteiclovnovtpdolgnislæ Nrpvgsdokavihsksspeislrfesgpgavihsllaekn
VVVFKITGVNGBIDIRGEDTBICLQVNQVTPDQLGNISLR NRPVGSDQKAVIHSKSSPBISLRFRSGPGAVIHSLLAEKN
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CHIKNFSTBFLTSSLMNIQHFLEDETVATVMPMKIQVSNT
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HHIKKMIVE
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TOUTOURTOTHOUT.DAPPINGDREPRIEDERSPEVER
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VTSMPSSMWSGQASVNPPLPGPKPSIPBEHRQAIPBSEAB EPPSATVSPGQIPBSDPADLSPRDTPQGEDMLWAIRRGVK
VTSMPSSMWSGQASVNPPLPGPKPSIPBEHRQAIPBSEABI EPPSATVSPGQIPBSDPADLSPRDTPQGEDMLNAIRRGVKI TINDRSAPRFS
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GKFFKGGGSSKSEAADSPOPEALURLRTTEEMGIKQEVILSRIEPG REALEKSHITTEVIRIMSTADULRRKERFEKQITQIDOTISTIEPG REALEKSHITTEVIRIMSTADULRRKERFEKQITQIDOTISTIEPG REALEKSHITTEVIRIMSTADULRRKERFEKQITQIDOTISTIEPG REALEKSHITTEVIRIMSTADULRRKERFEKQITQIDOTISTIEPG REALEKSHITTEVIRIMSTADULRRKERFEKQITATULTETE EQQDIAQBISEAFSGRVGFGDDFDEDEMABLEBELEQEBLIKKM THIRLPHYPSSSLIPAQPINREPGMSSTARRSRAASGRAEBEDDD IKQLAAMAT  5503  216. 654 KGVRRGGRVREDSEDSHLGYFKMSFLLFKLITSKREVQAIKSTA ERVIVLKLFGRDEDDVCLQLDDILSKTSSDLSKMAAIYLVDVDQT AVYTQYDISYIPSTVFFFNGQHMKVDYGGEDDALRSIKAVRRT SPASTIGKRFVKS  5504 58 3563 QLSFSFQAFVTFDDITVYLLQEEWVLLSQQQKELGGSNKLVAPL GPTVANPBLFRKFGRGPEPWIGSVGGGRSLLGBHFGKQMGYMG BSVGQFTRESGGSLDFPQKKAYLSHLSTGSGHIBEDMAGNRKL LKPRSIQKSWFVQFPWLIMMERQTALFCSACRRYPSIRDRRSPL LKPRSIQKSWFVQFPWLIMMERQTALFCSACRRYPSIRDRRSPL LKPRSIQKSWFVQFPWLIMMERQTALFCSACRRYPSIRDRRSPL BPGGGCAIPAWYLDCISDLRQKSITTGHSSSDINILYNDAVE SCLQDSAGGLSERVVVFPBELLYDDAVFYTERSEMGMLDKS GEDGGRAFFONKKWAVRRADTQASAADSALPGSSVBARASC CSSSICEGEGGGFRIKTRYTPRSIQRSWFGQFPMLVIDFKETKK, FCSACLERFNLHDKSSRLVRGYTGPFKVFTLKYHRVSKAHELCV NTVBIKKDTPHTALVPRISSDLAMHFPNAAYSIAVHSRPLAN DPSKILQLLQSTGTVILGKYRNRTACTQPIKTISTLKRBLLBD VRRSPCVSVLLDSTIDASEQACVGIYLTRYFKGMEVKSSYITLAP LYSSTADGYFFTUSALDELDIFFGWVGGGTGSAMLSGC GGLVEKFQEVIPQLLPVHCCAHRLHLAVVDACGSIDLWKKCDRH IRTVFKYYQSSKKINBLYGGAAPLEGBIIRKDLNAVRWASR RRTHALLJUSWPALARHLQRVVARAGQGIGRRAKCHLLIMRGFHFV VKFCHELLDFLSITAPLSEVCQKSIVLITEVNATIGRAYVALBS LRHQAGPKREEPNASPKGGRIHGICLDKLEVARGTGRAYVAVRS RRTHALLJUSWPALARHLQRVVARAGQGIGRRAKCHLLIMRGFHV VKFCHELLDFLSITAPLSEVCQKSIVLITEVNATIGRAYVALBS LRHQAGPKREPFNASPKGGRIHGICLDKLEVARGTERFOKDDI LNIARYFRCSLPTGVSSEALLBERGGLKTLAGHLPFSMLCKNAL AGGCRPFLLSKLMAVVCVPISTSCERFFKAMNITTETRATKI SNEVLNMLMMTAVNGVAVTESPERTQKPFLIDERSAABVI KQCIMBEPRELLYPITSQAPAGRA SSEVLSKRBMGGRANDNIKGSRUPPQLQMLIKRDPPAYIREFLQ QYMPKSSASARLKKBMGALVYBEPRTQKPFLIBERBAABVI KQCIMBEPRELLYPITSQAPAGRA		ļ		
REIALAKHGTONKRAALOALKRKKRPEKUPAJDIOTISTIEPO REALENSHINTEVLRINGSPAAKAMKSVIENMULNKIDDLMQEIT EQQUIAQEISRAFSCRVGFGDDFDEDELMAELEELEQEELMKKM TNIRLPNYPSSSLPAQPNRKFGMSSTARRSRAASSQRAEREDDD IKQLAAMAT  STORT KGVRRGRVRSDSEDSHLGYFKMSFLLFKLTSKKEVDQAIKSTA EKVLVLRFGRDEDDVCLQLLDDILSKTSDLSKMAAIYLJUDUQT AVYTOYVDISYIPSTVPFNGGHKVUPGGEDPALRSIKAVRRT SPASTIGEKPVNS  SPASTIGEKPVNS  SPASTIGEKPVNS  SPASTIGEKPVNS  SPASTIGEKPVNS  LEFSFQAFVTFDDITVYLLQESWVLLSQQKELGGSNKLVAPL GPIVANPELFRRFGRGPEPMIGSVOGGRSLLEHHFGKKQMGYMG EMSVQCPTRESGGELPPQKRAYLSHLSTGSGHLBGDNAGRRKL LKPKSIQKSMFVQFPWLIMNEEQTALFCSACR8YPSIRDKRSRL LKPKSIQKSMFVQFPWLIMNEEQTALFCSACR8YPSIRDKRSRL LKPKSIQKSMFVQFPWLIMNEEQTALFCSACR8YPSIRDKRSRL LKPKSIQKSMFVQFPWLIMNEEQTALFCSACR8YPSIRDKRSRL LKPKSIQKSMFVQFPWLIMNEEQTALFCSACR8YPSIRDKRSRL LKPKSIQKSMFVQFPWLIMNEEQTALFCSACR8YPSIRDKRSRL CRICKGRPGPORKWAYLSHLATGGSOGNABLLPSSREL EDTGGGGAIPAMYLDISDLGSUGGBMAELLPSSREL EDTGGGGAIPAMYLDISDLGSUGGBMAELLPSSREL EDTGGGGAIPAMYLDISDLASSAAKDHLISKHERAAPMITDDN GCHNEKGRPPORKWAVANRADIGHSHSSDLIHINLYNDAVS SCIQDESAEGLSEVPVVFEELPVVFEDVAVYFTREBMGMLDKR QKBLYRDVMRMYKELLASLGPAAAKPHLISHTSKSSEPSHVARASC CSSICEBCDGPRIKTYRPBSIQRSMFQQPHULVIDPKRTKL FCSACLBRPNIHDKSSRLVRGTTGBFWTTLKPHRUSKAHRLCV NTVBILKEDTPHTALVPBISSDLMAMMEHFFNAAYSIAVHSRPLIN DPKKILOLLQSTGTVILGKYRNRTACTQPIKYISSTLKREILBD VRNSPCVSVLLDSTGTSTSVTTLGKYRNRTACTQPIKYISSTLKREILBD VRNSPCVSVLLDSTGTSTTVSALDELDIFFRKGMVVGLGTDGSSAMLSCC GGLVERYGEVIPQLEPVALCUKANRTACTQPIKYISSTLKREILBD VRNSPCVSVLLDSTGTSTSTRUBLGGGAAPWAVGLGTDGSSAMLSCC GGLVERYGEVIPQLEPVARAGGQIGHRAKCMLKLMRGFHP VKPCHFLLDFLSIYRPLSEVCQKEIVLITKVWATIGRAYVALBS LRIQAGPKREBENASPKOGILHGICLKLBAVBORFQADRRTV LTGIBYLQQRPDADRPPQLKMMEVFDTMAWPSGIELASPCNDDI LNILARYFRCSIDFTMSSELLBEWLGIKTIAGHLFFRHICTANL AGGCRPPLLSKIMAPVVCVPITSTCGRGFKAMMRIRTDRRTKL SNEYLMMLMMTAVNGVAVTEVDPQPAIGHWITTSSGRPSHVYT CAQVPARSPASARLKKEBMGALYVEEPTQKPPILDSRRAABVL KOCIMSPPERLLYPHTSQPAPGRB.  S505 3312 1219 NCSPRSISAAKGNRNNKIGDSNLPQLQMLKILRDPPAYIERFLQ QYMYKSNVEIFKLQPNKPSKELBELVMFMQQISHCYPEYLSNF	5502	1 3	824	
REALERSHTNTEVLENMERAAKAMKSUHENMULNKTIDLIMGEIT EQQDIAGEISBAPSORVGFGDDFDBBELMAELBELEGEELNKM TNIELPNVPSSSLPAQPRRKEGMSTARBSRAASGRAEBEDDD IKQLAAMAT  SCHAMAT  KURRIGEWASDS BOSHLGYFKMSFLLPKLITSKKEVDQAIKSTA EKULVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT AVYTQYFDISY1PSTVPFFBAQEHKVDYGGEDPALRSIKAVRRT SPAGTIGEKPVAS  SPAGTIGEKPVAS  S504  58  3563  QLSFSPQAPVFPDDITVYLLQBEWVLLSQOQKELGGSNKLUAPL GPYVANPELFRKFGRPPEPBUGSVQQGSLLBHPGKKOMGYMG EMSVQCPYTESSQSLPPQKKAYLSHLSTGSGHIEBDMAGRARKL LKPRSIQKSMFVQFPWLIMMERQTALFCSACRRYPSIRDRKSRL LKPRSIQKSMFVQFPWLIMMERQTALFCSACRRYPSIRDRKSRL LKPRSIQKSMFVQFPWLTMFERGTALFCSACRRYPSIRDRKSRL LKPRSIQKSMFVQFPWLTMFERGTALFCSACRRYPSIRDRKSRL LKPRSIQKSMFVQFPWLTMFERGTALFCSACRRYPSIRDRKSRL LKPRSIQKSMFVQFPWLTMFERGTALFCSACRRYPSIRDRKSRL LKPRSIQKSMFVQFPWLTMFERGTALFCSACRRYPSIRDRKSRL CREATERPHLAUGLSPROKENTOLHSSDLINLLYNDAVS SCIQDPSAGGLSEBVPVFEELLYVPEDUAVYFTEEBEMGHLDKR QKKLYRDWRMMYBLLASLGPAAKPDLISKLERRAADMINDPW GPXMGKGRPPGRNKMVAVRRADTQASAADSALLPGSPVBRRASC CSSICEGEGGRRIKKTYRPRSIQESWFGQPPMLVIDPKETKL FCSACLERPHLIDKSSRLVRGYTGPFKVETLKYBBVSKAHRLCV NTSHKERDTPHTALVPRISSDLAMMSHFFNAAYSIAVHSKPLIN DFEKILQLLQSTGTVILGKYRNRTACTQPIKYISSTLKRBILED VRNSPCVSVLLOSSTDASEGACVGIVILTKYRMEVKSYTITLAP LYSSTADGFFTUSALDELDIFFRRGGWVGLGTDSSAMLSCR GGLVERPOSVIPOLLPVHCVAHRLHLAVVDACGSIDLVKKCORH IRTVFKFYQSSNKRIMELQSGAAPLEGIIRLKGLMAVRWVASR RRTLHALLVSWPALARHLQRVARRAGGGIGHRAKCKLKLMRGFHF VKPCHFLLDFLSITRPLSEVCQKEIVLITKVNATLGRAYVALBS LRIQAGPKREBFNASPKORLHGICKLKLENSPAGRADRATHV VKPCHFLLDFLSITRPLSEVCQKEIVLITKVNATLGRAYVALBS LRIQAGPKREBFNASPKORLHGICKLGLKATLAGHLPFSMLCKNAL AGGCRPPLLSKLMAVVCVVPISTSCERFFKAMNTRITTERTKK SNEVLNMLMMTAVNGVAVTESTGCRFFKAMNTRITTETRTK SNEVLNMLMMTAVNGVAVTESTGCRFFKAMNTRITTETRTK SNEVLNMLMMTAVNGVAVTESPDPQDAIGHWYLTSSGRPSHVYT CAQVPARSPASRARLKRBMGALVVEEPFTQKPFLIDERRAABVI KQCIMBPPSELLYPITSQPARGEN  S505  3312  1219 NGSPRISAAKKGNRNNKKDSNLPQLQMLKRDPPAYIBRFLQ QYMYKSNVEIFFLQDBLRKELBELUWFMAQISHCYPEYLSNF	i	j	1	
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THIRLPHVPSSIPAQPNRKPGMSSTARRSRAASSQRAEREDDD IKQLAAMAT SCHORTINGRAWAT KGYRRGRVRSDSEBSHLGYFKMSFLLPKLTSKKEVDQAIKSTA RKVLVLRFGRDBDPVCLQLDDLLSKTSSDLSKMAALTLVDVDQT AVYTOYFDISYIPSTVFFFNGQMKVDYGGEDPALRSIKAVRIT SPAGTLGEKPVKS  5504 58 3563 QLSFSPQAPVFPDITTVLLQREWVLLSQQQKELGSNKLVAPL GPTVANPBLFRKFGRGPBPWLGSVOGQRSLLEHHPGKKQMGYMG EMSVQCPTRESGQSLPPOKKAYLSHLSTGSGHIBGDWAGRNRKL LKPKSIQKSMFVQFFWLLNNERQTALFCSACREVPSIRDKRSRL LKPKSIQKSMFVQFFWLLNNERQTALFCSACREVPSIRDKRSRL LKPKSIQKSMFVQFFWLLNNERQTALFCSACREVPSIRDKRSRL LKPKSIQKSMFVQFFWLLNNERQTALFCSACREVPSIRDKRSRL LKPKSIQKSMFVQFFWLLNNERQTALFCSACREVPSIRDKRSRL SCTQDPSAEGLSEEVPVVFBRLPVVFDVAVYFTREBMGMLDKR GCHANGKGPPGNKKWVAVBADTQASAADSALLPGSSPAEL EDFGGCKAIPAWALDCIBDLRQRETTDGIHSSDINILYNDAVE SCTQDPSAEGLSEEVPVVFBRLPVVFBDVAVYFTREBMGMLDKR GKLYRDVMRMNYBLLASIGPAAKPDLISKLERRAAPMIKDEN GCHANGKGPPGWKKWVAVBRADTQASAADSALLPGSPVBRASC CSSSICEBGDGPRIKRTYRPRSIGSSWFGQPPMLVIDPKETKL FCSACLERINLHUKSSRLVRGYTGPFKVETLKYBRVSKAIRLCV NTUBILKBTPHTALVPBISSDLMAMMRHFWAAXSIAYHGRPLN DPEKILOLLQSTGTVILGKYRMARTCTQPFKYLBSTLKRRELND VRISPCVSVILLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFFTUSALDBLDIP FRREDWVGLGTDGSSAMLSCR GGLVERKQEVIPOLLPWHCVARRACQVGRAKCKLKIMRGFHF VKPCHELDPLSTYRPLSSVCQKEIVLTTEVMATTGRAVVALSR RRTHALLUSWPALARHLQRVARAGGGIGRAKKCKLKIMRGFHF VKPCHELDPLSTYRPLSSVCQKEIVLTTEVMATTGRAVVALSR RRTHALLUSWPALARHLQRVARAGGGIGRAKKCKLKIMRGFHF VKPCHELLDFLSTYPLSSEDLGKENGLTYTIGRAVVRIS LRRQASPKBEBFNASPKDGRIHGICLDKLEVAPGRFQADRRRTV LTGIBYLQQRPDADRFPQLKNMKYPDTWARPSGLELASPGNDDI LNIARYFBCSLPTGYSPEALLBEWLGLKTIAQHLPFSMLCKNAL AQUCRFPLLSKLMAVVVCVPISTSCCERGFKAMMRIRTDERKKL SNEVLMMLMMTANNGVAVTEYNPQPAIGHWIITSSGRRFSHVYT CAQVPARSPASALKREBMGALYVEPFTOKPPILFSRAAPUL CQVPARSPASARLKREBMGALYVEPFTOKPPILFSRAAPUL CCGIMPEPERLLYPHTSQEADMS  5505 3312 1219 NCSPRSLSAAKMSNRNNNKLPSDNLPQLONLIKRDPPAYIERFILG QYMHYKSNVEIFFLQPNKPSKELAELVMFNAQISHCYPPYLSNP PQEVKDLLSCNITYLDPDLRMYPCKALLLLARKMLINPSSLLEL	ì	ł	i	
1 IKQLAAMAT  5503  216. 654 KGVRRIGKUNESEDSHLGYFKMSFLLEKLTSKEVDQAIKSTA REVLIVLIKFGREBDPVCLQLDDILSKTSSDLSKMAAIYI.VDVDQT AVYTQYFDISYIPSTVPFFNGQHMKVDYGGEDPALRSIKAVRRT SPAGTIGEKRVES  5504  58 3563 QLSFSFQAPVTPDDITVYLLQEEWVLLSQQQKELGGSNKLVAPL GPTVANPELFRKFGRGPEPWLGSVQQRSLLEHHPGKKQMGYMG EMSVQCPTEESGGSLPPQKAXISHLSTGSCHIEDDMAGRNEKL LKJRESIQKSMFVQFPWLIMNERQTALFCSACREWSIRDRAKGRNEKL LKJRESIQKSMFVQFPWLIMNERQTALFCSACREWSIRDRAKGRNEKL DPFGDVLASPEPLFTADCPIFTPCFLGGFDEMAELLPSSRAEL BUPGGDAIPAWLDCISDLRGKTTDGIHSSSDINILIVANDS SCIQDESAEGLSEEVPVVFEELPVVFEUPAVYFTREBMGMLDKR QKKLYRDVMRMNYBLLASIGPAARFDLISKLERRAAPWINDRN GPXMGKRPPGRKKWVAVRRADDASADSALIHGSPVPARASC CSSSICEEGGGPRRIKRTYRPRSIQRSWFQQFPWLVIDPKRTKL FCSACTERPRIHNKSSRLVRGTTGFFKWTLKYHRUSKAIRLCV NTVBIKEDTPHTALVDEISDLMAMMEHFMAAYSLAYHSRPLM DPEKKILOLLQSTGTVILGKYRNRTACTQPIKYLSETLKREILBD VRRSPCVBVLLDSSTDASSQACVGIYIRIFRQMBVKBSYTTLAP LYSSTADGYPETIVSALDELDIPFRRGGUGHRAKCMLKLMRGPHF WKPCHFLLDFLSTYRPLSEVQKELVLITEVNATIGRAYVALSS RRTLHALLVSWPALARHLQRVARAGGIGHRAKCMLKLMRGPHF VKPCHFLLDFLSTYRPLSEVQKELVLITEVNATIGRAYVALSS LRHQAGFKERFMASPKOGRLHGICLDKLEVABGRFQADRRTV LTGIEYLQQRFDADRPPQLKNNEVPDTMAWPSGTELASPGNDDI LNILARYFECSLPTGYSEPLIKBEMLGILTILGHLPFSMLCKNAL AQHCRPPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNRVLMMLMMTAVNGVAVTEVDPQPALQHWVITSSGRRFSHVVT CAQVPARSPASARLKREMGBATYVEEPRTQKPPILFSRRAAPVL KDCIMEPPERLLYPHTSQEAPGMS  5505 3312 1219 NGSPRSLSAKKBNRNNNININIDERNPQLIALIKRDPAYIEEFLQ QYMHYKSNVEIFRLQPNRPSKELAELVMFNAQISHCYPEYLSNP PQSVKDLLSCNITVLDPDLRMTPCKALTLLARKMLINPSSLLLEL	j			EQQDIAQEISRAFSQRVGFGDDFDRDELMABLEELEQEBLNKKM
216. 654 KGVRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA ERVIJVILEGERDEPVCLQLDD ILSKTSSDLSMAAITLUDVDQT AVYTOYDISTYPENVEFMSQHMKVDYGĞEDPALRSIKAVRIT SPASTLGEKEVNS  5504 58 3563 QLSFSRQAFVTFDDITVYLLQESMVLLSQQKELGSNKLVAPL EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHI EGDMAGRNRKL LKPRSIQKSMFVQFPMLIMMEEQTALFCSACREYPSIRDKRSEL LKPRSIQKSMFVQFPMLIMMEEQTALFCSACREYPSIRDKRSEL LKPRSIQKSMFVQFPMLIMMEEQTALFCSACREYPSIRDKRSEL LKPRSIQKSMFVQFPMLIMMEEQTALFCSACREYPSIRDKRSEL LKPRSIQKSMFVQFPMLIMMEEQTALFCSACREYPSIRDKRSEL LKPRSIQKSMFVQFPMLIMMEEQTALFCSACREYPSIRDKRSEL LKPRSIQKSMFVQFPMLIMMEEQTALFCSACREYPSIRDKRSEL LKPRSIQKSMFVQFPMLIMMEQTALFCSACREYPSIRDKRSEL LKPRSIQKSMFVQFPMLIMMEQTALFCSACREYPSIRDKRSEL LKPRSIQKSMFVQFPMLIMMEQTALFCSACREYPSIRDKLSKLSC SCHOLDSABGLSERVPVVFRBLPVVFBDAVYFTREMGHLDKR QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAPWIKDPM GPYMKMGRPPGNRIKMVAVRRADTQASAADSALLPGSPVRARASC CSSICLEGEGGPRRIKRTYRPRSIQRSWFGQYPMLVIDFMRTKL FCSACIERPNLHDKSSRLVRGYTGPFRVFTLKYHRVSKAIRLCV NTVEIKEDTPHTALVPSISDLMANMEHFFNAAYSIAYHSRPIL DPEKILQLLQSTGTVILGKYXRNETACCQPFRLVKTHSTLKREILBR VRNSPCVGVLLDSSTDASEQACVGIYIRYFKQMVGKESYTTLAP LYSETADGYFETIVSALDELDIFFRGWVGLGTTGSAMLSCR GGLVEKFQEVIPQLLPVHCVANRIHLAVVDACCSTDLVKKCORR IRTVFKPYQSSNKRLNELQEGAAPLEQBIIRLKMRGFHF VKPCHFLLDFISTYPLISEVQCKEIVLITKVNATIGGRYVALBS LREQAGPKREEFFNASPKDGRLHGICLDKLEVABQRFQADRRTV LTGIETLQQRFDADRP PQLKMMSVFDTMANFSGIELASFONDDI LNILARYFBCSLJETYPISEVQCKEIVLITKVNATIGGRYVALBS LREQAGPKEEFFNASPKDGRLHGICLDKLEVABQRFQADRRTV LTGIETLQQRFDADRP PQLKMMSVFDTMANFSGIELASFONDDI LNILARYFBCSLPTAYSEBEALLEBMLGIKTIAGHLPFMLCKNAL AQUCRPPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNSVIMMIMTANNGVAVTEYDPQPATQHVITTSSGREPSHVTT CAQVPARSPASARLKKERMGALYVEEPRTQKPPILLPSRAAEVL KCCIMEPPERLLYPHTSQEAPGMS  5505 3312 1219 NCSPRSIAAKKGNRNNNKLDPSNLPQLQNLIKRDPPAYLERFIQ QYMYKSNVEIPKLQPNKPSKELAELVMFMAQISHCYPEYLSNP PQSVKOLLSCCNHTYLDPDDRMTPCKALLLKRNNLLNPSSLLEL	l	ì	ì	TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEREDDD
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AVYTOYFDISYIPSTVFFFRQHMKVDYGGEDPALRSIKAVRT SPASTIGERCVNS  QLSFSPQAPVTPDDITVYLLQEEWVLLSOQQKELGSNKUVAPL GPYVANPELFRKFGRGEPBWLGSVGGQRSLLEHHPGKKQMGYMG EMSVQGFTRESGQSLPPQKKAYLSHLSTGSGHI BGDNAGRNRKL LKPRSIQKSMFVQFPWLIMNEGTALFCSACREYPSIRDKRSRL LKPRSIQKSMFVQFPWLIMNEGTALFCSACREYPSIRDKRSRL LKPRSIQKSMFVQFPWLIMNEGTALFCSACREYPSIRDKRSRL DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL EDPGGGAI PAMYLDCISDLRQKETTDGIHSSSDINILINNDAVE SCTQDPSAGGISBEWPVERLPVVFERWAVVFTRERSMGHIDKR QKELYRDVMRMNYBLLASLGPAAAKPDLISKLERRAAPWIKDPN GPKMGKGPPGNKKMVAVRRADTQASAADSALLPGSPVBRARSC CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL PCSACLERPNIHDKSSRLVRGTTGPFKVETLKYHRVSKAHRLCV NTWEIKBDTPHTALVPBISSDLMAMMEHPFNAAYSIAYESPLM VRMSPCVSVLLDSSTDASEQACVGIYIRFKQMEVKESYITLAP LYSETADGYPETIVSALDELDIPFRRPGWVGLGTDGSAMLSCR GGLVERKQEVIPQLLPVHCVARRILLAVVDACGSIDLVKCCDRI IRTVFKPYQSSNKRINBLQEGAAPLBQBIIRLKDLMAVRWASR RRTHALLUSWPALARHLQRVARAGGQIGHRAKCKLKLMRGFHP VKPCHFLLDFLSIVRPLSEVCQKEIVLITWANTIGRAYVALES LENQAGPKEEFNASPKDGRHGICLDKLEVABCRFQAVRALES LENQAGPKEEFNASPKDGRHGICLDKLEVABCRFQAVRALES LLEQAGPKEEFNASPKDGRHGICLDKLEVABCRFQAVRALES LLEQAGPKEEFNASPKDGRHGICLDKLEVABCRFQAVRALES LLEQAGPKEEFNASPKDGRHGICLDKLEVABCRFQAVRALES LNLARYFCSLPTGYSEEALLEEWLGLKTIQHLPFSMLCKNAL AQHCRPPLLSKLMAWVVCVPISTSCCERGFKAMNTIRTDERTKL SNEVLNMLMMTAVNGVAVTEUPDQPAIQHWYITSSGREPSHVYT CAQVPARSPASARIKKEMGALYVEEPRTQKPPILDSREAABCU, KDCIMEPPERLLYPHTSQEAPGMS  5505 3312 1219 NGSPRSLSAAKMARNNNKLDENLPQLQNLIKRDPPAYIEFFLQ QYMYKSNVZIFKLIQNLOPPLAYLEFFLQ QYMYKSNVZIFKLAELVWFMAQISHCYPEXLSEP		}	}	
SPAGTLGEKPVNS  5504  58  3563  QLSFSPQAPVTFDDITVYLLQEEWULLSQQQKELCGSNKLVAPL GPYVANPBLIPKKPGRGPEPWLGSVOGQRSLLRHIPGKKQMGYMG EMEVOGPTRESGQSLPPQXKAYLSHLSTGSGHIBGDMAGRNRKL LKPKSIQKSMEVQFPWLIMNERQTALFCSACRRYPSIRDKRSRL 1EGYTGPFKUETLKYHAKSKAHMPCVNALAARDPIWAARFRSIR DPPGDULASPEPLETADCPIFYPEGFLGGFDSMAELLPSSRAEL EDPGGGGAIPAMYLDCISDLRQKETTDGHSSSDINILYMDAVE SCIQDFSAEGLSEEVPVVFEULAVYFTREBMGMLDKR GPKMGKGRPPGNKMVAVRRADTQASAADSALLPGSPVBARASC CSSSICEGGGPRIKKTYRPRSIGRSWEGGPPMLVIDPKRTKL FCSACIERPMIHDKSSRLVRGYTGFFKVETLKYHRVSKAIRLCV NTVEIKEDTPHTALVPRISSDLMANMBHFFNAAYSIAYHSRPLN DPSKILQLLQSTGTVILGKYNNRTACTQPIKYISBTLKREILBD VRNSPCVSVILLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYPETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVERKQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKCORR IRTVFKPYQSSNKRLNELQEGAAPLEGBIIRLNDLNAVRWASR RRYTHALLVSWPALARHLQRVARAGGQIGHRAKGLLKLMRGFHF VKFCHFLLDFLSTYRPLSEVCQKEIVLITEVNATLGRAYVALES LRRQAGFKEEFFNASPKDGRLHGICLDKLEVABGRQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFENDDI LNIARYFECSLPTAYSEEALLEBWLGLKTIAQHLPPSMLCKNAL AQHCRPPLLSKLMAWVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGREPSHVYT CAQVPARSPASARILKRENGALYVEEPFTQCKPPILFSRRABEVL KDCIMEPPERLLYPHTSQEAPGMS  5505 3312 1219 NGSPRSLSAAKMSRNNNKLDENLPQLGNLIKRDPPAYIEFFLQ QYNHYKSNVEIFFKLQPNKPSKELAELVWFMAQISHCYPEYLSSH PQSVKDLLSCNHTVLDDDLRMTFCKALLTLLRKNNLINPSSLLEL		1	i	
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GPTVANPELFRKPGRGPEPWLGSVOGQRSLLKHHPGKKOMGYMG EMSVOGPTRESGOSLPPOKRAYLSHLETGSSHIEDDMAGRNEKI, LKPRSIQKSWFVQFPWLINNEGYTALFCSACREYPSIRDRESRL LKPRSIQKSWFVQFPWLINNEGYTALFCSACREYPSIRDRESRL LEGYTGFYKVETLKYHAKSKAHMPCVNALAARDPIWAARPRSIR DPPGDVLASPEBLFTADCPITYPEGPLGGFDSMAELLPSSRAEL EDPGGDGAIPAMYLDCIEDLRQKEITDGIHSSGDINILYNDAVE SCTQDESAEGLSERVPVVFELEVVFBUVAVYFTREBMOMLDER QKELYRDVMRMNYBLLASLGPAAAKPDLISKLERRAAPWIKDPN GPKMIKGRPPONKKWVAVRRADTQASAADSALLPGSPVBARASC CSSSICEEGDGPRIKRTYRPSIQRSWFGGPPBLVIDPRRTYL PCSACIERPNIHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLCV NTVBIKRDTPHTALVPBISSDLMANMEHFFWAAYSIAYHBRPLM DPEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILBD VRRSPCVBVLLDSSTDASSQACVGIYLTFFKQMBVKESYITLAP LYSSTADGYPETIVSALDELDIPFRRPGWVGLGTDGSAMLSCR GGLVEKFQCVIPQLSTALDELDIPFRRPGWVGLGTDGSAMLSCR RRTHALLVSWPALARHLQRVARAGGQIGHRAKGKLKLMRGPHP VKPCHFLLDFLSIYRPLSSVCQKEIVLITEVNATLGRAYVALES RRTHALLVSWPALARHLQRVARAGGQIGHRAKGKLKLMRGPHP VKPCHFLLDFLSIYRPLSSVCQKEIVLITEVNATLGRAYVALES LRHQAGPKHEBFNASPKJGRIHGICLDKLEVABQRFQADDRRTV LTGIBYLQQRPDAURPPQKMMSVFDYMAWPSGIBLASPGNDDI LNLARYPBC9LPTGYSEBALLEBWLGIKTIAQHLPFSMLCKNAL AQHCRPPLLSKIMAVVVCVPISTSCCERGFKAMNIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDDPQPAIQHWYLTSSGREPSHVYT CAQVPARSPASARLKREMGALYVEEPRTQKPPILDSRRAABVL KDCIMEPPERLLYPHTSQEAPGMS  5505 3312 1219 NGSPRSLSAAKMSNRNNNINGLSBLLVWFMAQISHCYPEYLSMP PQBYKDLLSCNHTYLDDPDLRMTPCKALILLERNKMLINPSSLLEL	F-53	ļ <u></u>	200	
EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIBGDWAGRNRKL LKPRSIQKSWPVQFPWIIMMEEQTALFCSACREYPSIRDKRSRL LKPRSIQKSWPVQFPWIIMMEEQTALFCSACREYPSIRDKRSRL IEGYTGPFKVETLKYHAKSKAHMFCVNALAARDPIWAARFRSIR DPPGDVLASPBELFTADCPIFYPPGELGGFDSMAELLPSSRAEI, EDPGGDCAIPAWYLDCISDLRQKEITDGIHSSSDINILYNDAVE SCTQDESABGLSERVPVVPEBLPVVFDWAVYFTREBWGMLDKR QKELYRDVMRMNYBLLASLGPAAAKPDLISKLERRAAPWIKDPN GFMGKGRPPGNKKWAVRRADTQASAADSALLFGSPVBARRSC CSSSICEEGDGPRIKRTYRPRSIGRSWFGQPPWLVIDPKRTKL PCSACIERPINHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLCV NTTUSIKEDTPHTALVVPSISSDLMAMMEHFFNAAYSIAYHSRPIN DPEKILQLLQSTGTVILGKYRNRTACTQPIKYLSETLKREILED VRMSPCVEVLLDGSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFFTIVSALDELDIPFRRPGWVGLGTDGSAMLSG GGLVEKFQEVIPQLEPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKPYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVABAGGQIGHRAKCKLKLMRGFHF VKFCHFLLDFLSIYEPLSEVCQKEIVLITEVNATIGRAYVALES LRHQAGPKREBENASPKDGRILHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVPDTMAWPSGIELASFGNDDI LNILARYFRCSLPTGYSEBALLEBWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMRIRTDERTKL SNEVINNILMMTAVNGVAVTEVDPQPAIGHWILTSSGREPSHVYT CAQVPARSPASARLRKEBUGALYVEEPRTQKPPILPSREAAEVL KOCIMEPPBERLLYPHTSQEAFGMS  5505 3312 1219 NCSPRSLSAAKMSNENNNINLEDNLPQLQNLIKRDPPAYIEEFLQ QYMHYSNVEIFRLQPNKPSKELAELVMFMAQISHCYPEYLSNF PQEVKDLLSCNHTYULDPDLRMTFCKALLILLERKNLINPSSLLEL	5504	58	3563	1
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SCIQDPSAEGLSEEVPVVFBELPVVFBUVAVYFTREBMGMLDKR QKELYRDVMRMNYBLLASLGPAAAKPDLISKLERRAAPWIKDPN GFRMGKGRPPGNKKWAVRBADTQASAADSALLPGSPVBARASC CSSSICEEGGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIBRPNIHDKSSRLVRGTTGPFKVETLKYHBVSKAHRLCV NTVEIKEDTPHTALVPBISSDLMANMBHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNTTACTQPIKYISBTLKREILBD VRMSPCVBVILDGSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFFIIVSALDELDIPFRKPGWVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCORH IRTVFKPYQSSNKRUNELQEGAAPLEQBIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAKAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATIGRAYVALES LRHQAGPKREEFNASPKDGRLHGICLDKLEVAEQRFQADRERTV LTGIBYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNIARYFBCSLPTGYSEEALLEBWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQYPARSFASARLKKEMGALYVEEPRTQKPPILPSRKAABVL KOCINEPPERLLYPHTSQEAPGMS  1219 NCSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAYIEBFLQ QYMHYKSNVEIFKLQPNKPSKELAELVWFMAQISKCYPEYLSNF PQEVKDLLSCNHTVLDPDLRMTPCKALILLENKNLINPSSLLEL	ĺ	1		DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL
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				POEVKOLLSCNHTVLDPDLRMTFCKALILLRNKNLINPSSLLEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid residue of	P-Proline, Q-Glutamine, R-Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	1 1 1	ļ — — — — — —	YTMLRDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACFSK
Į.			VTKILVAALTFFIGKDEDEKQDSDSESEDDGPTARDLLVQYATG
1			KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPODFA
1			EKLLKQLECCKERFEVKMMLMNLISRLVGIHELFLFNYYPFLQR
I	1	{	FLOPHOREVTKILLFAAQASHHLVPPEIIQSLLMTVANNFVTDK
			NSGEVMTVGINAIKRITARCPLAMTERLLQDLAQYKTHKDKNVM
ŀ			MSARTLIHLFRTLNPQMLQKKFRGKPTEASIBARVQBYGBLDAK
			DYIPGARVLEVEKERNAKNDEDGWESISLSKREDADGRWIDVQH
l	ļ		SSDEBQQEISKKLNSMPMBERKAKAAAISTSRVLTQBDFQKIRM
l			AQMRKELDAAPGKSQKRKYTEIDSDEEPRGELLSLRDIERLHKK
1			PKSDKETRLATAMAGKTDRKBFVRKKTKTNPFSSSTNKKKKKQK
5506			NFMMMRYSQNVRSKNKRSFREKQLALRDALLKKKRNK
5506	1	1531	FRGDLCGQRGGSAPGEGGSSAWPAPAHPLPERERREALCPGRS
1			CSGGGGETPGTTPVWSPLEGGGDRELRPNPYVRFPYRWWAVVV
1			LAAFPSLGAGGETPEAPPESWTQLWFFRPVVNAAGYASFMVPGY LLVQYFRRKNYLETGRGLCPPLVKACVPGNEPKASDEVPLAPRT
1			EAAETTPMWQALKLLPCATGLQVSYLTWGVLQERVMTRSYGATA
1			TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY
ŀ	·		SFASLSNVLSSNCQYRALKFVSFPTQVLAKASKVIPVMLMGKLV
I			SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL
ł			LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL
l .			LEQGALLEGTRFMGRHSRFAAHALLLSICSACGQLFIFYTIGQF
[			GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
5507			LRVYARGRLKQRGKKAVPVE9PVQKV
3507	3704	1271	PROTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK
1	· —		VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACKKAGFK
}			CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVVRRVDREELSVMPPISAGFTRRYVENPNIMACY
]	İ		NELLQLEFGEVESQLKLRACNSVFTALENSEDAIEITSEDRFIQ
1			YANPAPETTMGYQSGELIGKELGBVPINEKKADLLDTINSCIRI
1			GKEWQGIYYAKKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC
}			NGNNKAEKISECVQSDTHTDNQTGKHKORRKGSLDVKAVASRAT
			EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA
			LORVLEILRTTELYSPOFGAKODDPHANDLVGGLMSDGLRRLSG
l i	Ì		NBYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENERYWDFDI
			PELEAATHNEPLIYLGLEMFARFGICEFLHCSESTLESWLQIIB
			ANYHSSNPYHNSTHSADVIHATAYFISKRRIKBTLDPIDEVAAL
•	j	,	IAATIHDVDHPGRTNSFI.CNAGSELAILYNDTAVLESHHAALAP
			QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KPVNSINKPLATLBENGBTDKNQBVINTMLRTPENRTLIKRMLI
<b>(</b>			KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV
ł i	ļ		FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF
<u> </u>			KYWKGLDEMKLRNLRPPPB
5508	1151	691	LSSVPSRRSASMFAVGCSMGPFLHYWYLSLDRLPPASGLRGFPN
	1		VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGRSCQELREKPW
	1		EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL
			KYRSPVPLTPPGCVALDTRAD ·
5509	1238	619	RKSRGCONALSASGPAAAAAAIMVRKLKFHEQKILKQVDFLNWE
			VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP
1	1	İ	RRDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR
	}		LPTVLLKLRMAQHLQAAVAFVBQGHVRVGPDVVTDPAFLVTRSM
5510	96	1365	RDFVTWVDSSKIKRHVLEYNEERDDFDLEA
3310	50	1195	PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM
		j	AEGEROPPPDSSEEAPPATONFIIPKKEIHTVPDMGKWKRSQAY
	ļ		ADYIGFILTUNEGVKGKKLTFEYRVSEAIEKLVALINTLDRWID
. 1	1	ł	ETPPVDQPSRFGNKAYRTWYAKLDERAENLVATVVPTHLAAAVP
,	ļ.	J	EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI
ł	l		WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT
	}	j	GPFAEHSNOLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF
<u> </u>			KFGSLLPIHPVTSG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
30:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ł	\=possible nucleotide insertion)
5511	276	1980	KLSRVLNLPPENLITSISAVPISQKBEVADFQLSVDSLLBKDND
1		1	HSRPDIQVQAKRLAEKLRCDTVVSBISTGQRTVNFKINRELLTK
l			TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEF9SPNVAKKFHVG
: 1		'	HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL
		i	FGYBEKLQSNPLQHLFEVYVQVNKBAADDKSVAKAAQBFFQRLE
i 1		}	LGDVQALSLWQKFRDLSIEBYIRVYKRLGVYFDEYSGESFYREK
, ,	ļ	1 .	SQBVLKLLESKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT
i 1		1	SLYATRDLAAAIDRMDKYNFDTMIYVTDKGQKKHFQQVFQMLKI
1		}	MGYDWAERCQHVPFGVVQGMKTRRGDVTPLEDVLNEIQLRMLQN
		\	MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR
1 1	}		VFQSRGDTGVPLQYTHARLHSLEETFGCGYLNDFNTACLQEPQS
		1 .	VSILQHLLRFDEVLYKSSQDFQPRHIVSYLLTLSHLAAVAHKTL
			QIKDSPPEVAGARLHLYKAVRSVLANGMKLLGITPVCRM
5512	120	1015	DPSLLLTITVTGVTVLVLVLKSMNSRRRBPITLQDPEAKYPLPL
			IEKEKISHNTRRFRFGLPSPDHVLGLPVGNYVQLLAKIDNELVV
1 1	}		RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK
. !			IGETIFFRGPRGRLFYNGPGNLGIRPDQTSEPKKTLADHLGMIA
1 1	}		GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE
	i	·	RIARTHPDOFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK
		1	STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWKLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPPPEPSSFPS
1 55.25	[ ~		PPTSRGGPGSRDTMSDSEERSQDRQLKIVVLGDGASGKTSLTTC
, ,	}		FAORTPGKOYKOTIGLDFPLRRITLPGNLNVTLQIWDIGGOTIG
1 1	Ì		GKMLDKYIYGAQGVLLVYDITKYQSFENLEDWYTVVKKVSEESB
1 1	}		TOPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG
1	1	]	DSVFLCFQKVAABILGIKLNKABIEQSQKVVKADIVNYNQEPMS
(	[ *		RTVNPPRSSMCAVQ
5514	1295	449	VNRPSWIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKOKRT
3322			CYLGSKTLFYRLEILEGITIVGMALTGMAGEQFIPGGPHLMLYD
1 1	1	ì	YKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSLTKL
	1		MLSNALFVEAPIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFL
(	ł	1	EFLVRNNVLLELLR9SLILLQGSWFFQIGFVLYPPSGGPANDLM
		] .	DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS
( )	<u>'</u>		EVGLLKNABREQESEREM
5515	1572	260	PVRLVGRGDCDPLLSVCLTTMPLYEGLGSGGEKTAVVIDLGEAP
ا کندو			TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEBLYSYL
, ,	}	}	KRFIHILYFRHLLVNPRDRRVVIIBSVLCPSHPRETLTRVLFKY
	]	1	PEVPSVILAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP
		(	VINCWGALPIGGKALHKBLETOLLBOCTVDTSVAKEQSLPSVMG
	1	]	SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP
[	[	1	NVDYPLDGEKILHILGSIRDSVVBILFEQDNEEQSVATLILDSL
	I	Į	IOCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY
			KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE
}	1		YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK
CE12	3	735	NSREPPOAGPGPSPRKSPTASSFLFPWRPLASSFWGAQGAQES
5516	( 3	( '35	IKAMWRVPGTTRRPVTGESPGMHRPBAMLLLITLALLGGPTWAG
<b>l</b> 1	l .	1	KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW
	1		DAKTGYTGEALGCHATCEALTGURGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
] 1	Ì	]	
1	1		YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY
	}	<del> </del>	PLEEPTTEPPVNLTYSANSPVCR ·
5517	246	499	SBIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA
			TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK
5518	3	1375	DAWADAWYRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMBA
[	1	<b>\$</b>	FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP
1	1	1	EPRYVANMHGDETVGRBLILHLIDYLVTSDGKDPBITNLINSTR
,	1		IHIMPSMNPDGFBAVKKPDCYYSIGRBNYNQYDLNRNFPDAFBY
·	L		
		1	NNVERQPETVAVMKWLKTETPVLSANLHGGALVAGYPFDNGVQA
			TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	
NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	) amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	1 1		HICPYRTNKYGEYYLLLLPGSYIINVTVPGHDPHITKVIIPEKS
1		1	QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT
	L		KPSLFLFLVSLLHIFFK
5519	87	477	IKSKLNQQVEVQESEWRLTEAKGPTMGKBSGWDSGRAAVAAVVG
			GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA
j			AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS
5520	117	943	PTEGROKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYTFLNYYI
1			SQEGKDEVKPKILANGARWKYMTLLNLLLQTIFYGVTCLDDVLK
1			RTKGGKDIKFLTAFRDLLFTTLAPPVSTFVFLAFWILFLYNRDL
i	]	1	
	Í	[	IYPKVLDTVIPVWLNHAMHTPIPPITLABVVLRPHSYPSKKTGL
	1		TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLAAPFSLS
1	i	[	YVFIASIYLIGEKLNHWKWVSVQILQRWRLESVGICFQWPDWKS
		<u></u>	PAKHQLVKNIR
5521	546	911	KILNMQKSCERNEGKPQNMPKAERDRPLEDVPQEAEGNPQPSEE
1	1	}	GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDELER
			LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
5522	1224	637	GSRPLGQRSREKMWVPGYGSLIWKVD5PYQDKLVGYITNYSRRP
			WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK
) .	ļ	j	AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG
1	l	ļ	PAPLEDIAEQIFNAAGPSGRNTEYLYELANSIRNLVPEKADEHL
5523			FALRKLVKERLEGKQNLNCI
5523	3	1280	SKCKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG
	•		KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELBILQBIE
ł			HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV
1			RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI
1 1			ATIIKDGBRATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV
			GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM
1	1		VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSRKRVEPG
1 1			FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRD
1			SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES
			RDAAEPVEDEAERSALPMCGPICPSAGSG
5524	85	2318	
3324	0.5	2310	RERERDHRPGESSQGQGGGGCFPSPTMELRCGGLLFSSRFDSG
1 1			NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEPNVWTRPD
1 1		·	CARTEFENGNRSNFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG
1 1			MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGA
1 1			TTFFAFCYPFSYSDCQKLLNQLDQRFPENHPTHSSPLDTIYYHR
1 1			KLLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPP
1 1			RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLR
( 1	i		RLFVFKLIPMINPDGVVRGHYRTDSRGVNLNRQYLKPDAVLHPA
1 1			IYGAXAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKAN
( I			NIQNEAQCGHSADRHNABAWKQTEPAEQKLNSVWINPOOSAGLE
1 1		i	ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE
1 1			NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV
1 1			
1		**	AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA
1 1	Į	,	FPSRYTVBLFEQVGRAMAIAALDMABCNPWPRIVLSEHSSLTNL
1 1	ŀ		RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE
1 1			NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL
			PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK
5525	105	834	SNILDFERHLFIMGQQISDQTQLVINKLPEKVAKHVILVRESGS
1			LTYEBFLGRVABLNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV
j 1	ļ		VVRVVCTKINKSSGIVEASRIMNLYQPIQLYKDITSQAAGVLAQ
į i		i	SSTSBEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD
) l			
1 1	ļ	ŀ	LILPCAHSFCQKCIDKNSDRHRNCPICRLQMTGANESWVVSDAP
			TEDDMANYILNMADEAGQPHRP
5526	3	853	RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT
Į l	]		QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR
ļ Ì	1		LDDDPPPSTLLKDYQNVPGIRKVDDVVKRLLSLEMANKKEMLKI
) (	1	i	KQEQFMKKIVANPEDTRSLBARIIALSVKIRSYEBHLEKHRKDK
1 1	1	ł	AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL
į l		j	YYRRAHRRFVTKKALCIRVPQETQKLKKRRRALKAAAAAQKQAK
	L		THE WATER TOWN TOWN THE WATER THE TOWN THE TRANSPORTER TO THE TOWN THE TRANSPORTER TO THE TOWN THE TRANSPORTER TOW

SEG   Predicted on   Predicted on   Predicted on   Incleotide   Cocation   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Courseponding   Course				
Mocation   Corresponding	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cocresponding to first anio acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acquence   Security	1			
CONTRESPONDING   Co first anino acid anino acid anino acid acid cest-due of anino acid acid acid cest-due of anino acid acid acid cest-due of anino acid acid acid acid acid acid acid acid	NO:	4		
to first anio acid residue of anio acid sequence	1			
amino acid residue of amino acid adino acid anino acid anino acid acquence control anino acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acid acquence control acquence control acquency control acquenc	(		i e	;
remidue of anino acid sequence (Codon, /=possible nucleotide deletion, Codon, /=possible nucleotide deletion, Codon, /=possible nucleotide deletion, Codon, /=possible nucleotide insertion)  5527 3225 565 LERYILMORFILLERIGONETE SPANHERICHORSONE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANAYAGE PROPERTY OF ANNOYAGE PROPERTY OF ANAYAGE PROPERTY PROPERTY OF ANAYAGE PROPERTY OF ANAYA	1			
amino acid acquence Coden, /-possible nucleotide insertion) RENEDSPAKAIRETHOSS  5527  3225  565  LEREYLINGSPLIKERUSCHEENTLOSS  LEREYLINGSPLIKERUSCHEENTLOSS  RENEDSPAKAIRETHOSS  RENEDSPAKAIRETHOSS  LEREYLINGSPLIKERUSCHEENTLOSSPROSSEC  RENTEKLINGSPLIKERUSCHEENTLOSSPROSSEC  RENTEKLINGSPLIKERUSCHEENTLOSSPROSSEC  RENTEKLINGSPLIKERUSCHEENTLOSSPROSSEC  RENTEKLINGSPLIKERUSCHEENTLOSSPROSSEC  RENTEKLINGSPLIKERUSCHEENTLOSSPROSSEC  RENTEKLINGSPLIKERUSCHEENTLOSSPROSSEC  RENTEKLINGSPLIKERUSCHEENTLOSSPROSSEC  ARTOSEKTIAPATHEMIKUNGERAAPPSTALDILIJE  ARTOSEKTIAPATHEMIKUNGERAAPPSTALDILIJE  ARTOSEKTIAPATHEMIKUNGERAAPPSTALDILIJE  ARTOSEKTIAPATHEMIKUNGERAAPPSTALDILIJE  ARTOSEKTIAPATHEMIKUNGERAAPPSTALDILIJE  RENTEKLITILIVOORSTIKKOOMARAIPSTUVATUSCHEENTEKLITI  THEMIKUNGERACHEENTEKSPROSSELIRERUVARQUSHEENTEKLITICI  RENTEKLITILIVOORSTIKKOOMARAIPSTUVATUSCHEENTEKLITICI  THEMIKUNGERACHEENTEKSPROSSELIRERUVARQUSHEENTEKLITICI  THEMIKUNGERACHEENTEKSPROSSELIRERUVARQUSHEENTEKSPROSSEC  RENTEKLITICI  RENTEKLITIC  RENTEK	ŀ		I .	
Sequence   N-possible mucleotide insertion	ļ		P .	
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SODAL PRODDAGESPSSLIREKEVPRQNEMERENIDEROTON LKQRIDNKSATCKNYP KRPLIGUTLTPTPELGVQRHINGURGHENERNIDEROTON LKQRIDNKSATCKNYP KRPLIGUTLTPTPTELGULERLIGKH YHLRINLRQIRCLVVDEADRWVERGHERELGQLESHLEDSGYNPK RQTEVVIDLTRINRATVETLETTRIHCETDEKDFYLTYFHQYPC RSUVPANSISCIKRISGILKHKHIKKMKKKMKGKQRKJENLEGGYNPK RQTEVVIDLTRINRATVETLETTRIHCETDEKDFYLTYFHQYPC RSUVPANSISCIKRISGILKHUKULHWFUTHARKQRIRNLEGG RTARATNBOLLSHILGPBUTWKKI YRTIKGDEDIP.PPVQTK YMDVVERHIRLANGIERSGYRNPQACHHNSWTEQAAAALBILBE EDWYKGKADQGERRROKGWKVIKKELRILKKDEDIP.PPVQTK YMDVVERHIRLANGIERSGYRNPQACHHNSWTEQAAAALBILBE EDWYKGKADQGERRROKGWKVIKKELRILKKDEDIP.PPVQTK YMDVVERHIRLANGIERSGYRNPQACHHNSWTEQAAAALBILBE EDWYKGKADQGERRROKGWKVIKKELRILKGEDIP.PPVQTK YMDVUERHIRLANGIERSGYRNPQACHHNSWTEQAAAABILBER EDWYKGKADQGERROKGWKWIKKELRILKGEDIP.PPVQTK YVENPSADDITCLAHCMVVVELDGRAFHRPAERIMPARADANDRAL  5528 3 895 GPFISACRIMMGACKVKVEDSLATISTTERRYLLGATMAKSKFP YVENPSADDITCLAHCMVVVELDGRAFHRPAERIMPARADANDRAL LKYLSWRADCHINLINTYPHAAGOGSEVSEVYHAGGENGGTIC LKYLSWRADCHINLINTYPHAAGOGSEVSEVYHAGGENGGTU- LKYLSWRADCHINLINTYPHAAGOGSEVSEVYHAGGENGGTU- LKYLSWRADCHINLINTYPHAAGOGSEVSEVYHAGGENGGTU- AADRINELLFISEFHINYNSEPPHYRRIBOSGGGWLSVARQRVSGL LSWILSPEHERUFVARSCURLUPFALIGERSCHUNGTHTERL PTEMEKSWADVITSTTEVCYTHAALOGSESPHYLLTRITUNGKOP PERKENTERLEVVSESCURVQEINERSTIVLITRITTPVEHCSLATI. IGGLGRVIKIGRCLPFRHILIGETDEKAALEVYLLTRITLDFG KRYTLEELEVVSESCURVGEINERSTIVLITRITTPVEHCSLATI. IGGLGRVIKIGRCLPFRHILIGETDEKAALEVYLLTRILTPE KRYTLEELEVVSESCURVGERDEKPENVYPFREQLIVKLTDFGFSNK POPCKKLTTSGSLAYSAPBILLGEBERSED PROKKLTTHAAG POPCKKLTTSGSCANSTANDANDANTYPELGERDELTRILGEN QUESCIJTESASPSTIKADPROCONSTINITGENDATATPLSH VCSQPPFGEANGSETLTHINDCKTYVSHVSKRCKOLTITHILOG POPKKRATITSGSCANSTANDANDANTYPELGERDELTPATTSTALLERI QUESCIJTESASPSTIKADPROGSGSCOSSESTEDDDSESRRELDKUNGG TYSHKRISSIEGPPSGGGGGGGSCSPSTANSAGDURATPLSCHILDEN QUESCIJTESASPSTIKADPROGSGDDEFDRANGSTIVSKLKNOTI. ASKTIVHRYBRITGSTTRIRGGRSTOLGSSTDDDSESRRELDKUNGG TYSHKRISSIEGPPSGGGGGGGSCSPSTANDASDELTPSILKNMULTDAN TNUPLISSLEGEPPSGGGGGGGSCDDSFDMAGNISTSTIVLIGKPG TYSHKRISSIEGPPSGGGGGGGSCSPSTANGSKUNGSLYSSIK LMSLICLIGGGUIR		1	ĺ	AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGETRTE
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PTGIKTALINGGSSTOKOOMILARREBILVATEGELEBILKEKE YHLENINGGURE(UVUDEADRAWEGIBFAELGOLLEBINDSCYMPE) RQTLVFSATLTI.VHQAPARILHKRHTKKMDRTAKLDILMQKIGM RGERVIDLTINDRIVERLIBETTSHIRGEDBKDPYLYFIAQYFG RSIVFNATSISCIKRISGILAVILDIPLITHAGHQKQRIRNLEG PARLEGUVILATOVAARGLDIPKUTHAGHQKQRIRNLEG RTARATNEGILAHLIGPEDUVIHVQVBETSEITYHBGG RTARATNEGILAHLIGPEDUVIHVQVBETSEITYHBGG RTARATNEGILAHLIGPEDUVIHVQVBETSEITYHBGG RTARATNEGILAHLIGPEDUVIHVQVBETSEITYHBGG RTARATNEGILAHLIGPEDUVIHVQVBETSEITYHBGG RTARATNEGILAHLIGPEDUVIHVQKUTHEQUPETSGICTK YHTOSGKPPLLUSABSISSALSCISKOKKKITKREKEPQPEQD QPSTSAN  5528 3 895 GPPLSACRIMGACKUVUDSLATISTITLRYLEILEAMARKSKEE YVRIPRADDITCHACHVUVURLDGRIPHRPAREINPRAKDNDSRAL QUMKCAGTYVBEHBIGDIVIHAGGSDENSEYTERKINMFRKRASKEE YVRIPRADDITCHACHVUVRLDGRIPHRPAREINPRAKDNDSRAL LKDYLSHWADACHINLINTYHVALOQSGLITYVQAGGRIQGTI, AADRINELIPSEPHINYNBEPPHYRRGIVLTWQKUDEWYTERIKL PTEMEKKGMAJORITHIKTRICTYBALOGGSUMSSUKWRQKVSGL LKDYLSHWADACHINLINTYHVALAIQGSDENSEYTERVANGRUSGIL LKDYLSHWADACHINLINTYHVALAIQGSDENSEYTEVAGRUSGIC LSWITLSRVIHASGISBPCARAGORIMERKALAYDLIRTIRDGR REPTLEBELEVVSSCUEVQEINBERYLJIRTPTPVBHCSLATI. GLCLRVKLQSCLPPRIKLBYJISEGTHSTEEDINGINKRVA AAMBINPHLISGISBPCARAGORIMERKALEYDLIRTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISLAYSAPJILLGBETDARAVINTIRHOGR PQCKKLTITSGISTYLTIPONGCKYPTKLTOVOLDITATPLSAT ATVPQSPARAADEVINGERSGICCSSARSODIDATAPPLSAT ATVPQSPARAADEVINGERSGICCSSARSODIDATAPPLSAT PATRATARASGICKSTYLTIPONGCKSTSTANCISSTSTONGCORYNASSPENNAG GSPSSGGGRPTNTTSGTTRCAGPSSNOMLASSPENNAG GSPSSGGGGGGSGSGSGSGSGSGSGSGSGNSTANSSPENNAGESTANCTLSTST TYSHRRINSBREPPESGICGGGSGSCSSSTODIDSESRRILLDRIGH LMSILGGGGIGSTYLTIAGGGRSTYCGSBILMSTUCCHUSISK LMSILGGSGICHGSTYLTIPONGCKSTSTONGCHUNGARAVINTIALGUE TYSHRRINSBREPPESGICHGGGGSSTSTONGSPEN	ĺ	1		VSDQALLFGDDDAGEGPSSLTREKPVPKQNENEEENLDKEQTGN
HILBRIDGCILVUBEADEMVERGHPAELSQULLEMILDSCYNEPS ROTLVPSATITLVUQAPALTEKHTKKMDETAKLDLINGKIGM ROKRYVIDLTRNEATVETLITETXIHCSTDEKDPYLYYPIMOYPC RSLVPANSISCIRKESGLIKVIDIMPLITHAGMIQKGRENNLEQ BARIBGCULLATOVARREGULTRVQVIRUPSTESTIVHENG FARARINGOLSIMLIGGEDVINPKKIYKTLKKDEDIS LPPVQTYK MODVERE TRLARGIERSSYRNFQACIMBYEDAPALEIELB EDMYKKGKADQGEBRRQKOMKVLKKELRHLLSQPLETESQKTK YPTJGGKPPLUVSAPSESSSAISCLSKOKKKKTKKPKEPQPEQP QPSTSAN  5528 3 895 GPFISACRWWGACKVKHDLLATISITLRRYTELGATMAKSKP YVEDPSADDITCLAHCWVVRLDGRNPHRPAEREMFARPADSRAL OLM*KCAQTVWEELBDIVTANGQSDEYSFVFRRTINNFRRRASK ENTEVASQPASSYVFVKHDYFEDQPLLIPPGGRVVVYPSKCT LKYYLSWRQADCHINNLYNTVFHALIQQSGLTFVQAQBIQGTIL AANDRISLIPSEFNINNINSPPMYRGSTYLVFKRYKREPKEPPEPP TEMEGKGAAVTRITKYPCCKSSH.PRAPCLRWI  5529 48 640 TFRIVSAHLKTRKLINFEARERWRUNDSRQGALSVKNQRVSGL LSHTLSRVIMISGISSPGARQPFINEBERGLEVYDLIRTIRDPE KRYTLEELEVVSSSCVEVQEINBERTALVIIRTTFTVHCSLATL IGCLEVKUGCLPFPRILERIYISGSTERBRUNQINGKERV AAMENPHIRBIVZQCULEPD AQVANATSYKIKHIVOHRDLERIVVYPFKKGLLVKLITDFGYSNK POPKKRLATSGGSLAVSAPELLLGDBYDAPAVDINGLGVILFML VCGQPPPQEANDSSTLIMINDCKYTVPSHVSKEKCKULITRMLQR DFRRRASLEETENHWALGOVDPSPATKYNTIFLVSYKRLSBERGH SIQURVLGDIADRADAVEALETNRYNHTTATYFLLARRILRER ORBEITGFRASSPSNIKAGPRSWFTLIVPOPDLEDDLTATPLISH ATVQSPARAADSVLNGHRSGGLCOSAKRODLEPELARPLESLAVN PAGLEFTSASSPSNIKAGPRSWFTLIVPOPDLEDDLTATPLISH ATVGSPARAADSVLNGHRSGGLCOSAKRODLEPELARPLESLYNG PAGLEFTSASSPSNIKAGPRSWFTLIVPOPDLEDDLTATPLISH ATVGSPARAADSVLNGHRSGGLCOSAKRODLEPELARPLESTY PAGLEFTSANGRKCLFFRVEDBERBEDEDKFRNGLFSTQVVLRRKPS VTRAITSRKSSAPVANQIFFBGGSCSSSSTSTOSTGVDVLRRKPS VTRAITSRKSSAPVANQIFFBGGSCSSSSTSTOSTGVDVLRRKPS VTRAITSRKSSAPVANQIFFBGGSCSSSTSTSTOSTGVDVLRRKPS VTRAITSRKSSAPVANQIFFBGGSCSSSTSTOSTSTOSTGVDVLRRKPS VTRAITSRKSSAPVANQIFFBGGSCSSSTSTOSTSTOVLRRKPS VTRAITSRKCGRAPPSCELLSTANGRAVSKSPLEHGTVLFARLE LMSLCLGSGLIGSTXYI IDDNGLSFSSVAVQKRSTWMCLISST GARGQVPAVGGIKFFRSDHADTTTGLER LRRKKNIKNIVLQLPLC EKTISUNTORRYFRSGGACOGGSSTVAVARSPERGELVESLLAV LGSBFTPATRAANSQLYGRVGARSFWDGGS SSHVOKGRKRWITESTOCSBLLAVBRANCAGGGGSTSVAVARSPROBERGENILAGCHAL CRABTPATRAANGGVRLSSPSTCCBSLLIVPLIKE CPHDFKLEDFYSASSELPPPYGGG	ļ	1		LKQBLDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
ROTLVESATLITUNDAPARTLIKKHTEKBORTAKIJLIMOKIGE ROKKVIJILITRIKATVETLIBEXTHCETUROVILOTIVOYPE RSLVFANSISCIKRISGILKVIDIMPLITHAUMIQKORIZMILEQ RALBERCVILATROVARGIDIPKVQHVIHYQVPRISTIVHESG RTABATINGILSIMILIGEPUNIPKKIY KIYLIKDEDIPLPPVQTK YMDVVKERIRILARQIEKSSYRNFQACIHNSWIEQAAAALEIELIE ROMYKGKAKOQGERERRQKOMVLKKKELHISQPLETISSQKTK YPTQSGKPPLLVSAPSESSALSCLSKOKKKKTKKPKEPQPPQQ QPSTSAN  5528 3 895 GPFISACRWĞACKVKVHDSLATISITLERYLRIGATMAKSKYP YVRDPBADDITCLAHCWVVVRLDGRWPHRPAEHEMFAKPDGSAL OLMYKCAQTVHEBLBIDIVANGQGBESTYRTKINNFKRRASK EMTHVASQPASSYVFWRDYFEDQPLLYPPGFGGRVVVTPSKCT LKDYLSWRADCHINNLYHVFWALIQOGS LKDYLSKRAGVENSTUNTWERPKRASK EMTHVASQPASSYVFWRDYFEDQPLLYPPGFGGRVVVTPSKCT LKDYLSWRADCHINNLYHVFWALIQOGS LSWILLESSFRILWINNSEPRVRKGTVLIWQKVDEWMTKEIKL PTENISGKWAVTKTRTKPCKPSHLPRAPCLIRH PTENISGKWAVTKTRTKPCKPSHLPRAPCLIRH SPENIEGKWAVTKTRTKDCKPSHLPRAPCLIRH LIGHLEVKLORCLPFHIKLEYISGGTHSFRADEWINDRINGINDKERV AAAMENPHILBELVESCULEPD  5529 48 640 TFRIVSSAHLKTRKLINFERAEKRRONDSSIGWMISVKMQRVSGL LSWILLSRVLMILSGISSFGAARQPRIMEBERALEVVZILHTINDPG KPRITEBLEVVSSCULEPD  5530 4541 2606 AQIVHATSYCHKLHVGHRDLKPENVVPFEKQGLVKLIDFGFSNK VOQOPPFPGEAMDSETLTHINDCXYTYPSHVSKKCKOLITRINQR PQFKKRIATISCGSLAVSAPELILGDBYDAPAVDINGLVILFINDLY VOQOPPFPGEAMDSETLTHINDCXYTYPSHVSKKCKOLITRINQR DFKRRASLERIENHPHLQCVDPSSATKVATIFLINSYKKLEBEEN SILQMVILGDIADRDAITVENLEFMYNHUTAYFILLBEKILBEK QEKSIQTISASPSRCHUNTAYFILLBEKSHNISHLENG SILQMVILGDIADRDAITVENLEFMYNHUTAYFILLBEKSHNISH ANTVPQSPARAADSVINGHRSKGLCSKSTSTDDDSFSRRRLDKNOG GCSSGSGGGGGTHVTTSGTTRRCAGPSSCUNGASPSANGHUSSLKWNI ASSCTVHKRYRKRSGGGGSGCSSSSTSDDSFSBRRLDKDSGF TYSHHERDSSGPPGSGGGGGGGGKPSNASGGUNKASPSENAGG GCSSGSGGGTPTNTTSGTTRRCAGPSSACVINGARSHADELVSLK LMSLCLGSQLHIGSTKYIIDPONGLSFSSVVQBKSTWKMCISST CHAGQVPAVGGIKFRSDHAADTTELERIKKMALKNIVLQLFILC EKTISVNICHNYRKSGGGRSPSSCGGGASPSACGGUNGASPSENAGG GCSPSGGGGGTPTNTTSGTTRRCAGPSSACCHUTARAL ANTVPGLESPALLTVALVCAGSPSSCCUNGASPSACCHUTARAL CHAGARATARANDYPREGLAGAGGPSSVVGGRASHADELTITHRENDSYG RATKRNPYRMI IBBOTTSPCGGEBLHINGKILKDRINT LIGHTGGGFFTLAKAGRAMAMDPVPDRMFRRNSTG CHAGQVPAVGGIKFRYNITERSTGCGEBLHINGELLSCHLINGTHRONSYG KRYUND	l	1	}	FTGIKTAILVGGMSTQKQQRMLNRRPBIVVATPGRLWRLIKEKH
RGERVIDLITRIBATURETI, HICETOBROPYLLY PIMOPYCE RSLVFANSISCIKKLSGLIKVLDIMPLITHAUMOKORILEO PARIBOCVILATIOVARGIODIRVQIVI HYQVPRITSETYVHESG RTARATINEGLISMI, IGPEDVINYKKI YKTLKKDEDIR JEPVUTK YMDVUKRI RILARQI RESKYNYRQACHHNINYEQAAALEI ELE EDMYKKGKADQGERRRQKOMKVLKKELHILLSQPLETISQKTK YPTYGGKRPELUVSAPSESESALSCLSKOKKKKTKKKEREPQPEQE QPSTSAN  5528 3 895 GPFLSACRWIGACKVKVHBLATISITLERYHLIGATMAKKEP PARIBODITCLAHCWVVRLDGRNPHRPAREHHFARPADSRAL QLM*KCAQTVMEELBOIVTANGQBEYSPVFKRITINYKRRASKP HTHIVASQPASSYVFVWBDYEDDPLLLYPOGGRVVVYPSKÇT LKDYLSKRQADCHINILYNTVFHALIQQSGLTPVQAQGRLQGTL AAKNBILPSBFNIHVANEPENFRRTVLIQKVDDEWTKERIK, PTEMECKOMAVTRIKTINPEKAREKRINDIOSKOĞWLSVUKQKVGSL LKDYLSKRQADCHINILYNTVFHALIQQSGLTPVQAQGRLQGTL AAKNBILPSBFNIHVANEPENFRITVLIQKVDDEWTKERIK, PTEMECKOMAVTRIKTINPEKAREKRINDIOSKOĞWLSVUKQKVGSL LKDYLSKRULISGISBREQARAPGPI HEREKEVD'LLIFTI RDPE KPYTLEELEVVSSCO'EVQBINRERYLJ'LIRTPTTVPHCSLATI, IGLCRYKLQRCLPFKHKLEIYISGSTHSTERDINGVIDNKERV KPYTLEELEVVSSCO'EVQBINRERYLJ'LIRTPTTVPHCSLATI, IGLCRYKLQRCLPFKHKLEIYISGSTHSTERDINGVIDNKERV LVGGOPPFQEANDESTLTJHILMCXYTYPSHVSKKCKOLITRHLQR POKKLITINGSIANTAGERILLGGERYDAPAVDINSLGVILFML VCGOPPFQEANDESTLTJHILMCXYTYPSHVSKKCKOLITRHLQR POKKLITINGSIANTAGERILLGGERYDAPAVDINSLGVILFML VCGOPPFQEANDESTLTJHILMCXYTYPSHVSKKCKOLITRHLQR PASLRPTASGRKCLFRVEEDBEBDEBOKKPMSLSTQVVLRRKPS VTNRITSRSSAPPINIQPPSBETLINGPENDYLORDEDDILTATPLSH ANTYQSPRAADSVLNGHESGELCOASKONDLASRSENIAD. SIQUMVUGRIPTRCGGPSDEXPOHLPPLAGPLATISH ANTYQSPRAADSVLNGHESGELCOASKONDLASRSGRUDARSPENNAG GSPSSGSGGOGOSKPSNASGGUVARSPENNAG GSPSSGSGGOFPTNTSGTTRCAGPSINGVLANKINSPENNAG GSPSSGSGGOFPTNTSGTTRCAGPSINGVANGARSAGELVESLK LMSLCLGSGLIGSTKYI IDPONGLSFSSVKVOKSSTKNCISST CNGQVPAVOGIKFSDHANTTTELERILPKYLKKNIKNIVLQLIPLC EKTISVNIQNPKEGLLCASSPASCCIVI  5531 24 515 GSOPRAPRFROSMERPEPELITRGSWRAVSRSPLEHDHIKVMLVIDAAV TNVEOLSSLERYLASLGRKHRAVGVKLSSPSTVCESLLYMLEKC LGPATTPATRAANSQLYQAVQAMSRGWDGE FRATRANPYTENI ROVEFLINAANKMAMDPVPCRMTPRENSYG KPLVJORRSKILLYPAVCAGGGFSEVYLMRKMHAKGFGHTLK GPHDEKLBOPYNSSELLEPYYGGGGTDGODITRPENI SAFRN VILDNTDRKGVHPLAADGGFSVEGGINGDILTRERDISLA GPHOKERICHTENINGHENIN	į.			YHLRNLRQLRCLVVDRADRMVBKGHFABLSQLLEMLNDSQYNPK
RSLUPANSISCIKKISGILKVIDITMPLITLHAGMIGKGRIZMILEQ PARLEDCVILLATDVAARGIDIPKVONVIHYQVERTSEITVÜREG RTARATMBÖLSILMIIGPBOVINPKKI YRTIKKDEDIPLPPVQTK XMDVVKERI RLARQIBKSSYNNIQACIARISHIEGANALBIELIS EMMYKGKARQOGERRIRQKOMVLIKKELLSQPLETSSQKTK YPTOGGRPPLLVSAPSESSAISCISKOKKKKTKKPKEPQPPCOP OPSTSAN  5528  3 895 GPPLSACRMIGACKVVHDSLATISITLRRYLRIGATMAKSKEP YVRNPBADDTCLAHCWVVRLIGENPHRZAEKHPRAKBORZAL GUNTKCAGTVERELBUIVIANGGSDEYSYVKRIKIMPKRRASK PHTHVASQPASSYVFWRDYFEOQPLLYPPGDFORVVYPSRCT LKDYLSWRADCHINNIKHTVFWALIQGSD LKDYLSKRAGNCHINGHATVFWALIQGSD PERBECKOMAVTERTRIKDEVCESSHUPRAPTVAQGGELGGTI AADRIBLIPSSENINYNNEPPMYRRGTVLIMGKVDEWMYREIKL PTEMECKOMAVTERTRIKDEVSSHUPRAPTVAQGGELGGTI AADRIBLIPSSENINYNNEPPMYRRGTVLIMGKVDEWMYREIKL PTEMECKOMAVTERTRIKDEVSSHUPRAPTULIMGKVDEWMYREIKL PTEMECKOMAVTERTRIKDEVSSHUPRAPTULIMGKVDEWMYREIKL PTEMECKOMAVTERTRIKDEVSSHUPRAPTULIMGKVDEWMYREIKL PTEMECKOMAVTERTRIKDEVSSHUPRAPTULIMGKVDEWMYREIKL PTEMECKOMAVTERTRIKDEVSSHUPRAPTULIMGKVDEWMYREIKL LSHTLSRVIMISGISSPGAARQPRIMEBRALEVZULIRTIRDPS KRYTLEBELEVVSSSCUWEQUEINEBRIVLITIRTIPTUPHCSIATI IGICLEVKLQRCLPFRHKLBIYISBGTHSTEEDINKQINDKRV AAMENPHIRBIVSOCULEDP  AAMENPHIRBIVSOCULEDP  AAMENPHIRBIVSOCULEDP  AAMENPHIRBIVSOCULEDP  AAMENPHIRBIVSOCULEDP  AAMENPHIRBIVSOCULEDP  AAMENPHIRBIVSOCULEDP  DPKRRASLEETEMHPHLQCVDPSSATKYNTELUSYKNISBEEHN GURGIQTRRASPENTALDEVSKRKCKOLITRHLQR DPKRRASLEETEMHPHLQCVDPSSATKYNTELLARIKUNISBEEHN ATVOGSPBAADSVINGHESSEULOGASKUSKINSLEELEMMI ASSCTVHKRYRRKSQGGSSCSSSTSIDDSSRRRILDKSIG GESSGSGGGOGNITHTSGTTRRCAGDSSMONGLARISAGEUNSLK LMSLCLGSQLHIGSTKYIIDPONGLSFSSVKVQBKSTWRMCISST GRAGGVPANGGILKFSDHHADTTTELBEI KRKNILKNNVLQLFLC EKTISVNIORNPREGILCAGSPASCCULVLARILE  SS31 24 515 GSOPRAPREPRISHERPEPELIRGSWANVSRSDEHGTVLFARLE  GSOPRAPREPRISHERPEPELIRGSWANVSRSDEHGTVLFARLE CHAPTIVARARSQLESPASCCULVLARILE CHAPTIVARARSQLESPASCGUNGANSKASPENIAGE RATRANPYNENIBGVFLINRAAKKMAMDPVPCRMFTRIPRISYG KPLVJOBRAGLLYPANCAGGSPASCCULVLARILE CPHDFKLBCPYNCROGFSSTYCHWRKMHAGGGGMYLL CPHDFKLBCPYNCROGGOFSSTYCHWRKMHAGGGGMYLL CPHDFKLBCPYNCROGGOFSSTYCHWRKMHAGGGGMYLL CPHDFKLBCPYNCROGFSTYCHWRKMANDENDFCHTLAG LIQUALCQFI	l	Į.		RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
# RABLEDCVILATDVARGILDIR RVOJNVIHYQVPRTSEITVÜHESG RTARATNEGLSIMLIGPEDVINKKI YKIKDEDIPLPPVQTK YMDVVERIR ILARQIBESBVRBFQACHINSNIEQAAAALBI ELB EDMYKGGKADQGERRRQKOMKVLKKELRILLSGPJPFTBSQKTK YPTQSGFPLIVSABSESBASIGSKKKKKTKRKEPGPDP QPSTSAN  5528 3 895 GPPLSACRMGACKVKVHDSLATISITLRRYLRGATMAKSKPB YVRNPRADDTCLAHCMVVVELDGR#PREPBERINFAKNDGRAL QLM*KCAQTVMEBLEDIVIAYGGSDEYSFVEKKTWKFRRASK EMTEVASQASSYVYEWDDYFEDQPLIAYPGFDGRVUYPDSGT LKDYLSWRQADCHINNLYNTVFMALIQGGIFPYQAGGELQGTI- AADRISLITJESFENINNBEPBYNRRGILAYDGKUDEWMYKRIKL PTEMEGKKMAVTRTTKPCKPSHLPRAPCLRWL  5529 48 640 TPRIVSAHLKTIKLINDEAAERRWEDNDSRQGMISVKMQRVSGIL LSWILSGRVILAGGLSPFENALDEYDLIRTIRDPE KPRTLEELEVVSSCVEVQEIMEBRYLVIIRFTPTVPHCSLATL IGGLEVKULAGGLSPFENALDEYDLIRTIRDPE KPRTLEELEVVSSCVEVQEIMEBRYLVIIRFTPTVPHCSLATL IGGLEVKLQRCLPPRIKLBEIVISEGTHSPEDINKQINDKERV AAMENPNLRBIVEQCVLEPD  5530 4541 2606 AQIVHAISYCHKLHVGREDKRENVYFPEKQGLVKLIDFGFSNK VCGSPFPCPARINSSTLIMLINDCKTYVPSHVSKKKKDLITRRIQD PFKRRASLERIENHPHQGOUPSPATAPILUSYCNILSBESH SILQRMVLGDLADRAIVRALBTNRYNHITATYFLLARRILREK QBREIQTRSASFSNIKAQPRGSWPTKLDVCPQLEDDLTATPLSH ATVYGSPRAADSVILNGHGSRGLICASRKKDLIPELLSPLATIV PASLRFTASGRKCLFRVEEDEBEDEENKMSISTQVVLRRKPS VTRILTSRSSAPLNAQ (FREGSSDDEYNDLIPPLATIVE PASLRFTASGRKCLFRVEEDEBEDEENKMSISTQVVLRRKPS VTRILTSRSSAPLNAQ (FREGSSDDEYNDLIPPLATIVE PASLRFTASGRKCLFRVEEDEBEDEENKMSISTQVVLRRKPS VTRILTSRSSAPLVAQ (FREGSSDDEYNDLIPPLATIVELMSIL ASPGTVHKRYHRRNSGGRGSSCSSSETSDDDSESRRRLDKDGG GSPSSGSGGFTTTTSCAGFSSPMQLASRSBERINGL GSSPSSGSGGFTTTTSCAGFSSPMQLASRSBERINGLENSLL LMSLCLGSQLHGSTKY11DPQMICSFSSPMCLASRSMQLASRSBERING GSSPSSGSGGFTTTTSCAGFSSPMCDLASRSRGLIVSLE LMSLCLGSQLHGSTKY11DPQMICSFSSPECLISTRICKHRNVLQLBLC EKTISVNTQRNPKEGLLCASSPASCCIVI  5531 24 515 GSQFRPRRDSMERPEPBLIRGSWRAVSSSPLERGTVLPARLF CRAFTRANFYTENIRGVFFLMRAMKMAMMDEVEFDRAFTFRBDSYC RAFTRANFYTENIRGVFFLMRAMKMAMMDEVEFDRAFTFRBDSYC KPLVVDRRBEILLYRADCGGPGSFSPECLORMTTRPRBDSYC KPLVVDRRBEILLYRADCGGPGSFSPECLORMTTRPRBDSYC KPLVVDRRBEILLYRADCGGPGSFSPECLORMTTRPRBDSYC CPHOFALBOPFSVECTOLALLCCCFREVCLFFRUTLA	}	j	l.	RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFLMQYPG
RTARATNBELSIMLIGGEDUINPKKI YKTILKKDEDI PLPPUTJIK YMDVVKERI RLARQIEKSEYRNFQACIHNSWI EQAAAALSIELE EDMYKGGKADQOERRRQKQMKVIKKELRHLLSQPIPTISQKTK YPTQGCRPPLLVSAPSISSAJICLSKQKKKKTKKPKEPQPPQP QPSTSAN  5528 3 895 GPFLSACRNWGACKVKVHDSLATISITLRRYLRIGATMAKSKPB YVRDPRADDITCLAHCWVVVRLDGRPPHREPAEKINFAKNDGSAL OLMYKCACYVMERLEDIVI AYGGSDEVSFYPVKRKTRWFKRRASK EMTHVASQPASSYVPYWRDVFBQPLLVPPGFDGRVVVYPSNCT LKDYLSWRQADCHINNLYNTVPMALDSGITPVQAQGELQGTL AADKNEILFSEPNINYNNEPPMYRRGTVLIWQKVDEVMYKRIKL PTEMBGKKRAVIKTRYTRPCKPSELPRAPCCRWI  5529 48 640 TPRIVSAHLKTKKIINPEAAEKRRRBNDSRGGWLSVKMGRVSGL LSWYLSRAHLKTKKIINPEAAEKRRRBNDSRGGWLSVKMGRVSGL LSWYLSRAHLKTKKIINPEAAEKRRRBNDSRGGWLSVKMGRVSGL LSWYLSRAHLKTKKIINPEAAEKRRBNDSRGGWLSVKMGRVSGL LSWYLSRAHLKTKLINPEAAEKRRBNDSRGGWLSVKMGRVSGL LSWYLSRAHLKTKLINPEAAEKRRBNDSRGGWLSVKMGRVSGL LSWYLSRELEVVSSCOVEQSILBERBYLIFPTPTPESLATI. IGLCLRVKLQRCLPPKHKLETYISEGTHSTEEDINKQINDKERV AAMENPHILRBUVSCOVLBPD AAMENPHILRBUVSCOVLBPD FORSKLITTSCSSLAYSAPPILLGDEVDAPAVDINSLGVILFM UVGQPPPPGEANDSETLTMIDCKYTVPSHVSKKCKDLITRRLQR PORKKLITTSCSSLAYSAPPILLGDEVDAPAVDINSLGVILFM UVGQPPPPGEANDSTLTMIDCKYTVPSHVSKKCKDLITRRLQR PORKRASLERIENBPWLQGVOPSPATKYNTELTSYKNISEBERIN SIIQMVLGDIADEDATVRALETNRYNHITATTFILARRILREX QEKRIGTRSASPSKAUGPRGWSTYRCHDEDLEDLERLGPALSTUP PASLKPTASGRKCLFRVEEDEEBEERKWRSISTQVVLRRKPS VTRALTSRGSAPVLNQTFESGGSGGGGGSPSRRGLDVSLERGHANT ASSCTYHKRYHRRSGGRGSGGGGGGGSPSNAGGGUDKASPSRNAGG GSPSGGGGGTMTTSGTTRCAGPSNSMQLASRSAGELVESLK MSLCLGSQTAIGSTKYIIDPONGLSFSSVKVORSTRINKCISST TYSHRENISSRGPPGSGGGGGGGGGSPSNAGGGUDKASPSRNAGG GSPSGGGGGGNAPHNTSGTTRCAGPSNSMQLASRSRRILDRING FKYSHRENSGRPFEFELHRGWRAVSKSPERHGTVLFARLF ALEPOLLEPLEPYNGGILCASSPAGGGUNASPSERNAGG GSPSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	ļ	ł	RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQRLRNLEQ
MIDUVKERI RLARQIBESENERO ACLINISHI EQARAALETELE   EDMYKGKADQQEERERQKOMKVILKELIRLLSQPILPTESQKTK   YPTQSGKPPLLVSAPSESSASIASICISKOKKKKIKKERGEQEPQQP   QPSTSAN     SPS	1	ĺ	ì	FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
### BOMYKGGKADQGERRRQKQMKVLKKELRILLSQPLPTTESQKTK YPTQGKPPLLVSAPSKSESALSCLSKQKKKKTKPKEPQPEQP QPSTSAN  5528 3 895 GPFLSACRMIGACKVKHDSLATISTITLRKYLLEATMAKSKFE YVRDFRADDTCLAHCWVVVRLDGENPHRPAREKHNPSKRNDSRAL OLMCKCAQTVMEELEDIVIAYGQSDEVSPVFKKTNWFKRRASK FMTHVASQPASSYVPYWALLQGGELTFVQAQGRLQGTL, AADENEILFSEFNIHYNNEPPMYRRGTVLIWQKVDEVMTKEIKL PTEMEKKMAVTRITKIKCCKSHLAPRAPCLRWI.  5529 48 640 TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL LSWYLSERVLMILSGISBPGAARQPRIMEBKALEVYDLIRTIRDPE KPWTLEELEVVSESCEVEVQEINBERKLUVIJIRTIPTPURGSLATI. IGLCLRVKLQRCLPPKHILBIYISEGTHSTEEDINKQINDKERV AAAMENPHLREIVEQCVLEPD  5530 4541 2606 AQIVHALSVCHKUHWGREDLKPENVVPFEKQGLVKLITDFGFSNK FQPGKKIATISCGSLAYSAPBILLGDEVDAPADINSLGVILIPHL VGGPPPQFQSANDSTILTHIMCKYTYVPSHVSKCKGULTHNIQR DPKRRASLEBIENHPWLQGVDPSPATKYNIPLVSYKNLSEESHN SIIQRWLGDIADRDAIVALDETNRYNHTTAYFILARRILREK QRESIGTRSAFSPNIKAQPRGSWFTLIDVPQDLEDDIATFILSH ATVQGSPARAADSVLNGHRSRGLCDSAKKODLPELAGPALSTVP PASLKPTAGSRKCLPRVSEDESEBERKMENGMISSTOVVLRKKPS VINRLTSRKSAPVLNQIFEBGESDDEFDMDENLPPKLSRLKMNI ASSCTVHKRYHRRKSQGRGSSCSSSTSTDDDDSSKRRLDKDSGF TTSWHREDSSGPPGSEGDGGGGKPSNAGGBUKASSPENNAG GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGMTMYTSGTTRRCAGPSNSMOLARSBSRRING GGSPSGGGGGGGGGGGGGGGGGGTHPATREKVELIFICK CRAGQYPANGGIKPFSDHADDTTTELERLKSKNILKNNVLQLIPLC EKTISVNIQRNPKGGLLCASSPRSCCLIS GGDFRAPRPROSHERPEFELIRGSWRAVSRSPDEBIGTVLPARLF ALEPDLLPLEPQVNCRYPSSPROCISSPFICHGTVLPARLF GGDFRAPRROSHERPEFELIRGSWRAVSRSPDEBIGTVLPARLF GGDFRAPRTRAMSGCGGGSSVAVRNSRBDGBDVARRHTMPRBDSVG KPLVKDRRABALILYPADVCAGPGGFSSFVLWRRKMHARGFGMTLK GPHDFKLEDPTSASSELFPBYYGGGGTDGGGITTPFRRISSAFRN FULINTDRKCVHPI	i			RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLPPVQTK
S528 3 895 GPFISACRIMIGACKVKVHDSLATISITIRRYLRIGATMAKSKFR YVRDFRADDTCLAHCWVVVRIDGRNPHRPARKINFAKENDSRAL OLM-KCAQTVMEBLED IVIAVGQSDEVSPVFRKTNWFKRRASK FMTHVASQRASSVVFYMDDYFBOPILLYPPGFDGRVVVYPSNQT LKDYLSWRQADCHINNILNTVFWALIQQSGUTTVQAQGRLEYDT AADKBELIFSERVIHANINEPPMYRGRYVLIWQKDDEVMYKRIKL PTEMEGKKMAVTRTRTKPCKFSHLPRAPCLRWI  5529 48 640 TPRIVSAHLKTRKLINFEARERKRINDBSKOKWLSVKMQRVSGL LSWILSRVLMLSGISEBCAARQPRIMERKALEVYJLIRTIRDPE KPPTLERLEVVSSSCUEVQRINERRYLVJIRTPTPVPHCISLATL IGLCLRVKLQRCLPPKHKLBIYISEGTHSTBEDINRQINDKERV AAMMENPINRBLVDGCVLEPD  5530 4541 2606 AQVWALISVCHKIHVGHRDLKPRWVVPFKQGLVKINTDGFSNK POSKKLITTGGSLAYSAPBILLGDBYDAPAVDINSLGVILFH UCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKOLITRMLQR DPKRRASLERIENHEWLQGVDPSPATKYNIPLVSYKNLSBESHN SIQRWALGDIADRBATVPALETRHYTTATFILARRILRER QEKSIQTRSASPSNIKAQPRGSWFTXIDVPQDLEDDLTATFILSH ATVPQSPARAADSVLINGHRSKGLCDSAKKODLPELAGPALSTVP PASLRYTASGRKCLFUVEEDEKEDEBKKPMSLSTQVVLRRKPS VTNKLTSRKSAPVLNQIFBSGSSDSFDDDGSSRKRRLKMNI ASPGTVHKYHRRYSGGRSSCSSSFSDDDDSFDMBLIPKLSRLLKMNI ASPGTVHKYHRRYSGGRSSCSSSFSDDDDSFDMSLPFKLSRLKMNI ASPGTVHKYHRRYSGGRSSCSSSFSDUDGSBARRILDKDSGF TYSMRRDSSGPPGSBGDGGGG KYSNASGGUDKSBLKM GGSPSSGSGGWFTNTSGTTRRCAGPSNSVQLASRSAMELVESIK LMSLCLGSQLHGSTKY1 IDDPONLSRRSAMGELVESIK LMSLCLGSQLHGSTKY1 IDDPONLSRRSAMGELVESIK LMSLCLGSQLHGSTKY1 IDDPONLSRRSAMGELVESIK CRAGQVPAVGGIKFFDHMADTTTELERIKSKNIKNNILQLFLC EKTISVNIORBPKSGLLCASSPASCCHVI  5531 24 515 GSGRPRAPRFDSMERPEPELIKGSWRAVSKSPLERGTVLFARLF ALEPOLLPLOPVNCRQPSSPROLSSPRIDHIRKVMLVIDAAV TNVEDLISSLEVLLASLERRHRANGVKLSSFSTVGESLLYHLEKC LGFAPTPATRAMSQLVGAVVQAMSRSWDGB  5532 3195 1402 SDMWVGKRKMITBDETTFCGERILHSVLQCKSVPDVLDGRENR GPDFKLEDFYSASSELFPRYVGRGGIDGDGITTPRRISSRFN FVLUNDRKGVHPIMADGGFSVEYGRILMGILSTLERGLITGCHTKR GPPDFKLEDFYSASSELFPRYVGRGGIDGDGITTPRRISSRFN FVLUNDRKGVHPIMADGGFSKSVENGRIBTRGGOTTLK GPPDFKLEDFYSASSELFFBYYGRGGIDGDGITTPRRISSRFN FVLUNDRKGVHPIMADGGFSKSVENGRIGBILKGQLLLCQFLMA LSIVRTGGHFICKTFDLFTFFNSGLVYLLKCLFKFRITS			ļ	YMDVVKERIRLARQIBKSEYRNFQACLHNSWIEQAAAALEIBLB
S528 3 895 GPFISACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKEP YVRDPEADDTCLAHCMVVVRLDGRDFHRFAREKINFARKNDSRAL QLM-KCAQTVMEELEDIVIANGQDEKSFVYRKKTMWFKRRASK EMTHUAGQRASEVVYRHDYEEDQPLLYPPGFDGRVVVYPSDKT- LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTL AADKNELLFSERNIHYNNEPFMYRKGTVLLIMQKUDEVVTKEIKL PTEMEGKKMAVTRIKTKYCKYSHLBPRAPCLRWI  S529 48 640 TPRIVSAHLKTRKLINPEAABKRRRDWDSKQGWLSVKMQRVSGL LSWTLSRVINLISGLSBPGARQPRIMEEKALEVYDLIFTIRDPE KRATILEELEVVSESCVEVQEINEERTIVIIRTPTYPDECSLATI TGLCLRVKLQRCLPPKHKLBTY1SEGTHSTEBDINKQINDKERV AAMEMPRILRETVEGVULEPD  S530 4541 2606 AQIVHAISYCHKLHVGHRDLKFENVVFFEKQGLVKLTDFGFSNK PQBCKKLITISCOSLAYSAPELLIADBEVDAPADUNSLGVILIFML VOGSPPPQRANDSETLIMIMDCKYTTVPSHVSKKCKOLTITMIOR DFKRRASLERIENHEWLQGVDPSPATKYNIPJUSVKNILSRESHN SIIQMWILGDIADRDAIVRALETNRYNHTTATYFILAERILREK QREKIQTRASEFSNIKAQPRSSMPTKIDVPQDLEDDLTATPLSH ATVQSPARAADSVINGHRSRGICDSAKKODLPELAGPALSTVP PASLRFTPTSGRKCLFRVEDEKBEDKKMMSISTVVINIRKPS VTNRLTSRKSAPVLNQIFEBGESDDEFSKRKDLKDSGF TTSWHRENDSKGPPGSBGGGGGSKSSISTSDDDSFSRRRLDKDSGF VTNRLTSRKSAPVLNQIFEBGESDDEFSKRRLDKDSGF TSWHRENSSKGPPGSBGGGGGSKSSISTSDDSFSRRRLDKDSGF CGSPSSGGGGMFTNTSGTTRRCAGPENSMOLASRSAGELVESLK LMSLCLGSQLHIGSTKYIIDPOMGLSFSVKVQBKSTKMCISST CRAGQVPANGGIKFFSDHADDTTELERIKKRNINNOLQLPIC EKTISVNIORIPKEGLLCASSPASCCHVT ALEPULLPLFQYNCRQPSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC GSPRAPARPROBMERPEPETLTGSRRAVSKSPLRHGTVLFARLF ALEPULLPLFQYNCRQPSSPEDCLSSPFTUDHIRKVMLVIDAAV TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGRAPTPATARAMSQLVANVQNARSRMDGB  5532 3395 1402 SDMWVGKRRMITEDETBFCGEELLHSVLQCKSVPDVLDGREMR RARTANNFYRHRYGRVFTLIRAANKMANNDMPCDMFTNPRBSYG KPLVKDRRSRLITFRYRGROUPLAARKMANNDMPCVDMFTNPRBSYG KPLVKDRRSRLITFRYRGROUPLAARKMANNDMPCVDMFTNPRBSYG KPLVKDRRSRLITFRYRGROUPLAARKMANNDMPCVDMFTNPRBSYG KPLVKDRRSRLITFRYRGROUPLAARKMANNDMPCDMFTNPRBSYG KPLVKDRRSRLITFRYRGROUPLAARKMANNDMPCVDMFTNPRBSYG KPLVKDRRSRLITFRYRGROUPLAARKMANNDMPCDFORMTNPRBSYG KPLVKDRRSRLITFRYRGROUPLAARKMANNDMPCDFORMTNPRBSYG KPLVKDRRSRLITFRYRGROUPLAARKMANNDMPCDFORMTNPRBSYG KPLVKDRRSRLITFRYRGROUPLAARAKMANNDMPCDFORMTNPRBSYG KPLVKDR		Í	ł	EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLFTBSQKTK
S528   S95   GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKPF YVRDPRADDYCLAHCWVVVRLDGRAPHRPAKHMFAKRMDSRAL OLM-KCAQTVMERIBIDIVIANGOSDEYSFVERKTANDSRAL LKDYLSWRQADCHINNLYNTVFRALIQQSGLTPVQAQGRLQGTL LKDYLSWRQADCHINNLYNTVFRALIQQSGLTPVQAQGRLQGTL AADKNELLFSEPRINNNNEPPHRRSTVLIMQKVDEWATKRIKL PTEMEGKGMAVTRTRYKPCKPSHLPRAPCLRRIL TYPKLVSAHLKTRKLIMPERABERRRDWDSHGGWLSVKMQRVSGL LSWTLSRVLMLSGLSBPGAARQPRIMEBRILVLIRFTPTVPHCSLATL IGLGLRVKLQRGLPFHKLBIVISSGTHSTBEDINKQINDKERV AAAMENDNLBSUVGCULBPD KRYTLERLEVVSSSCVEVQEINEBRILVLIRFTPTVPHCSLATL IGLGLRVKLQRGLPFHKLBIVISSGTHSTBEDINKQINDKERV AAAMENDNLBSUVGCULBPD		j	į	YPTQSGKPPLLVSAPSKSBSALSCLSKQKKKKTKKPKBPQPEQP
YVRPPEADDTCLAHCWVVRLDGRNPHRPAEKHNFAKPNDSRAL OLMTKCAGTVMERLBIDIVIAYGGSDEYSEVKRKTNWFKRRASK FMTHVAGQPASSVFVKRDYEBQPILVPPGFGGRVVYPSNCT LKDYLSKRQADCHINNLYMTVFMALIQQSGLTPVQAQGRLQGTL AADENEILIPSEPNINYNNEPFMYRRGTVLIWQKVDDWTKEIKL PTEMEGKMAVTRITRIKPCKPSHLERAPCLERBL  5529 48 640 TPRIVSAHLKITKALINPEAAERRWRDWDSHGGWLSVKNQRVSGL LSWTLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDPE KPRYLEELEVVSSSCVEVQEINBERYLVIIRFTPTVPHCSLATL IGLCLRVKLQRCLPFKHKLBYYISBGTHSTBEDINKQINDKERV AAAMENPNLRBIVEQCVLEPD  5530 4541 2606 AQIVHALSYCHKLHVGHRDLKPENVVFFEKQGLVKLIDFGFSNK FQPGKKLATTSGSLAYSAPBILLGDBYDAPAVDINSLGVILFML VCQPPPQEANDSSTLTMINDCKYTVPSHVSKECKDLITRMLQR PKRRASLEEIBHBWLQGVDPSPATKNIPLVSYKALSBESHN SILQRWILGBIADRDAIVEALETNRYNHITATYFILABRILRER QBKRIQTRSASPSNIKAQPRQSWPTKIDVPQDLEDDLTAPTLSH QBKRIQTRSASPSNIKAQPRQSWPTKIDVPQDLEDDLTAPTLSH ATVYQSPARAADSVLNGHRSKGLCDSAKKDDLPRLAGPALSTVP PASLKPTASGRKCLFRVEEDBEEDBEDKKMSLSTQVVLRRKES VTNRLTSRSSAPVLNQIFFSEGSDDEFDMDRNLPPRLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRBGLSSBGPPGSBGDGGGGSKPSNAGARSGUPKASPERNAG GGSPSSGGGGNPTWTTGTTTRCAGPSNAMDLASRSAGELVENSL GGSPSSGGGGNPTWTTGTTTRCAGPSNAMDLASRSAGELVENSL GGSPSGGGGNPTWTTGTTTRCAGPSNAMDLASRSAGELVENSL GGSPSGGGGNPTWTTGTTTRCAGPSNAMDLASRSAGELVENSL GRAGQVPAVGG IKFPSDIMADTTTEILRRIJKKNILKNAVLQLPLC EKTISVNITQRNEREGLLCASSPSSCLGVI  5531 24 515 GSQFRAPRPROSMERPEPELIRGSWRAVSKSPLEHGTVLFARLF ALEPDLLPLGVNCRQFSSPBCLSSPSTVGESLLYMLEKC LGPAPTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDMNVGKRRMIIEBETBFCGEBLLHSVLQCKSVPDVLDGEBMR RATRANPYEMIRGVPFLURAAMKMANDFVPDRMFTNPRDSYG KPLVVDDRRASHLIYFADVCAGGGFSBTVLWRKKMHARGFGMTLK GPNDFKLBIPTYSASSELPBTYGGSGTDGDDITTPENTSAFRN FVLINTDRRGSVPFLURADGGFSPEVGLNQBTLISQULLLCQFLMA LSIVRYGGBFICKSTPDLFTPSVGLVJLLSCQCLLLCQFLMA		ł		QPSTSAN
QLMCKCAQTVMERLEDTVI AYGQSDEYSFVEKRTINFKRRASK FMTHVASQPASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNCT LKDYLSKRQADCHINNLYNTYFWALIQQSGLTFVQAQGRLQGTL AADRIELLFSEFNINYNEPEMYRRGYVLIMQKUDEVMTKEIKL PTEMEGKIMAVTRITKPCKPSHLPRAPCLRWL  5529 48 640 TPRLVSAHLKTRKLINPEAARRRRIDDDSRQGWLSVKMQRVSGL LSWILSRULMISGLSBPGAARQPRI IMBEKALEVYJLTRITRDPB KPWTLERLEVVSSCVEVQBINERBYJLVI IRFTPTVPHCSLATL IGLCLRVKLQRCLPFKHKLBIYJSGGTHSTREDINKQINNKERV AAAMENIPHILBELVQCULBPD  5530 4541 2606 AQIVHALSYGKIKLWGGREDEKAPRVVFPEKQGLVKLTDFGFSNK VCSQPPPQEANDSSITJMIHDCKYTVPSHVSKRCKDLITRMLQR PQRKKLTTSCGSLAYSAPBILLGDEYDAPAVDINSLGVILFML VCSQPPPQEANDSSITJMIHDCKYTVPSHVSKRCKDLITRMLQR PKRRASLEBI ERNHPWLQGUDPSPATTYNITPUSYKNLSEBEN SIIQRMVLGDIADRDAIVRALETNRYNHITATYFLLABRILREK QBKRIQTRSASPSNIRAQPRQSWPTKUDVGDEDDLTATPLEH ATVVQSPARAADSVINCHRSKGLCDSAKKODLPELASPRASTVP PASLKPTASGRKCLFRVEEDEBEDEEDKRMSLSTQVULRRKPS VTNRLTSRKSAPVLNQI IFBEGSCDSEFNAGGGVKSPSKNNAG GSPSGGGGGNFTNTSGTTRCAGPSNSMQLASPSRNNAG GCSPSSGGGGNFTNTSGTTRCAGPSNSMQLASPSRNNAG GCSPSSGSGGGNFTNTSGTTRCAGPSNSMQLASPSRNNAG GCSPSSGSGGNFTNTSGTTRCAGPSNSMQLASRSAGELVBSILK LMSLCLGSQLHGSTKYI IDPONGLSFSSVKQBKSTHKMCISST GNAGQVPAUGI KFFSDHADDTTTBLER IKSKNLKNNVLQLFLC EKTISVNIQRNPKEGILCASPASCCHVI  5531 24 515 GSQFRAPRPRDSNERPEPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLIPLGYNCRQFSSPBOLCISSPFLDHTRKVMLVIDAAV TNVEDLSSLESYLASLGRKHRAUGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAANSQLYGRVVQAMSRKWDGB 5532 3395 1402 SDMNVVGKRMI IBDETBFGGBELLHSVLQCKSVFDVLGGERBY KPLVKDRBABILLYFADVCAGPGGFSRYVLWRKMHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGIDGDGTTPPENTSAFRN FVLINTDRKSVHFLNBAMKMANMDPVFDRMFTNPDSYG KPLVKDRBABILLYFADVCAGPGGFSRYVLWRKMHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGIDGGDTTPPENTSAFRN FVLINTDRKSVHFLNBAMKMANMDPVFDRMFTNPLSAFRN FVLINTDRKSVHFLNBAMKMANMDPVFDRMFTNPLSAFRN FVLINTDRKSVHFLNBAGGGFSVEGGRDGGDTTRPENTSAFRN FVLINTDRKSVHFLNBAGGGFSVEGGRDGGDTTRPENTSAFRN FVLINTDRKSVHFLNBAGGGFSVEGGRNGLKGCLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGGRIDGGDTTRPENTSAFRN	5528	3	895	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFB
FMTHVASQPASSYVEYWRDYFEQPLLYPPGFOGRVUVYPSNQT LKYYLSWRQADCHINNLYNTVFWALLQSGLITVQAGGRLQGTI, AADENBILIFSEFNINYNNEPFMYRRGYVLIWKYDEWMTKRIKL PTEMEGKMAVTRITKIPCKESHLPRAPCLRWL  5529 48 640 TPRIVSARIKITRKLINFEAAERRWRDWDSRGGWLSVKMQRVSGL LSWTISRVLMISGISBPGAARQPRIMERKALEVYDLIRTIRDPE KPWILBELEVVSBSCVBVQBINERRYLVIIRFTPTVPHCSLATI, IGLCLRVKLQRCLPFKHKLBTYISBGTHSTREDINKQINNKERV AAAMENPILREIVEQCVLLEPP  5530 4541 2606 AQIVHAISYCHKLHVGRDEKPENVVPFEKQGLVKLTDFGFSNK FQFRKKLIATSCGSLAYSAPBILLGDEYDAPAVDINSLGVILFFHL VCSGPPPQEANDGSTLTMINDCKYTVPSHVSKRKCKDLITMINQR DPRRASLERIEMPHILGGVDPSPATKYNTPLVSYKRILSBESH SIIQBMVLGDIARDAIVEALETINFYNHITATYFLLARRILREK QRKEIQTRSASPSNIKAQFRGSWFTKIDVPQDLEDDLTATPLSH ATVPQSBARAADSVLNGHRSRGLCDSAKKODLPBLAGPALSTVP PASLKPTASGRKCLFRVEEDBEEDBEKKPMSLSTQVVLRKPS VTNRLTSRKSAPVINQIFFBESGDDEFDMENLPPKLSKLKMIT ASPGTVHKRYHRRKSGCRGSSCSSSTSDDDSESRRRLDRDSGF TYSWHRDSSGPPGSBGDGGGGKPSNASGGVDKASPSENNAG GCSPSSGSGOPPTNTSGTTTRCAGPSNSMGLAGRSAGELVESIK LMSLCLSSQLHGSTKYIIDPONGLSPSSVKVQBKSTKKMCISST CNRGQVPAVGGIKFSDHADTTTBLERIKSKNILKNVLQLPLC EKTISVNTORNFREGLLCASSPASCGHV SSVKVQBKRSTKKMCISST CNRGQVPAVGGIKFRRAGGVKLSSFSTYGESLLYMLEKC LGPAPTPATRAMVSQLYGAVVQAMSRGWDGB  5531 24 515 GSQPRAPRPRDSMERPEPETIRGSWRAVSKSPLEHGTVLPARLF ALEPOLLPLGYNCROPSSPBCLASSPSTUGESLLYMLEKC LGPAPTPATRAMVSQLYGAVVQAMSRGWDGB  SDMNVGKRRMIIBDETBPGGBELLHSVLQCKSVPDVLLGERMI KPLVKDREAKLLYFADVCAGPGGFSBYVLWRKMHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGIDGDDITTRPNTSAFRN FVLINTDRKSUMFLINAAMKMAMMDFUPDRMFTNIPRDSYG KPLVKDREAKLLYFADVCAGPGGFSBYVLWRKMHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGIDGDDITTRPNTSAFRN FVLINTDRKSUMFLINAAGGFSVEGGRILDGILLCOFIMA LSIVRTGGHFICKTFDLFFFFSGLUVLLCKFRPTTSAFRN		ļ		YVRDFEADDTCLAHCWVVVRLDGRNFHRPAEKHNFAKPNDSRAL
LKDYLSWRQADCHINNLYNTVFMALIQQSGLTPVQAQGRLQGTL AARKBELIFSEFNINYNNEPEMYRRGTVLIWQKVDEWMTKEIKL PTEMEGKMAVTRITKTPCKYSHLPRAPCLEWL  5529 48 640 TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGKLSVKMQRVSGL LSWILSRULMISGISBEGAARQPRIMBEKALEVYZLIRTIRDPE KPHYLBELEVVSSCVEVQEINERRYLVIIRTPTVPHCSLATL IGLCLRVKLQRCLPPKHKLBIYISBGTHSTEEDINKQINDKERV AAAMENPHILBELTVEQCVLEPD  5530 4541 2606 AQIVHALSYCHKLHVGHERDKYPENVVPFEKQGLVKLTDFGFSNK PQRGKKLITISGSLAYSAPRILLGDEYDAPAVDINSLGVILFML VCGQPPPQEANDSSTITMINDCKYTVPSHVSKRCKDLITMMLQR DPKRRASLERIENHPWLQVDPSPATKYNIPLVSYKNLSBEENN SILQRWIGDIADRDAIVRALETINKYNHTIATYFLLARRILREK QKKSIQTRSASPSNIKAQPRQSWFTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEBEDEBCKKMSISTQVVLRRKES VTNRLTSRKSAPVLNQIFEBESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRKSGGRGSSCSSSETSDDDSFSRRLDKDSGF TYSWHRDSSBGPPGSBGDGGGQSKPSNASGGDVKASPSENNAG GGSPSSGGCMPTNTSGTTRRCAGPSSNWQLASRSAGELVESIK LMSLCLGSQLHGSTKYIIDPQNGLSFSVKVQKKSIFMKMCISST CNAGQVPAVGGIKFFSDHAADTTTELERIKGSKNLKNNVLQLFLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQRRAPRPRDSNERPEPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLPQVNCRQFSSPBCLISSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKRRAVGVKLSSFSTVCESLIYMLEKC LGPAFTPATRAARSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWNVGKRMIIEDETBFCGEELHSVLQCKSVPDVLDGEEMR RARTRNPYBMIRGVFFLNRAMKMANMDFVFDRMFTNPRDSYG KPLVKDREABLLYFADVCAGPGGPSBYVLWRKMHAKGFGMTLK GPMDFKLEDFYSASSELFBPYYGRGGIDGGDLTRFENISAFRN FULLNTDRKSUMPLMADAGGFSQCRORLDKILSSCLLLCCFINA LGIVRTGGHPICKTFDLFFFYSVGLVYLLYCCFRRVCLFKPITS			i	QLMTKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK
AADKNEILPSEFNINYNNEPPMYRRGTVLIWQKVDEVMTKEIKL PTEMEGKKMAVTRITKTKCKSBILBERAPCIRWI  5529 48 640 TFRIVSAHLKITKLINDERAPEGRHENDENGGISVKMQRVSGE LSWTLSRUIMISGESEPGARQPRIMEERALEVYDLIRTIRDE KPRILEELEVVSESCVEVQEINERBYLVIIRFTPTVPHCSLATL IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEBDINKQINDKERV AAAMENPILREILVSCULEPD  5530 4541 2606 AQIVBAISYCHKLHVGHRDLKPENVVFPEKQGLVKLTDFGFSNK FQPSKKLITISGSIAYSAPBILLGDEYDAPAVDINSLGVILIPHL VCGQPPPGEAMDSETLITHIMDCKYTVPSHVSKKCKOLITAMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPILVSYKNLSEEEIN SIIQRMVLGDIADRDAIVVALETNEYNHTTATTFLLABRILREK QEKELQTTRSASPSNIKAQFRQSWPTKLDVPQDLEDDLTATPLSH ATTVQSFARAADSVLNGHRSKGLCDSAKKODLPELAGPALSTVP PASLKPTASGGKCLFVVEDEBEDEBDKKPMSISTQVVLRRKPS VTNRLTSRKSAPVINQIFPEGESDDEFDMCDENLPPKLSRLKMNI ASPGTVHKRYTRRRGGGRSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSEGPPSBEGGGGGKKPSNASGGVDKASPSENNAG GGSPSSGGGMPTTNTSGTTRRCAGFSNMQLASREAGELVESLK LMSLCLGSQLGSTKYIDPONGLSFSSVKVORKSTWKMCISST TYSWHRRDSSEGPPSBEGGGGGKKPSNASGGVDKASPSENNAG GGSPSSGGGMPTTTSGTTRCAGFSNMQLASREAGELVESLK LMSLCLGSQLGSTKYIDPONGLSFSSVKVORKSTWKMCISST TYSWHRRDSSEGPPSBEGLGGSGKSCSSETSDDDESRRRLDKDLGPLC EKTISVNIORNPRKGILCASSPASCCHVI SCHRGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIORNPRKGILCASSPASCCHVI ALEPDLLPLFQYNCRQFSSPBCLSSPREIDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAMSQLYGAVVQAMSGRØDGB SDMVVGKRKMITEDETEPCGERLIHSVLQCKSVPDVLDGEEMR RARTRNPYEMIRCVFFINRAAMKMAMDPVEDRMFTNPRDSYG KPLVKDREAELLYPADVCAGPGFSRYVLWRKKMHAKGFGMTLK GPNDFKLEDFYSASSELFEPTYGGSGIGDGDDITRPENTSAFRN FULINTDRKGYPTINRAAMKMANDPVEDRMFTNPRDSYG KPLVKDREAELLYPADVCAGPGGFSRYVLWRKKMHAKGFGMTLK GPNDFKLEDFYSASSELFEPTYGGSGIGDGDDITRPENTSAFRN FULINTDRKGGYPTLAKAGGSVFGGRUDGBTLSKQLLLCOFILMA LSIVRTGGHPICKTFDLFTDFFVSGLVVILLYCCFERVCLFKPITS				FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNCT
PTEMEGKKMAVTRITKPCKPSHLPRAPCLRWL  5529  48  640  TPRIVSARILKTIKLINPERAERERMENDESKOGWLSVKMQRVSGL LSWILSGULINGGLSBEGARQPR IMBERALEVYDLIRTIRDPE KRYTLEELEVVSESCVEVQEINEBRYLVIIRTIPTVPHCSLATL IGLCLRVKLQRCLPPKHKLBIYISBSTHSTEEDINKQINDKERV AAAMENPHLREIVEQCVLEPP  AAAMENPHLREIVEQCVLEPP  5530  4541  2606  AQIVHALSYCHKLHVGHEDLKPENVVPFEKQGLVKLTDFGFSNK FQPGKKLTTSGSILAYSAPEILLGDBYDAPAVDINSLGVILPHL VCGQPPPGEANDSETLTMIMDCKYTVPSHVSKEKCHLITMLQR DPKRRASLERIENHPWLGGVDPSPATKYNIPLVSYKNLSEBEIN SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK QEKRIQTRSASPSHIKAQFRGSWPYKIDVPQDLEDDLTATPLEH ATVPQSPARAADSVILGHERGSKILCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEBEDEEKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEGESDDEFDMDERLPPKISKLKMMI ASPGTVHKRYRRRRSQGGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSEGPPGSBEDGGGGKPSNASGGVDKASPSEENNAG GGSPSSGGGMPTNTSGTTRRCAGPSNASGGVDKASPSEENNAG GGSPSSGGGGPTTNTSGTTRRCAGPSNASGGVDKASPSEENNAG GGSPSSGGGGPTNTTGTTRRCAGPSNASGGVDKASPSEENNAG GGSPSSGGGRPTNTSGTTRRCAGPSNASGGVDKASPSEENNAG GGSPSGGGGPTNTTGTTRRCAGPSNASGGVDKASPSEENNAG GGSPSGGGGPTNTTTELERIKGKNIKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531  24  515 GSQPRAPRPRDSNERPPEELIRGKRAVGNKLSSFSTVGESLLYMLEKC LGPAFTPATRAAMSQLYGAVVQAMSGGMDGB  5532 3395 1402 SDMVVGKRRMITEDETEFCGEELLHSVLGKSVPDVLDGEEMR RARTRANPYEMIRGVFFILNRAAMKMANDPVEDRMFTNPRDSYG KPLVKDRBABLLYFADVCAGPGGPSRYVLWRKKMHAKGFGMTLK GPNDFKLEDPYSASSELFRYYGGGSIGGGDICDEITRPENTSAFNN FULINTDRKGVPHTIMAGGSVFGGIDGGDITTRPENTSAFNN FULINTDRKGVPHTIMAGGSVFGGNUGBTLSKQLLLCOFLMA LSIVRTGGHPICKTFDLFTDFFSVGLVYLLYCCFERVCLFKPITS				LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTL
TPRIVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL   LSWTLSRVIMLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDPE   KPNTLEELEVVSSSCVEVQEINERBYLVIIRFPTTVPHCSLATI   TGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV     AAMENPHIRELVEQCULBPD     S530   4541   2606   AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK     VCGQPPFQEANDSETLTMINDCKYTVPSHVSKBCKDLITMLQR     VCGQPPFQEANDSETLTMINDCKYTVPSHVSKBCKDLITMLQR     DPKRRASLERIENHPWLQGVDPSPATTYNTELVSYKNLSEBERIN     SIIQRWLGDIADRATVRYNHITATYFLLABRILREK     QRKEIQTRSASPSNIKAQPRQSWPTKLDVPQDLEDDLTATPLSH     ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP     PASLKPTASGRKCLFRVEEDBERDERKMSLSTQVVURRKES     VTNRLTSRKSAPVLNQIFESGSDDBFDMDRNLPPKLSRLKMMI     ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF     TYSWHRBISSRSPPGSBGDGGGSKPSNASGGVDKASPSENNAG     GGSPSSGSGGNPTNTSGTTRCAGPSNSMQLASRSAGELVESIK     LMSLCLGSQLIGSTKYIIDPONGLSPSSVKVQBKSTWKNCISST     GNGQVPAVGGIKFPSDHMADTTTELERIKSKNLKNNVLQLPLC     EKTISVNIQRNPKEGLLCASSPASCCHVI     ALEPOLLPLPQYNCQPSSPRCLSSPETDHIRKVMLVIDAAV     TNVEDLSSLEEVLASLGRHRAQGVKLSSPTVGESLLYMLEKC     LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB     SDWAVGGRRMIIEDETBFCGEBLHSVLQCKSVFDVLDGREMR     RARTRANPYENIRGVFFINRAAMKMANMDPVFDRMFTMPRDSYG     KPLVKDREABLLYPADVCAGPGGFSKYVLMRKNHAKGFGMTLK     GRODFKLEDFYSASSELLEPYLGGGGTGDGDITRPRNISAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGLLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGLLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGLLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGLLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGLLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGLLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGLLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGLLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGLLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGCHLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGCHLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGNILGBILSKGCHLLACFMATSAFRN     FVILINTDRKGVHFIMADGGFSVEGGRNILGBILSKGCHLACFMATSAFR     FVILINTDRKGVHFIMADGGFSVEGGLTREFT     FVILINTDRKGVHFIMADGGFSVEGGLT		<u> </u>		AADKNEILFSEFNINYNNEPPMYRKGTVLIWQKVDEVMTKBIKL
LSWTLSRVLMLSGLSEPGARQPRIMEEKALEVYDLIRTIRDPE KPRTLERLEVVSESCUEVQELIRBERYLVIIRTPTPYPHCSLATL IGLCLRVKLQRCLPPKHKLBIYISEGTHSTBEDINKQINDKERV AAMMENPHLRELVEQCVLEPD  5530 4541 2606 AQIVHAISYCHKLHVGHRDLKPERVVFPEKQGLVKLTDEGFSNK FQPGKKLTTSCGSLAYSAPBILLGDEYDAPAVDINSLGVILFML VCGQPPPGANDSETLTMUMDCKYTVPSHVSKRCKDLITRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEN SIIQRMVLGDIADRDAIVERLETNRYNHITATYFLLARRILREK QEKRIQTRSAFPSNIKAPKLDYPQDLEDDLTATPLEK ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEBEDEEKKPMSLSTQVVLRRKES VTNRLTSRKSAPVLNQIFEBGESDDEPDMDERLPPKLSRLKMNI ASSCTVHKRYHRRNSGGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGMPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLIGSTKYLIDPQNGLSFSSVKVQBKSTWKMCISST GNAGQVPAVGGIKFPSDHMADTTTELERIKGKNLKNNVLQLPLC EKTISVNIORNPKEGLLCASSPASCCHVI  5531 24 515 GSGFRAPRPSMERPEPELIRGSWRAVSKSPLEHGTVLFARLF ALEPDLLPCHYNCRQFSSPBCCISSPETDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB 5532 3395 1402 SDMVVGKKMITEDETBPGGPSELHSVLQCKSVPDVLDGREMR RARTRANPYEMIRGVFFLNRAAMKMANDFVFDRMFTNPRDSYG KPLVKDREABLLYPADVCAGPGGFSRYVLWRKKMHAKGFGMTLK GPMDFKLEDFYSASSELERBYYGGGGTGGDITRPRNISAFRN FULINTORKGVHFILMBADGGFSVEGGRNLQBILSGALLLCOFIMA LSIVRTGGHPICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS				PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL
KPNTLEELEVVSESCVEVQBINEBERYLVIIRFTPTVPHCSLATL IGLCLRVKIQRCLPPKHKLBIYISBGTHSTEEDINKQINDKERV AAAMENPHLREIVEQCVLEPD  5530 4541 2606 AQIVHAISYCHKLHVOHRDLKPENVVFFEKQGLVKLTDFGFSNK FQPGKKLTTSCGSLAYSAPBILLGDEYDAPAVDINSLGVILFML VCSQPPFQEANDSETTTMIMDCKYTVPSHVSKECKDLITRMLQR DPKRRASLEBIENHPWLGVDPSPATKYNIPLVSYKNLSBEERN SIIQRWULGDIADRDAIVEALETINEYNHTTATYFLLABRILBEK QEKBIQTRSASPSNIKAQPRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRESGLCDSAKKDDLPELAGPALSTVV PASLKPTASGRKCLFRVEEDEBEDBEKKFMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFBEGSDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSSBRRRLDKDSGF TYSWRRDSBGPPGSEDGGGQSKPSNAGGVDKASPSENAG GCSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESIK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQBKSTWKMCISST GRAGQVPAVGGIKFPSDHMADTTTELER KBKNILKNNVLQLFLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQPRAPRPRDSMERPEDELTRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLPQYNCRQFSSPEDCLSSPBFLDHIRKVMLVIDAAV TNVEDLSSLEBYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAPTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDMNVGKRKMIIEDBTBPCGBBLLHSVLQCKSVPDVLDGEBMR RARTRANPYEMIRGVFFLNRAAMKMANMDPVFDRMFTNPRDSYG KPLVKDRBABLLYFADVCAGPGGFSBYVLWRKKMHAKGFGMTLK GPMDFKLEDFYSASSELLEBPYYGEGGIDGDGDTRPENISAPRN FVLINTDRKGVHFLMADGGFSVFGGBNLQBILSKQLLLCQFLMA LGIVRTGGHPICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS	5529	48	640	TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL
IGLCLRVKLQRCLPPKHKLBIYISBGTHSTBEDINKQINDKERV AAAMENPHIRBIVEQCULEPD  5530 4541 2606 AQIVHAISYCHKLHVQHRDPD FORGKKLTTSCGSIAYSAPBILLGDBYDAPAVDIWSLGVILFML VCGQPPFQEANDSBILTMIMDCKYTVPSHVSKBCKDLITRMLQR PORKKLTTSCGSIAYSAPBILLGDBYDAPAVDIWSLGVILFML VCGQPPFQEANDSBILTMIMDCKYTVPSHVSKBCKDLITRMLQR DPKRRASLEBIRHPWLQGVDPSPATKYNTPLVSYKNLSBEBIN SILQRWYLGDIADRDAIVRALETNRYNHITATYFILLARRILERK QKRSIQTRSASPSHIKAQFRGSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVBEDBEBEDBEDKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFBEGSDDEFDMDRNLPPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSBGPPGSEGSDGSQSKPSNASGGVDKASPSENNAG GGSPSSGGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVQKKSTHKMCISST GRAGQVPAVGGIKPFSDHADDTTTELERIKSKNIKNNVLQLPLC EKTISVNTQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQPRAPRPRDSMERPEPETIRQSWRAVSRSPLEHGTVLFARLF ALEDDLEPLGYNCRQFSSPBCLSSPBFLDHTRKVMLVIDAAV TNVEDLSSLEBYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB 5532 3395 1402 SDMVVGKRKMIIBDETBFCGEBLLHSVLQCKSVFDVLDGREMR RATRANPYEMIRGVFFLNRAMKMANMDFVFDRMFTNPRDSYG KPLVKDRABALLYFADVCAGPGGFSBYVLWRKKMHAKGFGMTLK GPNDFKLBDFYSASSELLFBPYYGEGGIDGDGDTTRPENISAFRN FVLINTDRKGVHFIMADGGFSVECGBNLQBILSKQLLLCQFIMA LGIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS				LSWTLSRVLWLSGLSBPGAARQPRIMEEKALEVYOLIRTIRDPE
AAAMENPNLRBIVEQCVLEPD  5530  4541  2606  AQIVHAISYCHKLHVGHREDKPENVVFPEKQGLVKLTDFGFSNK FQPGKKLTTSCGSLAYSAPBILLGDBYDAPAVDINSLGVILFML VCGQPPFQEANDESTLTMINDCKYTVPSHVSKECKDLITRMLQR DFKRRASLEBIENHPWLQGVDPSPATKYNIPLVSYKNLSBEBEN SIIQBMVLGDIADRDAIVEALBTNRYNHITATVFLLABRILBEK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVINGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVBEDBBEDEBDKKPMSLSTQVVLRRKPS VTNRLITSRKSAPVLNQIFBGBSDDBFPMDBRLPPKLSRLKNNI ASPGTVHKRYHRRKSQFGSSCSSETSDDDSESRRRLDKDSGF TYSWHRRNSBGPPGSBCDGGGGSKPSNASGGVDKASPSENNAG GCSPSSGSGMPTNTSGTTRRCAGPSNSMQLASRSGELVBSLK LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVQBKSTNKMCISST GNAGQVPAVGGIKFFSDHMADTTTBLBRIKSKNLKNNVLQLPLC EKTISVNIQNRPKEGLLCASSPASCCKVI  5531  24  515 GSQPRAPRPDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQPSSPBDCLSSPBFLDHIRKVMLVIDAAV TNVEDLSSLEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGMDGB  5532 3395 1402 SDMNVGKRKMIIEDBTBFCGEBLLHSVLQCKSVPDVLDGBEMR RARTRANPYEMIRGVFFLNRAAMKMANMDPVFDRMFTNPRDSYG KPLVKDRABRLLYPADVCAGPGGFSBRVLWRRKMHARGFGMTLK GPNDFKLEDFYSASSELFBPYYGEGGIDGDGDTRPENISAFRN FVLINTDRKGVHENLANGGFSVFGGRINLGRILSKQLLLCQFIMA LGIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS		,		KPNTLEELEVVSESCVEVQEINEERYLVIIRFTPTVPHCSLATL
5530  4541  2606  AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK FQPGKKLITEGGSLAYSAPKILLGBYDAPAVDINSLGVILFML VCGQPPFQEANDSETITMIMDCKYTVPSHVSKEKDLITRMLQR DPKRRASLEEIBNHPWLQGUOPSPATKYNIPLVSYKNLSEEEIN SIIQBMVLGDIADRDAIVERLETNEYNHITATYFLLAKRILKEK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVVQSPARAADSVLNGHRSKGLCDSAKKDDLPBLAGPALSTVP PASLKPTASGRKCLFRVEEDEBEEDEKKPMSLSTQVVLRRKPS VTNRLITSRKSAPVLNQIFBEGESDDEFDMDENLPPKLSRLKNNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSEGPPGSBGDGGGQSKPSNASGGVDKASPSENNAG GGSPSSGGGCNPTNTTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVQBKSTWKMCISST GRAGQVPAVGGIKFFSDHADTTTBLERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASPASCCHVI  5531  24  515 GSQPRAPRPRDSMERPEPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLFQYNCRQFSSPBOCLSSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAMSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWMVGKRKMITEDETBPCGEBLLHSVLQCKSVPDVLDGREMR RATTRANPYEMIRGVFFLNRAAMKMANMDPVFDRMFTNPRDSYG KPLVKDRBARLLYPADVCAGPGGFSBYVLWRKWBAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGTDGDGDITRPENISAFN FVLINTDRKGVHFLMADGGFVEGGDDLOSILSKQLLLCQFIMA LGIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLPKPITS		İ	· ·	IGLCLRVKLQRCLPFKHKLBIYISEGTHSTBEDINKQINDKERV
FQPGKKLTTSCGSLAYSAPBILLGDBYDAPAVDINSLGVILFML VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKRCKDLITRMLQR DPKRRASLERIENIPWLQGVDPSPATKYNITIVSYKNLSBERIN SILQRMVLGDIADRADAIVRALETINRYNHITATYFLLAERILREK QEKBIQTREASPSNIKAQPRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDBEEDEEDKKPMSLSTQVVLRRKPS VTNRLITSRKSAPVLNQIFBRSGSDDFPDMDERLPPKLSRLKNNI ASPGTVHKRYHRRKSQGRGSSCSSETSDDDSESRRRLDKDGGF TYSWHRRDSSBGPGSGGGGSKPSNASGGVDKASPSENNAG GGSPSSGGGMPTNTSGTTRRCAGPSNSMQLASRSAGELVESIK LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVQBKSTWKMCISST GRAGQVPAVGGIKFFSDHMADTTTELBRIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASPASCCHVI SETTISVNIQRNPKEGLLCASSPASCCHVI ALEPDLLPLFQYNCRQFSSPBCLLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAPTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWMVGKRKMIIBDETBPCGEBLLHSVLQCKSVPDVLDGREMR RARTRANFYEMIRGVFFLNRAAMKNANMDPVFDRMFTNPRDSYG KPLVKDREABLLYFADVCAGPGGFSBYVLWRKKWHAKGFGMTLK GPNDFKLBDPYSASSELFBPYYGRGGIDGDGDITRPENISAFRN FVLUNTDRKGVHFLMADAGGFSVEGGBNLQBILSKQLLLCQFIMA LGIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS		į		AAAMENPNLRBIVEQCVLEPD
VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR DPKRRASLERIENHPHIQGVDPSPATKYNIPLVSVKNLSEBERN SIIQBMVLGDIADRDAIVEALETINRYNHITATYFLLAERILIREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATTVPQSPARAADSVLNGHRSKGLCDSAKKDDLPBELAGPALSTVP PASLKPTASGRKCLFRVEEDEBEDEEDKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFBEGESDDEFDMDENLPPKLSRLKNNI ASPGTVHKRYHRRKSQGRGSSCSSSETDDDSESRRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGQSKPSNASGGVDKASPSENNAG GGSPSGSGGEMPTNTSGTTRRCAGPSNSMQLASRSAGELVBSLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQBKSTWKMCISST GNAGQVPAVGGIKPFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQPRAPRPDSMERPEPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLPQVNCRQFSSPBDCLSSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWMVGKRKMIIEDBTEPCGEBLLHSVLQCKSVPDVLDGEEMR RARTRANPYEMIRGVFFLNRAMKMANMDFVFDRMFTNPRDSYG KPLVKDRBAKLLYPADGGGSGFSBYVLWRKKMHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGIDGDGDITRPENISAFRN FVLINTDRRGVHFLMADGGFSVFGGRNLQBILSKQLLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS	5530	4541	2606	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK
DPKRRASLEBIENHPWLQGVDPSPATKYNIPLVSYKNLSBEEIN SIIQRMVLGDIADRDATVRALETNRYNHTTATYFLLAERILREK QRKBIQTRSASPSNIKAQPRQSWPTKIDVPQDLEDDLTATTELSH ATVPQSPARAADSVLNGHRSKGLCDSAKKODLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEEDEEDKRPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEBGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSGGRGSSCSSETSDDDSESRRRLDKDGGF TYSWHRRDSSBGPDGGGGSKPSNASGGVDKASPSENNAG GGSPSSGSGCNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVQBKSTWKMCISST GNAGQVPAVGGIKPFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQFRAPREDSMREPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLPQVNCRQFSSPBDCLSSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWMVVGKRKMIIEDETEFCGEBLLHSVLQCKSVFDVLDGREMR RARTRANPYEMIRGVFFLNRAMKMANMDFVFDRMFTNPRDSYG KPLVKDREABLLYPADVGGGFSBYVLWRKWHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGIDGDGDITRPENISAFRN FVLINTDRRGVHFIMADGGFSVFGGRNLQRILSKQLLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS				FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDINSLGVILFML
SIIQRMVLGDIADRDAIVEALETINEYNHITATYFILAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLMGHRSKGI.CDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEBEDEBEKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEBGESDDEFDMDENLPPKLSRLKMNI ASPCTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGCNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPOMGLSFSSVKVQEKSTWKMCISST GNAGQVPAVGGIKFPSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQFRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLPQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDMNVVGRRKMIIEDETEPCCEELLHSVLQCKSVPDVLDGEEMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDREAKLLYPADVCAGPGGFSRYVLWRKKMHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGTDGDGDTRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQRNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS				VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR
QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARADSVLNGHRSKELCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEBDEKKPMSLSTQVVLRRKPS VINRLTSRKSAPVLNQIFEBGESDDEFDMDENLPPKLSRLKMNI ASPCTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRRDSSBGPPGSBGDGGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGCMPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVQBKSTWKMCISST GRAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQFRAPRPDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPPGYNCRQFSSPBDCISSPRFIDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDMWVGRRKMIIBDETEPCGEBLHSVLQCKSVPDVLDGBEMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVEDRMFINPRDSYG KPLVKDRBAKLLYPADVCAGPGGFSEYVLWRKKMHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGTDGDGDTRPRNISAFRN FVLDNTDRKGVHFLMADGGFSVEGQRNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS	1			DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEERHN
ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEREDBEDKKPMSLSTQVVLRRKPS VTNRLITSRKSAPVLNQIFEBGESDDEFDMDRNLPFKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSETSDDDSESRRLDKDSGF TYSHHRDSBGPPGSGGDGGQSKPSNASGGVDKASPSENNAG GCSPSSGSGGPFNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQBKSTWKMCISST GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQPRAPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPDGYNCRQFSSPBDCLSSPRFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWMVVGKRMIIEDBTBPCGEBLLHSVLQCKSVPDVLDGREMR RARTRANPYBMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDRBAKLLYPADVCAGPGGFSBYVLWRKKHHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGIDGDGDITRPRNISAFRN FVLINTDRKGVHFLMADGGFSVFGQRRNLQBILSKQLLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS				SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK
PASLKPTASGRKCLFRVEEDEEDEEDKKPMSLSTQVVLRRKPS VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPFKLSRLKMNI ASPCTVHKRYHRRKSGGGSSCSSETSDDSESKRRLDKDSGF TYSWHRRDSSEGPPGSEGDGGCQSKPSNASGGVDKASPSENNAG GGSPSGSGGEMPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQBKSTWKMCISST GNAGQVPAVGGIKPFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQPRAPRPDSMERPEPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLPQVNCRQFSSPBDCLSSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWMVGKRKMIIEDBTEPCGEBLLHSVLQCKSVPDVLDGEEMR RARTRANPYEMIRGVFFLNRAMKMANMDFVFDRMFTNPRDSYG KPLVKDRBAKLLYPADCGGFGSBYVLWRKKMHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGIDGDGDITRPENISAFRN FVLINTDRKGVHFLMADGGFSVFGQRNLQRILSKQLLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS			*	QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH
VINRLTSRKSAPVLNQIFEBGESDDEFDMDENLPPKLSRLKMNI ASPCTVHKRYHRRKSQGRGSGSSSSETSDDDSESRRRLDKDGGF TYSWHRRDSSBGPGGGGSGSSSSETSDDDSESRRRLDKDGGF TYSWHRRDSSBGPGGGGGSKPSNASGGVDKASPSENNAG GGSPSSGGGMPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVQBKSTWKMCISST GNAGQVPAVGGIKPFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI ALEPDLLEPLGYNCRQFSSPBGCISSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAPTPATRAAWSQLYGAVVQAMSRGWDGB SDWMVVGKRKMIIEDBTEFCGEBLLHSVLQCKSVPDVLDGREMR RAFTRANPYEMIRGVFFLNRAMKMANMDFVFDRMFTNPRDSYG KPLVKDREABLLYPADVCAGPGFSBEVVLWRKWHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGDGDGDTRPENISAFRN FVLINTDRRGVHFIMADGGFSVFGQRNLQRILSKQLLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS				ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP
ASPGTVHKRYHRRKSQGRGSSCSSETSDDDSESRRRLDKDGGF TYSWHRRDSSEGPPGSEGDGGQSKPSNASGGVDKASPSENNAG GGSPSSGGGMPTNTGGTTRCCAGPSNOMQLASRSAGELVESLK LMSLCLGSQLHGSTKYLIDPQNGLSFSSVKVQBKSTWKMCISST GNAGQVPAVGGIKPSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQFRAPRFDSMERPEPELIRQSWRAVSKSPLEHGTVLFARLF ALEPDLLPLPQYNCRQFSSPBDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWNVVGRRKMIIBDETEPCGEBLLHSVLQCKSVPDVLDGREMR RARTRANPYEMIRGUFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDREAKLLYPADVCAGPGGFSRYVLWRKWHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGBGGTDGDGDTTRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQBNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS	İ	!		PASLKPTASGRKCLFRVEEDEBEDEEDKKPMSLSTQVVLRRKPS
TYSWHRRDSSEGPPGSEGDGGQSKPSNASGGVDKASPSENNAG GGSPSSGSGCNPTNTSGTTRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYLIDPONGLSFSSVKQEKSTWKMCISST GNAGQVPAVGGIKPFSDHMADTTTELERIKGKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLPQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDMNVVGRKKMIIEDETEPCCEELLHSVLQCKSVPDVLDGEEMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDREAKLLYPADVCAGPGGFSRYVLWRKKMHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGGGGTDGDGDTRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQBNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS				
GGSPSSGGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVQBKSTWKMCISST GRAGQVPAVGGIKFFSDHMADTTTBLERIKSKNLKNNVLQLFLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQPRAPRPDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF ALEPDLLPLGYNCRQFSSPBDCISSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDMWVGRRMIIBDETEPCGEBLLHSVLQCKSVPDVLDGBEMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVEDRMFINPRDSYG KPLVKDRBAKLLYPADVCAGPGGFSEYVLWRKWHAKGFGMTLK GPNDFKLBDFYSASSELFBPYYGGGGIDGDGDITRPRNISAFRN FVLDNTDRKGVHFLMADGGFSVEGQRNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS				ASPCTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF
LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQBKSTWKMCISST GNAGQVPAVGGIKPFSDHMADTTTELERIKSKNLKNNVLQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI  5531 24 515 GSQPRAPRPDSMERPEPELIRGSWRAVSRSPLEHGTVLFARLF ALEPDLLPLPQVNCRQFSSPBDCLSSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWMVVGKRKMIIEDBTEPCGEBLLHSVLQCKSVPDVLDGEEMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDRBAKLLYPADVCAGPGGFSBYVLWRKWHAKGFGMTLK GPNDFKLBDFYSASSELFBPYYGBGGIDGDGDITRPENISAFRN FVLINTDRKGVHFLMADGGFSVFGQRNLQBILSKQLLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS				TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG
GNAGQVPAVGGIKPPSDHMADTTTELERIKSKNIKNNVLQLPLC EKTISVNIQRNPKEGILCASSPASCCHVI  5531 24 515 GSQPRAPRPDSMERPEPELIRQSWRAVSKSPLEHGTVLFARLF ALEPDLLPLPQYNCRQFSSPBOCISSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASIGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWMVVGKRKMIIEDETEPCGEBLLHSVLQCKSVPDVLDGREMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDREAKILLYPADVCAGPGGFSBYVLWRKWHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGBGGIDGDGDITRPENISAFRN FVLINTDRKGVHFIMADGGFSVFGQRNLQRILSKQLLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS				GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK
GNAGQVPAVGGIKPPSDHMADTTTELERIKSKNIKNNVLQLPLC EKTISVNIQRNPKEGILCASSPASCCHVI  5531 24 515 GSQPRAPRPDSMERPEPELIRQSWRAVSKSPLEHGTVLFARLF ALEPDLLPLPQYNCRQFSSPBOCISSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASIGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWMVVGKRKMIIEDETEPCGEBLLHSVLQCKSVPDVLDGREMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDREAKILLYPADVCAGPGGFSBYVLWRKWHAKGFGMTLK GPNDFKLEDFYSASSELFBPYYGBGGIDGDGDITRPENISAFRN FVLINTDRKGVHFIMADGGFSVFGQRNLQRILSKQLLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS				LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQBKSTWKMCISST
5531 24 515 GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGIVLFARLF ALEPDLLPLFQYNCRQFSSPBCCLSSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB 5532 3395 1402 SDWMVVGKRKMIIBDFTBFCGEBLLHSVLQCKSVPDVLDGREMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDREABLLYPADVCAGPGGFSRYVLWRKWHAKGFGMTLK GPMDFKLEDFYSASSELFBPYYGRGGTDGDGDTTRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQRNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS				
5531 24 515 GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGIVLFARLF ALEPDLLPLFQYNCRQFSSPBCCLSSPBFLDHIRKVMLVIDAAV TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB 5532 3395 1402 SDWMVVGKRKMIIBDFTBFCGEBLLHSVLQCKSVPDVLDGREMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDREABLLYPADVCAGPGGFSRYVLWRKWHAKGFGMTLK GPMDFKLEDFYSASSELFBPYYGRGGTDGDGDTTRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQRNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS				EKTISVNIQRNPKEGLLCASSPASCCHVI
ALEPDLLPLPGYNCRQFSSPBCLSSPBFLDHTRKVMLVIDAAV TNVEDLSSLEBYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAPTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDWNVVGKRKMIIBDFTBPCGEBLHSVLQCKSVPDVLDGREMR RARTRANPYEMIRGFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDRBABLLYPADVCAGPGGFSRYVLWRKKMHAKGFGMTLK GPNDFKLBDFYSASSELFBPYYGBGGTDGDGDTTRPENISAFRN FVLDNTDRKGVHFLMADGGFSVEGQBNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS	5531	24	515	
TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB  5532 3395 1402 SDMMVVGRRKMIIBDETEPCGEBILHSVLQCKSVPDVLDGREMR RARTRANPYEMIRGVFLMRAAMKMANMDFVFDRMFINPRDSYG KPLVKDRBAKLLYPADVCAGPGGPSEYVLWRKKMHAKGFGMTLK GPNDFKLBDFYSASSELFBPYYGRGGIDGDGDITRPRNISAFRN FVLDNTDRKGVHFLMADGGFSVEGQRNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS				
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RARTRANFYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG KPLVKDREABLLYFADVCAGPGGFSBYVLWRKKMHAKGFGMTLK GPNDFKLBDFYSASSELFBPYYGBGGIDGDGDITRPENISAFRN FVLINTDRKGVHFLMADGGFSVBGQBNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS	5532	3395	1402	
KPLVKDREABLLYFADVCAGPGGFSBYVLWRKKMHAKGFGMTLK GPNDFKLBDFYSASSELFBPYYGBGGIDGDGDITRPENISAFRN FVLINTDRKGVHFLMADGGFSVBGQBNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS				
GPNDFKLEDFYSASSELFBPYYGRGGIDGDGDITRPENISAFRN FVLINTDRKGVHPLMADGGFSVEGQBNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFBRVCLFKPITS	j			
FVLDNTDRKGVHFLMADGGFSVEGQRNLQBILSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS			1	
LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS				
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		L		VEWIND VIA A CUOPVAGIIDIAKDI ILIAMI KUMANI KUMANI DEDAND

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Jouquesto	\=possible nucleotide insertion)
<b></b>		<del> </del>	VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVODTTL
1	1		SBPRQAEIRKECLRLWGIPDQARVAPSSDPKSKFFELIQGTEI
ı	}	}	DIPSYKPTILTSKTLEKIRPVFDYRCMVSGSEQKFLIGIGKSOI
I			YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAORKI
1	1	ł	
			SAIHILDVLVINGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN
1	i	İ	PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHP
1	}.	j	VPMGLYIVRTVNEPWTMGPSKSFKKKFFYNKKTKDSTFDLPADS
i			IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
6630		700	MHRA
5533	94	789	MKBRRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
1			TVFENYTACLETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV
J	}	•	LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
}	l		LSTLMBLSHQKQAPISYEQGCALAKQLGPEIYLEGSAFTSEKSI
1	l	}	HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSBLISPT
			FKKBKAKKCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK
	Ì	1	TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK
ļ			AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
1			CAFILFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG
			RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFWDSEARLCSLVELSDTQDETQKSDSENEDLKIDCLQESQEL
}			NLQKLKNSERILTBAKQKMRELITVNIKMKEDLIKELIKTGNDAK
			SVSKQYTLKVTKLEHDAEQAKVELTETQKQLQELENKDLSDVAM
			KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
1			ELEQSVDHMKYQKIQLQRKLQEENBKRKQLDAVIKRDQQKIKVI
			LSYIPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPPSAAPLPTGRAQMSP
			SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP
] '			DAVYTELQPTSPTPTWPADETPQPQTQTQQLEGTDGPLVTDPET
	"		HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKP8GFHEDDPF
			FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537	3	2391	RARVSSPOLRVPRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT
1			pghpgswemglltprdvavefsleewehlepaqknlyqdvmlen
1			YRNLVSLGLVVSKPDLITPLEQRKRPWNVKSRETVAIQPDVPSH
			YNKOLLTEHCTBASFOKVISRRHGSCDLENLHLRKRWKREECEG
<b>1</b>			HNGCYDEKTFKYDQPDESSVESLFHQQILSSCAKSYNFDQYRKV
		•	PTHSSLLNQQEBIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
1			EXNYHCNNSEKTLNOSSSPKNHORNYFLEKOYKCKEFSRALFOS
			MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
			DXDLSQSSNLRKQIIHNERKPYKCEKCGDSLNHSLHLTQHQIIP
			TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS
			FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
1 1			EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
1	'		SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY
			KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI
{ i	i		RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
	l		CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR
1	i		SHTGERPYKCBECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
} .	·		PSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHORSHTR
1 l			EKL
		161	HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG
5538	926	707	
5538	926	101	IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGTPCNP I
5538	926	101	IPGTPGPDGQPGTPGIKGERGLPGLAGDHGEPGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGAPGPKGRSGDYKATOKIAFSATRTI
5538	926	201	GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI
5538	926	101	GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA
5538	926	101	GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLBQ
5538			GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAYSATRTI NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYPTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIPSGPLLFPDMEA
	38	1258	GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAYSATRTI NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYPTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIPSGPLLFPDMEA HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG
			GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAYSATRTI NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPBTVPAVPGPYGPHRPPQPLPPGLDSDGLKREK
			GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYPTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMRA HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK DEIYGHPLFPLLALVFEKCKLATCSPRDGAGAGLGTPPGGUVCS
			GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAYSATRTI NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPBTVPAVPGPYGPHRPPQPLPPGLDSDGLKREK

SEO	Predicted	Predicted end	Drive acid compate washing
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	LaLeucine, Mamethionine, Nanagaragine,
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	WaTryptophan, YaTyrosine, XaUnknown, *aStop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	· ·	\=possible nucleotide insertion)
	<del>                                     </del>	<del> </del>	BLEKVHOLCONFCHRYITCLKGKMPIDLVIBDRDGGCREDFEDY
1			PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS
1		•	SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM
1			RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV
l			QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS
1			LNIEGEWHYL
5540	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
J	j		PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKRBKDEI
			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
l			FNEUNTAFAKOVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
ì			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
1			EDILDQEPRRNKKRGI PPKVATNIMRAWLFQHLSHPYPSERQKKQ
1			LAQDTGLTILQVNNNFINARRRIVQPMIDQSNRTGQGAAFSPEG
			QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
1			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1 .			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
			YGHPLFPLLALVFRKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1			FNEINTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHILELE
			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDONNIWIRDHED
1 1			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED EDLDQBPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSKEQKKQ
1			LAQDTGLTILQVNNWFINAKRRIVQPMIDQSNRTGQGAAFSPEG
	<u>.</u>	•	QPIGGYTET3PHVAFRAPASVGDEFGTRKEEWHYL
5542	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1 :		•	GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDKI
[			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1 1			PNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELB
1 :			KGKMPIDLVIEDRDGGCRRDFEDYPASCPSLPDQNNIWIRDHBD
1 1	į		SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGRD
			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEBQKKQ
l			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAF3PEG
			QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWYREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
1 1			KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPRPTRVHG
]	}		SSASRDRVLARTMIVADSECRABLKDYLRFAPGGVGDSGPGEEQ
			RESPARRED SAFIPVEEVLREGASSLEOHLGLEALMSSERV
			DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA ARHQCSYLVGSHMAEVLQTGGDPBWLLGLHRAPBKLRKLSBINK
i I			LLAHRPWLITKEHIQALLKTGEHTWSLABLIQALVILTHCHSLS
1 1	. 1		SPVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF
[ ]	Ì	,	ESARDVEALMERMOQLQESLLRDEGTSQEEMESRFELEKSESLL
1			VTPSADILEPSPHPDMLCPVEDPTFGYEDFTRRGAOAPPTFRAO
[	}		DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV
	1		DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNOLLERNLKVYIKTV
]			ACYPEKTTRRMYNLFWRHFRHSEKVIIVNLLLLEARMOAALLYAL
			RAITRYMT
5544	1895	514	LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD
			PEGRRQEPLRRRASSASVPAVGASAEGTRRDRLGSYSGPTSVSR
	i		QRVBSLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAEEBEEEV
	1		ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRRGNLHFIR
	1		PPTHDMPAFIQMGRDKNPSSLHTVFCATGGGAYKFBQDFLTIGD
] ]	1		LQLCKLDELDCLIKGILYIDSVGFNGRSQCYYFENPADSEKCQK
	1		LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKKVTGTSLGGGTF
	j		FGLCCLLTGCTTFERALEMASRGDSTKVDKLVRD1YGGDYBRFG
	į		LPGWAVASSFGNMMSKERREAVSKEDLARATLITITNNIGSIAR
i i	]		MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSRGQLKALF
			SEHEGYFGAVGALLELLKIP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Į į	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
Į į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGABLVTCGSVL
			KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG
i !			GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSNNOEV
			SAFGEDGEGDDLDLWTVRCSGCHWEREAAVRFQHVGTSVFLSVT
1			GROYGSPIRGOHEVHGMPSANTHNTWKAMRGIFIKPSVEPSAGH
) )			DRL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLBAYAANPHSFVFT
Į.			RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKENSLKDCVAVAGP
1			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
1 1			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1			NVHKVNLNTIKRCLLIDYNPDSQBLDFRHYSIKVVPVGASRGMK
( )			KLLQEKPPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
) 1			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
1			FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
1 1			RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
1 1			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
L			CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRPGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
( )			RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
1			LGVTHPLILSKTETNVYPKLMRLPGGPTLTFQVKKYSLVRDVVS
1 1			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1 1			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
1 1			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1 1			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
)	. *		FVSKTEBELQATIBAKEKKLRLKAQRQAQQAQQAQRVQRKQEQREAH
( I			RKKSLEGMKKARVGGSDEEASGIPSRTASLRLGEDDDEQEDDDI
1 1			EYFCQAVGEAPSEDLFPRAKQKRLAKSPGRKRKWEMDRGRGRI. CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRGRKVA
5548	1	2153	DOTGPPETIAFTFPRETMEPLCPLILLVGFSLPLARALRGNETTA
3340	*	23.55	DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLVLLLAAYFFRP
1	•		RKORKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI
1			PVEHLBEEIRIRSADDCKOPREEFNSLPSGHIOGTFELANKEN
1 1			REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
1 1			FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY
			WPDQGCWTYGNIRVCVBDCVVLVDYTIRKFCIQPQLPDGCKAPR
1 1			LVSQLHFTSWPDPGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC
1 1			SAGVGRTGTFIVIDAMMAMMHABQKVDVFBFVSRIRNQRPQMVQ
1 1			TDMQYTFIYQALLEYYLYGDTBLDVSSLEKHLQTMHGTTTHFDK
1 1			IGLBEBFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR
, ,			VILSMKRGQBYTDYINASFIDGYRQKDYFIATQGPLAHTVKDFW
			RMIWBWKSHTIVMLTBVQBREQDKCYQYWPTEGSVTHGEITIEI
)			KNDTLSBAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG
			IPABGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL
		•	SNILERVKAEGLLDVFQAVESLRLQRPHMVQTLEQYEFCYKVVQ
			DFIDIFSDYANFK
5549	915	256	PEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ
			CLARGSAGIKGLGRVFRINDDDNNRTLDFKBFMKGLNDYAVVME
			KEEVERLFORFDKOGNGTIDFNEFLLTLRPPMSRARKEVIMQAF
1			RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD
- <u></u> -			NFDSPYDKDGLVTPEEPMNYYAGVSASIDTDVYFIIMMRTAWKL
5550	2364	1210	RKRKVFLKMRRLNRKKTLSLVKELDAPPKVPESYVETSASGGTV
			SLIAFTTMALLTIMBFSVYQDTWMKYEYEVDKDFSSKLRINIDI
( I			TVAMKCQYVGADVLDI.AETMVASADGLVYEPTVFDI.SPQQKENQ
}			RMIQLIQSRLQBEHSLQDVIPKSAFKSTSTALPPREDDSSQSPN
1 1			ACRIHGHLYVNKVAGNPHITVGKAIPHPRGHAHLAALVNHESYN
]			PSHRIDHLSFGBLV9AIINPLDGTEKIAIDHNQMFQYFITVVPT
1			KLHTYKISADTHQFSVTERBRIINHAAGSHGVSGIFMKYDLSSL
į l		4	·
)			MVTVTEEHMPFWQPFVRLCGIVGGIPSTTGMLHGIGKFIVEIIC
\$551	211	1700	·

Bogianing   contion   cortesponding   contion   cortesponding   contion   cortesponding   to first   anino acid   anino acid   sequence   seq	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Not				
cortesponding to first anino acid residue of anino acid residue of anino acid anino ac				Clutamic Acid R-Dhanulalanine C-Clucina
to first mino acid residue of mino acid control of the control of mino acid control of mino acid control of mino acid control of the control of mino acid control of the co	NO:			
to first anino acid residue of anino acid anino acid cequence  ##TryPtophan, Y-Tyrosine, X-Unknown, *=Stop Codon, (-possible nucleotide deletion,	1	3		
anino acid residue of anino acid sequence  Gequence  Gequence  Whitepophan, N-Typosine, X-Dinkown, *=Stop Codon, /-possible mucleotide deletion, /-possible mu	Į.		i e	
residue of anino acid sequence (Codon, (-possible nucleotide deletion, (-possible nucleotide deletion) (-possible nucleotide deletion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible personation of the procession of the proces				
anino acid	1			
Image: A	l	residue of	amino acid	
WEVPERTABEDKINTLIKKOP PAMALALIDAKEI PSÖMEDDDITE   ORREGINETOKINTPOLITHEDTRA (OMDSTANGEDESED     DERSSOKLISTSONITH CPSCHWICKOPTOKINGSPEKKY     LIARKELOGKPYANKUJOKU VANRAKOMILANSYWI     PELUGIAYSHYOTEKUJYULDVINGGELPHILOKORSPEKKY     PELUGIAYSHYOTEKUJYULDVINGGELPHILOKORSPEKKY     PELUGIAYSHYOTEKUJYULDVINGGELPHILOKORSPEKKY     PELUGIAYSHYOTEKUJYULDVINGGELPHILOKORSPEKKY     PELUGIASDITITPOOTPEKLAPVILROPINTUDRALCANI, Y     EKICAISDITITPOOTPEKLAPVILROPINTUDRALCANI, Y     EKICAISDITITPOOTPEKLAPVILROPINTUDRALCANI, Y     EKICAISDITITPOOTPEKLAPVILROPINTUDRALCANI, Y     EKICAISDITITPOOTPEKLAPVILROPINTUDRALCANI, Y     EKICAISDITITPOOTPEKLAPVILROPINTUDRALCANI, Y     EKICAISDITITPOOTPEKLAPVILROPINTUDRALCANI, Y     EKICAISDITITPOOTPEKLAPVILROPINTUDRALCANI, Y     EKICAISDITITPOOTPEKLAPVILLAROPINTUDRALCANI, Y     EKICAISDITATEETUTISVILSTYOUSENDANINGKAKKIKKIKKIKEKEKEI     EKICAISDITATEETUTISVILSTYOUSENDANINGKAKKIKKIKKIKKIKKIKKIKKIKKIKKIKKIKKIKKIKK	{	amino acid	sequence	Codon, /=possible nucleotide deletion,
ORRAGIANETIONLYRYELINIHDURAFIQMOSPKRIGODISEDE BERSOKLAISTOON ILLAKKILOGEVAPUKULOKKUVANIKKOOKHUMAERIVULAKNIVAN PELVELAYTSEVTEKUVAUNIKKOOKHUMAERIVULAKNIVAN PELVELAYTSEVTEKUVAUNIKKOOKHUMAERIVULAKNIVAN PELVELAYSEVTEKUVAUNIKKOOKHUMAERIVULAKNIVAN PELVELAYSEVTEKUVAUNIKKOOKHUMAERIVULAKNIVAN REGIALSIOTITTEVOOTPEVIAPPUKURUSHILLIOSVAHVVITOPEILC REGIALSIOTITTEVOOTPEVIAPPUKURUSHILLIOSVAHVVITOPEILC REGIALSIOTITTEVOOTPEVIAPPUKURUSHILLIOSVAHVVITOPEILC REGIALSIOTITTEVOOTPEVIAPPUKURUSHILLIOSURUSHILLIONILlionill	i	sequence		\=possible nucleotide insertion)
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GSPERLSVGEQPDYTHIDPYBETQSPEPARAKT  1095  LGERAYILVSRMDGPVAEHAKQEPEHVVTPILESWALSQVAGMP  VPLACENVQPSGSPKIRGIGHVQENAKKGCHLVCSSGGNAGI  AAAYARKLGIPATIVLPESTSLQVVQRLQGEGAEVQLTCKVMD  EANLRAQELAKRDGWENVPPPDHPLIWKCHASLVQELKAVLRTP  PGALVILVAGGGGLLAGVVAGILLEVONQHVPIIAMETHGAHCFRA  AITAGKLVTLPDITSVAKSLGAKTVAARALRCMQVCKIHSEVVE  DTEAVSAVQQLLDDERMLVPPACGAALAAIYSGLLRRLQAGGCL  PPSLTSVVVIVCGGNINSREQAALAAIYSGLLRRLQAGGCI  S554  166  2318  CSGRTGGRGSLRPARWCLTCKLSGAETRGLCPALRTUKVI.  GRSFFWJLPPVLPWAVQAVEHEEVAAQRVIKLHRGRGVAAMQSRQ  WXRDSCRKLSGLLRQKNAVLNKLKTAIGAVERDVGLSDEKLEQ  VHTPEIFOKKLNESENSVPQAVYGLQRALQGDYKDVVNMKESGR  QBLEALREAAIKEBTEYMELLAARKHQVEALLUNMQCNQSLSML  BEILEDVRGAADRLEEBIEEHAPDDNKSVKGVMFEAVLRVEEER  ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH  HPIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN  GSARGDKECDIDYSTVLLGMLYDDVGLGLERAVMPTLIQAGAS  ASSIVVEVLRILVLIGQILPSLAAVFILCLVIKKYLIGPYYRK  LIMMSKGNKRILLIGGSPIPLAUFFASIGLHYPPTVAVS  LIMMSKGNKRILLIGGSPIPLAUFFASIGLHYPPTVAGAL  VSSGPVTERIATSIEPIRDPLAUFFASIGLHYPPTVAGAL  VSSGPVTERIATSIEPIRDPLAUFFASIGLHYPPTVAGAL  VSSGPVTERIATSIEPIRDPRCEAASQGRVGWRADAAEEAVRSVWNKTRDR  GYMPPORISTFCLLLLYLIGAVIAGRDFYKIIGVPRSASIKDIK  KAYRKLALQLHPDRNPDDDPQAQEKFDDLGAAYEVLSDSEKRQY  TYTGEBGLKOHQSSHGDIFSHFFGDFGFMGSTFRQODRNIPR  GSDITVULKVTLEKVYAGRFVENVUNNEVARQAFGRKKCNCRQE  MRTTQLGFGFPQMTQSVGCDECPNVLVLVSRERTLEVSEIEPGVRD  MRTTQLGFGFPQMTQSVGCDECPNVLVLVSRERTLEVSEIEPGVRD  GMRYPFIGGGEPHVDGROGDLAFRIKVVKHPIFBRRGDDLYTMV  TISLVESLVGFMDTTHLDGHKVHISPNKITRPGAKLMKGGGL  PNFDNINIKGSLIITFDVDFPKRQLITEEAREGIKQLLKQGSVQK  VYNGLGGY	Į.			
1095 LGREAVILVERMDEPVAEHAKQEPFHUVTFILESMAISQUAGMP VPLKCENVQPSGSFKIRGIGHFCQEMAKKGCRILVCSSGGNAGI AAAYAARKLGIPATIVLPESTSLQVVQRLQGGAGUQLTKKVMD EARLRAQELAKRICHRENPEPFHPHI MKGHASLUQELKAULRTP PGALVIAVGGGELAGVVAGILEVGNQHVPI IAMETHGAHCFNA AITAGKLVTLPDITSVAKSIGAKTVARALBCCHQUCKHSEVVE DTEAVSAVQQLLDDERRIVVEPACGAALAAI YSGLIARIQAGGCL PPSLTSVVVIVCGCSNIN NERBLQAIKTHLGQV  SSST 166 2318 CSGRTGGRSSLRPARENVCLTCKLSGASTRGLCPALRTWIMKVI GRSFFWULPVLEWAVQAVSHEEVAQAVKHKGRGVARMQSRQ WVRDSCKRLSGLLRQNAAVLANKLKTAIGAVRENUGLSDEKLIPQ VHTPEIPQKKLNESENSVPQAVYGLQBALQGDYKDVVNNKESSR QRLEALREAAIKESTEVMELLAARSHQVALMMOHQOSLSMI. DEILEDVKKAADRIKEBIEBERDPDINGSVKGVMFERVLRVEEBE ANSKQNITKREVEDDLGISMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTLAGLPTWFGYIIGGVLGFSGK. SIRSIVQVETIGERGVPFTHJVGLRFSPERKRVWKISLQGPC YMTLMIAFGLLWGGLLRIKPTQSVPISTCLSLSSTBLVSRFM GSARGDKEDIDISTULIGRUVTPLVGLRFSPERKRVWKISLQGPC YMTLMIAFGLLWGGLLRIKPTQSVPISTCLSLSSTBLVSRFM GSARGDKEDIDISTULIGRIVTPTQVGLGLFRANMPTLIQAGRS ASSSIVVEVLRILVLIGQIHFSLAAVFLLCIVIKKVLIGFYYRK LIBMSKGNKBILLIGISAPIPLALTVIFBLIDVSNEIGCFLAGAL VSSCGPVVTREIATSIEPIEDFLAIVFFSSIGLHVPFTPVAYEL TVLVPTLTSVVVNKYELABALVISLILFSSGYIKMIVSAGLAQV SSSSPVLGSRARRAGVISREVYLLJLSVTTLSILLAPVLWRAAI TRCVPRPERRSSI LSLETTETPAPPRCERAASQGRVGWRADAAEEAVRSVWNKTRDR GTMAPQNISTCCLLIVILGAVTAGRBPYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKKQY DTYGBGGLKDGHGSSHGDISHFFGDFGFFWGGTPRQODENIPR GSDIIVDLEVTLESVYAGNFVEVVRNEVARQAPGRKKCNCRGE MRTTDLGPGRPMTQBVGCDECPNVKLVMEERTLEVBEEPGVRD CMEYPPIGGEGPHVDGSPGDLRFRIKVVKUPIERRAGKLINKKGGGL PNFDNNNIKGSLIITFDVDPPREQLTEEAREGIKQILKQGSVQK VYNGLQGY	j		)	
VPLKCENVQPSGSPKIRGIGHPCQEMAKKGCRHLVCSSGGNAGI ANAYARKLGIPATIVLPESTSLQVVQRLQGEGABUQLTSKVMD EANLRAQELKRRIDWERNPPFDHPILINKGRASLUQELKAVLRTP PGALVIAVGGGGLLAGVAGLLEVGNQHVPILAMETHGARCFNA AITAGKLVTLPDITSVAKSLGAKTVARARLECMQVCKHSEVVD DTEAVSAVQQLLDDERMILVERACGAALAAIYSGLARLQABGCL PPSLTSVVVLVCGGNNINSRBLQALKTHLGQV  5554  166  2318  CSGRTGGRGSLRPARNVCLTCKLSGAETKGLLCPALRTWIMKVI GRSFFWVLPPVLPWAVQQAVEREVAQAVIKHRGRGVAAMQSRQ WVRDSCRKLSGLLRQRNAVLNKLKTAIGAVRRIDVGLSDERKLFQ VHTTEIFQKKLINSSENSVPQAVYGLQRAIKUMQHUNGSLSML DEILRDVRRAADRLEEBIEERDDDNSVRSVFERAVLRVEERE ANSKQNITRREVERDLGLSMLIDSQNDQYLITKPRDSTIPRABH HFINDIVTIGHALSLPCGWLCTAIGLPTWFGYIICGVLLGPSGLN SIRSIVQVETLGBFGVPFTLFLVGLRPSPERLRKVMKISLQGPC YMTILMHARGLLWGSHLIRIRPTGSVITSTLSISSTPLVSRFILM GSARGDXEEDIDTSTVLLGHLVTDQVGLGLFMAVMPTLIQAGAS ASSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LIBMSKGNKRILLIGISAPIFLMLTVTELLDVSMBIGGTLAGAL VSSGPVVTRESLATSIEPIEDPLAIVFFSLGHLVPFTPVAYSL TVLVPLTLSVVVMKYLLAALVLSLILPRSSQYIKWIVSAGLAQV S3FSPVIGSRARRAGVISRSVYLLILSVTTLSILLAPVLWRAAI TRCVPPPRRSSL  5555  212  1425  LSLETTETPAPPRCEAASGGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQMLSTFCLILLYLIGAVIAGRPYKLLGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQRKPQDLGARVEVLSBERKRQY DTYGBEGLKDGHQSSHGDIFSHPFGFFFFGFFRQQDRNIPR GSDIIVDLEVTLERVYAGNPVEVVNRVARAAFEGRKCCNCRQE MRTTQLGPGRFTQTGECCDECPNVKLVMEERTLRVEREPGVAD GREYPFIGGEGPHVDGEPGDLRFRIKVVKHPIPBRRGDDLYTNV TISLVESLVGFRWDTTHLDGHKVHISRDKITRNAKLMKGGGL PNFDNNNIKGSLIITPDVDPPREQLTEEAREGIKQLLKQGSVQK VYNGLQGY	1	1		
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EANLRAQELAKROGMENVPPFDHPLIWKGHASLVQELKAVLRTP PGALVIAVGGGGLLAGVVAGILEVCMQHVPIIMMETHGAHCFNA AITAGKLVTIPDITSVARSLGAKTVARARALECMQVCKHISEVVE DTEAVSAVQQLLDDERMIVEPACGAALAAIYSGLLRRLQAEGCL PPSLISVVVIVCGGGNINSRELQAKKTHAGAY  5554  166  2318  CSGSTGGGGSLRPARNVLSTCKLGGAETEKSLLCPALRTWIMKVI. CRSFFWVLFPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ WVRDSCRKLSGLLRQKAVAVLNKLKATIGAVRHUVGLSDEEKLPQ VHTTEIPQKKNINSESBLYALGDYKDVVMKESER QRLEALREAAIKEBTEYMELLAABKHQVEALKIMQHQNQSLSML DEILBDVRKAADRLBEBTERHAFDDNKSVKGVMFRAVLRVEEBE ANSKQNITKRRVEDDLGJALLDSQNMQYLTFRPRSTTPRADK HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIRSIVQVETIGBEFGVFFTLFLUGGEFSPERLRKVWKLSLQGFC YMTLLMIAFGLLWGHLRIKPTQSVPISTLGLLSSYNTYLYSPLSAM GSARGDREDDIDTSTVLLGMLVTQDVQLGLFNAVMPTLJQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKVLIGPTYNK LHMESKGNKRILVLIGGSLFFLAAVFLLCLVIKKVLIGPTYNK LHMESKGNKRILVLIGGSAPFIPLATVFFASIGLHVPPTFVAYSL VSSCGPVVTREIATSIBPIRDFLATVFFASIGLHVPPTFVAYSL TVLVPLTLSVVVMKELLAALVLSLILPRSSQYIKWIVGAGLAQV SSPSFVLGSRARRAGVISREVYLLLISVTTLSLLLAPVLMRAAI TRCVPPPERRSSL  5555  212  1425  LSLETRETPAPPRCEAASQGRVGWRADAAAEEAVRSUWNRTRDR GTMAPQNILSTTCLLLLLVILGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLGHPDRNPDDPQAQBKFQDLGAAVEVLSDSKKRGY DTYGEBGLKDGHQSSHGDIFSHFFGDFGFMFGSTPRQQDRNIPR GSDIIVDLEVTLEBVYAGNFVEVVYNKPVARQAPGKRKCNCRQE MRTTQLGFGRRQMTDEVCGBCPNVALVMERFTLEWEIBFGVRD GMEYPPIGEGEPHVDGSPGDLRFRIKVVKHPIFBRRGDDLYTNV TISLVESLVGFRMDITHLIGHKVHISRDKITRRGAKLMKGGSL PNFDNNNIKGSLIITFFDVDFPKBQLTEEAREGIKQLLKQSSVQK VYNSLQGY	( .	· .		VPLKCENVQPSGSFKIRGIGHPCQEMAKKGCRHLVCSSGGNAGI
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DTEAVSAVQQLLDDERMLVEPACGAALAA1YSGLLRRLQAEGCL PPSLTSVVIVCGGNNINSRELQALKTHLGQV  CSGRTGGRGSLFPAENVCLTCKLSGAETRGLICPALRTWIMKVI. GRSFFWVLFPVLPWAVQAVEHESVAQRVIKLHRGRGVAAMQSEQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVRRDVGLSDEKLFQ VHTPEIPQKKLNESENSVPQAVYGLQRALQGDYKDVVNNKESSR QREALRRAAIKEBTEYMBLLAARKHQVEALKHMQHQNGSLSML DEILEDVRKAADRLEBEIEHAPDDNKSVKGVMFEAVLRVEEEB ANSKQNITKRZVEDDLGLSMLIDSQNNQYIITKRRDSTIPRADH HFIRDIVTIGMISLPGGWCLTAIGLFYMFGYIICGVLGSGGIN SIRSIVQVETLGEFGVFFTLFLVGLEFSPERLRKVWKISLQGFC YMTLIMIAFGLLWGHLIKITGQTLFSLAVFFLCLVIKKYLIGPYYRK GSARGDKEEDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQTLFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKRILILGGIAPIFLAIVFFASIGLHVFPTYVAYEL VSSGFVVTREIATSIEPIEDFLAIVFFASIGLHVFPTYVAYEL TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIK WIVSGLAQV SSFSFVLGSRARRAGVISREVYLLILSVTTISLLAPVLWRAAI TRCVPRPERRSSL  5555 212 1425 LSLETRETFAPPRCEAASGGRVGWRADAAAEEAVRSVWNKTRDR GTMAPQNLSTFCLLLLLYLIGAVTAGRPFYKTLGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRQY DTYGEGGLKOCHQSSHGDITSHFFGDFGFMFGGTFRQODRNIFR GSDIIVDLEVTLEBVYAGRFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGFGRRQMTGSVGCDBCPNVKLVNEERTLEVEIEPGVRD GMEYPPIGEGBPHVDGSPGDLRFRIKVVKHPIFBRRGDDLYTNV TISLVESLVGFFMDTTHLDCHKVHISRDKITRPGARLMKKGRGL PNFDNNIKKGSLIITFDVDFPKBQLTEEAREGIKQLLKQGSVQK VYNGLQGY	1 .	1		
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ASSSIVVEVLRILVLIGQILFSLAVFLLCLVIKKYLIGPYYRK LIMMSKGNKRILILGISAPIFLMLTVTELLDVSMELGCFLAGAL VSSCGPVVTREIATSIEPIRDFLATVFFASIGHVPFTVAYEL TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SSFSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLMRAAI TRCVPRPERRSSL  SSSS 212 1425 LSLETRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKLIGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRQY DTYGEGGLKDGHQSSHGDIFSHFFGDFGFMGGTFRQODRNIPR GSDIIVDLEVTLEBVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMRYPFIGRGEPHVDGSPGDLFFRIKVVKHPIFBRRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRGAKLMKKGEGL PNFNNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	1		ì	
LHMESKGNKRILILGISAPIPLMLTVTELLDVSMELGCPLAGAL VSSQGPVVTREIATSIEPIEDPLAIVFYASIGLHVPPTVAYEL TVLVVITLSVVVMKYLLAALVISLILPRSSQYIKWIVSAGLAQV SSPSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLMRAAI TRCVPRPERRSSL  5555 212 1425 LSLRTRETPADPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDPYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR GSDIIVDLEVTLEBVYAGNEVEVVRKPVARQAPGRRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEETLEVEIEPGVRD GMEYPPIGEGEPHVDGEPCDLEFRIKVVKHPIFERRGDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	}	1	}	GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS
LHMESKGNKRILILGISAPIPLMLTVTELLDVSMELGCPLAGAL VSSQGPVVTREIATSIEPIEDPLAIVFYASIGLHVPPTVAYEL TVLVVITLSVVVMKYLLAALVISLILPRSSQYIKWIVSAGLAQV SSPSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLMRAAI TRCVPRPERRSSL  5555 212 1425 LSLRTRETPADPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDPYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR GSDIIVDLEVTLEBVYAGNEVEVVRKPVARQAPGRRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEETLEVEIEPGVRD GMEYPPIGEGEPHVDGEPCDLEFRIKVVKHPIFERRGDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY		Į.	l .	ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK
VSSCGPVVTREIATSIEPIEDFLAIVFFASIGLHVPPTFVAYEL TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SSPSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLMRAAI TRCVPRPERRSSL  5555 212 1425 LSLETTETPAPPRCEAASQGRVGWRADAAAEBAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDPYKIIGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQBVGCDBCPNVKLVNEERTLEVBIEPGVRD GMEYPPIGEGEPHVDGSVGCDBCPRVKLVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLMKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEARBGIKQLLKQGSVQK VYNGLQGY		Į.	1	
TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV S3PSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLMRAAI TRCVPRPERRSSL  5555 212 1425 LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGSTPRQQDRNIPR GSDIIVDLEVTLKEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVBIEPGVRD GMEYPFIGEGEPHVDGSPGDLRFRIKVVKHJERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	1	1	1	
SEPSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  SISTEPTPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDPYKILGVPRSASIKDIK KAYRKIALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEBGLKDGHQSSHGDIFSHFPGDFGFMFGGTPRQQDRNIPR GSDIIVDLEVTLEBVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQBVGCDBCPNVKLVNBERTLBVBIBPGUPD GMRYPFIGBGBPHVDGSPGDLRFRIKVVKHPIFBRRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKBGGL PNFDNNNIKGSLIITFDVDFPKBQLTBEARBGIKQLLKQGSVQK	1	1	1	· ·
TRCVPRPERRS9L  1425 LSLETRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRPYKLIGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSD9EKRKQY DTYGEGGLKDGHQSSHGDIFSHFFGDFGFMRGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMRYPFIGEGEPHVDGSPGDLAFRIKVVKHPIPBRRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITREGAKLMKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	}	1	1	
1425 LSLRTRETPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDPYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGSTFRQQDRNIPR GSDIIVDLEVTLEEVYAGHFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFGTVDGVGCDECPNVKLVNEERTLEVELEPGVRD GMEYPPIGEGEPHVDGSPGDLFRIKVVKHPIFBRRGDDLYTNV TISLVESLVGFBMDITHLDGHKVHLSPDKITRPGARLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	1		ŀ	
GTMAPQNLSTFCLLLLYLIGAVIAGRDPYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVELEPGVRD GMEYPPIGEGEPHVDGSPCDLEFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLMKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY		L	<del></del>	
KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY  DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR  GSDIIVDLEVTLERVYAGNEVEVVRKPVARQAPGKRKCNCRQE  MRTTQLGFGRFQMTQEVGCDECPNVKLVNEETLEVEIEPGVRD  GMEYPPIGEGEPHVDGEPGDLEFRIKVVKHPIFERRGDDLYTNV  TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLMKKGEGL  PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK  VYNGLQGY	5555	212	1425	
DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR GSDIIVDLEVTLEBVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGFGRFQMTQBVGCDECPNVXLVNEERILBVDIEPGVRD GMEYPFIGEGEPHVDGFPGDLLFRIKVVKHPFBRRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFFNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	1	ł	1 .	**
GSDIIVDLEVTLEBVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVBIEPGVRD GMBYPFIGEGEPHVDGSPCDLAFRIKVVKHPIPBRRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITREGAKLMKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	1	1		
MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPPIGEGEPHVDGEPGDLRFRIKVVKHPIFBRRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITREGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQG\$VQK VYNGLQGY	1	1	1	DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR
MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPPIGEGEPHVDGEPGDLRFRIKVVKHPIFBRRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITREGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQG\$VQK VYNGLQGY	ı	1	!	GSDIIVDLEVTLEEVYAGNEVEVVRNKPVARQAPGKRKCNCRQE
GMEYPPIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITREGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQG\$VQK VYNGLQGY	}		1	
Tislveslvgfemdithlochkvhisrdkitregaklwkkgegl Pnfdnnikgsliitfdvdfpkeqlteearegikqilkqgsvqk Vynglqgy		1		
PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQILKQG\$VQK			§.	
VYNGLQGY	1			
		Į .	1	· ·
2220 2832 3346 KIRGMSKNCVPMEREKATTWALGLIATPOVILLEPON		F635		
	5556	5835	3346	KIRCASVACABURKERAPTKULÖGILATPTÖYTIVDUNYHIAKER

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
[	sequence		\=possible nucleotide insertion)
<b></b>		<del> </del>	LEELDESYIEKFTDFLRLFVSVHLRRIBSYSOFPVVKYLTLLFK
ì		1	YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
ſ		1	DALVILLTEVINRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR
ļ		ļ	QSLEVVAKVMBLLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS
ł		1	GHRLNITAENDCRRLHCSLRDLSSLLOAVGRLAEYFIGDVFAAR
		•	FNDALTVVBRLVKVTLYGSQIKLYNIBTAVPSVLKPDLIDVHAQ
ł	1	ł	SLAALOAYSHWLAOYCSEVHRONTOOFVTLISTIMDAITPLIST
l			KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA
1		{	LRLVDKAQVLVCRALSNYLLLPWPNLPENEQQWPVRSINHASLI
ł	ł	}	SALSRDYRNLKPSAVAPORKMPLDDTKLIIHOTLSVLEDIVENI
}		]	SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL
1		}	TLFRGLRVOMGVPFTEQIIOTFLNMFTREOLAESILHEGSTGCR
ł		}	VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
		ì	PDVKAKLFELLFRTLHHNWRYFFKSTVLASVORGIABEOMENEP
1	Ī	[	OPSAIMOAFGOSFLOPDIHLFKONLFYLETLNTKOKLYHKKIFR
ł	}	1	TAMLFQFVNVLLQVLVHKSHDLLQEBIGIAIYNMASVDFDGFFA
1			APLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA
1	1		RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAATR
	]		KHLPARNHCGLSDSSPQLWPBPDFRNPPRKASKASLDFKRYVTD
1			RRLAETLAQIYLGKPSRPPHLLLBCNPGPGILTQALLRAGAKVV
1	l	1	ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP
ļ.	1		AMSSRGLPKNLGIRAVPNTADIPLKVVGNPPSRGBKRALWKLAY
l	ļ		DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVLSVI
	1		WQLACBIKVLHMEPWSSFDIYTRKGPLENPKRRBLLDQLQQKLY
ļ	1		LIQMIPRONLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
i			LTPLDARDILMQIGKQEDBKVVNMHPQDFKTLFETIERSKDCAY
1			KWLYDETLEDR
5558	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI
1			TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS
			LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
	l .		YTVTNLAGGPKPYSPYDSQYHETTLKGGMPAGQLTKVGMQQMFA
l		·	LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA
1	,		GLFQCQKEGPI1IHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
i	}		SLQPGISBOLKKVKDRMGIDSSDKVDFFILLDNVAABQAHNLPS
ł			CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
i '			NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
} ;	į		FAVDLTMBLYQHLESKBWVVQLYYHGKEQVPRGCPDGLCPLDMF
· '	ì		LNAMSVYTLSPEKYHALCSQTQVMBVGNKB
5559	150	1983	PLAATAHFAKMSRVAKYRRQVSBDPDIDSLLETLSPEEMEELEK
			ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK
			LMQREMSMDESKQVETKTDAKNGBERGRDASKKALGPRRDSDLG
			KEPKRGGLKKSFSRDRDEAGGKSGBKPKEBKIIRGIDKGRVRAA
		•	VDKKEAGKDGRGEERAVATKKEERKGSDRNTGLSRDKDKKREE
	Į į		MKBVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
	1		VKRGTGNTDTKKDDBKVKKNEPLHEKEAKDDSKTKTPEKQTPSG
<b>(</b>			PTKPSEGPAKVEBEAAPSIPDEPLERVKNNDPEMTEVNVNNSDC
			ITNEILVRFTEALRFNTVVKLFALANTRADDHVAFAIAIMLKAN
			KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHICG
	·		GKTEMELAKLLKENTTLLKLGYHPELAGPRMIVINLLSRNMDKQ
			RQKRLQEQRQAQBAKGBKKDLLEVPKAGAVAKGSPXPSPQPSPK
		•	PSPKNSPKKGGAPAAPPPPPPPPLAPPLIMENLKNSLSPATQRKM
			GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
5560	9	921	SSVVEPSALSVSMACLSPSQLQKFQQDGFLVLKGFLSAEECVAM
			QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK
1			IRFFFERGVFDERGNFLVPPEKSINKIGHALHAHDPVFKSITHS
j			FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT
			EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG
			SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL
			SDRSRQAYTPHLMEASGTTWSPENWLQPTABLPPPQLYT
5561	2175	1775	CYFIFQFFS8PYPGLHPHOTPAPLPNPGLYPPPVSMSPGQPPPQ
	L		

SEQ P	redicted	Predicted end	Amino acid segment containing signal peptide
	eginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO: n	ucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	ocation	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l c	orresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	o first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
1 1	mino acid	residue of	S=Serine, T=Threonine, V=Valine,
	esidue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	mino acid	sequence	Codon, /=possible nucleotide deletion,
St	equence		\=possible nucleotide insertion)
1 1	,		QLLAPTYFSAPGVMNFGNPSYPYAPGALPPPPPPPHLYPNTQAPS
1 1			QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVTIKPPPPEVVSRGS
5562	342	1385	
3304	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCBTLEDLKLH
1			LQSTDYGNFLANKASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP LASPLDFITYSYNIDNVILLITGTLHQRSIAELVPKCHPLGSFE
1 1			QMEAVNIAQTPABLYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1 1			IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
			INSPGTELSKEDRAKLPPHCGRLYPEGLAQLARADDYROVKNVA
1 1			DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAPLNOFHF
1 1			GVFYAFVKLKEQECRNIVWIABCIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLRDLKLH
			LQSTDYCNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
<b>1</b>			LASPLDFITYSYMIDNVILLITGTLHQRSIABLVPKCHPLGSPB
] ]			QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1			IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1 1			Insfgtelskedraklpphogrlypeglaqlaraddyeqvenva
1			DYYPEYKLLFEGAGSNPGDKTLEDRFFBHEVKLNKLAFLNQFHF
5564		A-4	GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL
)			LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC VPLTWRCDRDLDCSDGSDEECRIEPCTOKGOCPPPPGLPCPCT
1			GVSDCSGGTDKKLRNCSRLACLAGKLRCTLSDDCIPLTWRCDGH
1 1		i	PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM
1	ļ		GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV
1			TATLLLLSWLRAGERLRPLGLLVANKESLLLSEGKTSLP
5565	993	138	RWNSPNPARAGSISRPQRAPGSVSAVAMTAAVFFGCAFIAFGPA
i l			LALYVFTIATEPLRIIPLIAGAPFWLVSLLISSLVNFMARVIID
1	i		NKDGPTQKYLLIFGAFVSVYIQEMPRPAYYKLLKKASEGLKSIN
			PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH
]			GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL
1 1			LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS
5566	2043	1232	LRLCLLCODKNFILYNORSR
) 3300	2043	1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT KNVKEYVRWMYWIVPALYTVIETVADQTVAWFPLYYELKIAFV
	•		IWLLSPYTKGASLIYRKFLHPLLSSKEREIDDYIVOAKERGYET
1 1	j		MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTTIQG
1 1	j		DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEKA
[ ]	1		BGPYSDNEMLTHKG?RRSQSMKSVKTTKGRKEVRYGSLKYKVKK
	1		RPQVYP
5567	1554	233	RFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEAGANINA
			CDSECWTPLHAAATCGHLHLVELLIASGANILAVNTDGNMPYDL
1 1	1	ì	CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLQ
	j		AGADLHAPLDHGATLLHVAAANGFSEAAALLLKHRASLSAKDQD
l	į	ł	GNEPLHAAAYWGQVPLVEILVAHGADLNAKSIMDETPLDVCGDE
l ·	i	ľ	EVRAKLLELKHKHDALLRAGSRQRSLLRRRTSSAGSRGKVVRRV
!	Į		SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDDRQTGAELR PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYOLSPLD
	ŀ		STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPESPETABP
] ]	1		GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM
5568	1731	587	AEDROPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL
		50,	SLLVSGPRLFLLQOPLAPSGLTLKSKALRNWOVYRLVTYIFVYE
			NPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL
l	ì	į	SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG
	f		MVVPSVLVPWLLLGASWLIPQTSPLSNVCGLSIGLAYGLTYCYS
		ì	IDLSERVALKLDOTPPFSLMRRISVFKYVSGSSAERRAAQSRKL
l	l l		NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM
	I		PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP
5569	2	835	PTLPPYQPASGLCYVONHFGPNPTSSSVYPASAGTSLGIQPPTP VNSPGTVYSGALGTPGAAGSKESSRVPMP QTPCPLAWERGSRSEDISVPGQKPPTCSSFSCMDVGPSSLPHLG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide		
10.		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
I	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	1 -	\=possible nucleotide insertion)
<b></b>	<del> </del>		LKLLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP
1	}	l	KGEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPG
l .	1	ŀ	
i	1	1	PMGIPGEPGERGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL
ł		i	TNPQGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLLYRSGVK
I .	i .	l	VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG
L			SDSVFSGFLLFPD
5570	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
1		j	MSSPSPGKRRMDTDVVKLIBSKHEVTILGGLNEPVVKFYGPOGT
1	1	[	PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDKASGTVCL
}	}	}	DVINGTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
1	i	1	
1	ł	1	RPEBYKQKIKRYIQKYATEBALKEQEEGTGDSSSESSMSDFSED
			EAQDMEL
5571	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
1	İ	1	MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNBFVVKFYGPQGT
1	i	f	PYEGGVNKVRVDLPDKYPPKSPSIGFMNKIFHPNIDEASGTVCL
	Ì	1	DVINGTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
1	1	l .	RPBBYKQKIKBYIQKYATEKALKEQEKGTGDSSSESSMSDFSED
ı	i		BAODNEL
5572	2802	2085	RTDYRTGIPGRRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG
	1		DAGAAABGGGWAAAALALLTGGGBMLLNVALVALVLLGAYRLWV
,	}	j	RMCRRGLGAGAGEESPATSLPRMKKRDFSLEQLRQYDGSRNP
		İ	
ł		ł .	RILLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLD
1	1		KDALRDBYDDLSDLNAVQMESVREWEMQFKEKYDYVGRILKPGE
			EPSRYTDEEDTKDHNKQD
5573	2562	219 .	VPARTPNAEDQGPEARAATATPCQSGGRERAGEAAEDGVKMAAF
ì	1	ŀ	SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET
i	ł	ļ	GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWQ
ł		ı	MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYB
İ	ŀ		VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
ł			NYGERFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN
	İ	ì	QALFPACVLKNAËLKFNFGEEEFKPPPKDGFVALSKAPDGYIVK
1	i		SQHSGNAQVTQTKFLPNAPKALIVEPSRBLAEQTLNNIKQFKKY
[	(		IDNPKLRELLIIGGVAARDQLSVLKNGVDIVVGTPGRLDDLVST
1		}	
1	ł	į	GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR
1	1	[	LQVIVCSATLHSPDVKKLSEKIMHPPTWVDLKGEDSVPDTVHHV
1	ĺ		VVPVNPXTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA
1	(	Ì	IKILKGBYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG
1	J	ŀ	PDKKGHQFSCVCLHGDRKPHERKQNLERPKKGDVRFLICTDVAA
1			RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA
1		j	TEKEKVNYHVCSSRGKGCYNTRLKEDGGCTIWYNEMOLLSEIEB
1			HINCTISQUEPDIKUPUDEFDGRUTYGQKRAAGGGSYKGHVDIL
{	1	]	APTVQBLAALEKEAQTSFLHLGYLPNQLFRTF
5574	1731	952	NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG
1		734	LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS
1			1
1			TGITQCDIXSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM
j			RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD
			FYSPLVPDSMKFEIGRALYLGIISSLFSLIAGIILCFSCSCQRN
L			RSNYYDAYQAQPLATRSSPRPGQPPKVKSEPNSYSLTGYV
5575	456	766	LLNALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL
1			LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR
			SPDIGRNSPHYLMFP
5576	249	2146	RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR
1 33,0	447	2146	
1			BEATERPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA
I			QQTLFSINQSCLPGFYTPAELKPFWERPPQDFNAPGADGKAFQK
] .			SKWTPLBTQEKEEGYKKHCFNAPASDRISLQRSLGPDTRPPECV
1			DOKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK
1 .			EIILVDDASTEBHLKEKLEQYVKQLQVVRVVRQBERKGLITARL
1			LGASVAQAEVITPLDAHCECPHGWLEPLLARIARDKTVVVSPDI
j			VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFCWBTLPPHEKQRR
1 .	!		KDETYPIKSPTFAGGLFSISKSYPBHIGTYDNOMEIWGGENVEM
			. ROBERT ET ROBERT PARAGONES IN KNY VICH LETT VIRALIMIK I MERSKA VEM - 1

PCT/US00/34263

SEQ Predicted predicted end nucleotide nucleotide nucleotide location corresponding to first amino acid segment containing signal heat for first amino acid residue of amino acid sequence seque	*=Stop n,  VIARNOVR OLREGLHC DVCENNRG HVSKGALG TSQDKKPA ILLPVLLD IFKIDWTL CNDGSILL PKELWHV RYYHKLRM DGGNYTCS
location corresponding to first amino acid residue of amino acid sequence    Code, /-possible nucleotide deletion   Code, /-possible nucleotide nucleotide deletion   Code, /-possible nucleotide deletion   Code, /-possible nucleotide deletion   Code, /-possible nucleotide nucleotide deletion   Code, /-possible nucleotide nucleotide deletion   Code, /-possible nucleotide nucleotide deletion   Code, /-possible nucleotide nucleotide deletion   Code, /-possible nucleotide nucleotide nucleotide deletion   Code, /-possible nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucl	*=Stop n, VIARNOVR OLEBOLHC DUTENING HVSKGALG TSODKKPA ILLPVLLD IFKIDWTL CNDGSLLL CNDGSLLL RYTHKIRM DGGNYTCS
corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, Codon, /=possible nucleotide deletion sequence S=FRWQCGGQLEIPCSVVGHVFRTKSPHTFPKGTS LAEVWMDSYKKIFYRRNLQAAKMAQKESFGDISERLEHNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNQCLLLGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCLYMAPCNPSDEHQLWLFV  1275 RNSDCSCGEISVHCLDFWVLFILDLKVESSMFCFLKLSPGENAKMAQKESFGDISERLEGGNQYFRYTTQRDLRHNIAKQLCLLLGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCLYMAPCNPSDEHQLWLFV  5577 3 1275 RNSDCSCGEISVHCLDFWVLFILDLKVESSMFCFLKLSPGENAKMAQKESFGDISERLEGGNQYFRYTTQRDLRHNIAKQLCLLLGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCLYMAPCNPSDEHQLWLFV  SPGEHAKDEVVLYYYSNLSVPIGRFQNRVHLMSDILQDVCSSGEISVHCLGRUSGFTRLKGESQVPKKAVVLHVLPBERGGLIQMGCVFQSTBVKHVTKVEWIFSGRRAKBEIVFGSVYSQSWGHFQNRVHLVGDIFRNDGSIMLQGVRESSITHLGNLVFKTTGNLVSDIFTRNDGSIMLGGVRESSITHLGNLVFKKTTGNLYSDIFTVLFAALRPLVLGGIVCATILLLPVLLILVKTCGNKSSVNSTVLVKNTTEKPCHPBRCEGEKKHIYSPIIVREVIEREEPSEKSAV	*=Stop n, VIARNQVR QLREQLHC DVERNARG HVSKGALG TSQDKKPA ILLPVILD IFKIDWTL CNDGSILL PKELWHV RYYHKLRM DGGNYTCS
to first amino acid residue of amino acid residue of amino acid sequence  S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, K=Unknown, Codon, /=possible nucleotide deletion >=possible nucleotide insertion)  SFRWQCGGQLEITPCSVVGHVFRTKSPHTFPKGTS LAEVWMDSYKKIFYRRNLQAAKMAQEKSFGDISERL HNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNOCLE GKPLIMYSCHGLGGNQYFETTORDLRHNIAKQLCLE LGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCL MAPCNPSDPHQLWLFV SSIGINDLWSPPELTVHVGDSALMGCVFQSTEDKC SPGEHAKDEYVLYYYSNLSVPIGRPQNRVHLMGDIL QDVQEADQGTYICEIRLKGESQVPKKAVVLHVVLPBEL GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFI SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESJ IHLGNLVFKKTIVLHVSPBEPRTLVTPAALRPLVLGG GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTT EKPCHPBRCEGEKHIYSPIIVREVIEEEEPSEKSEA	*=Stop n, VIARNQVR QLREQLHC DVERNARG HVSKGALG TSQDKKPA ILLPVILD IFKIDWTL CNDGSILL PKELWHV RYYHKLRM DGGNYTCS
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, K=Unknown, Codon, /=possible nucleotide deletion sequence SprvwqcgGQLbiipcSvvGHVFRKSpHTFPKGTS    SFRVWQCGQLbiipcSvvGHVFRKSpHTFPKGTS	N, VIARNOVR QLREQLHC DVGENNRG HVSKGALG TSQDKKPA ILLPVLLD IFKIDWTL CNDGSLLL CNDGSLLL RYCHKIRM DGGNYTCS
residue of amino acid sequence	N, VIARNOVR QLREQLHC DVGENNRG HVSKGALG TSQDKKPA ILLPVLLD IFKIDWTL CNDGSLLL CNDGSLLL RYCHKIRM DGGNYTCS
amino acid sequence   Codon, /=possible nucleotide deletion	N, VIARNOVR QLREQLHC DVGENNRG HVSKGALG TSQDKKPA ILLPVLLD IFKIDWTL CNDGSLLL CNDGSLLL RYCHKIRM DGGNYTCS
sequence    =possible nucleotide insertion	VIARNOVR QLEBQLHC QLEBQLHC DVGENNRG HVSKGALG TSQDKKPA ILLPVLLD IFKIDWTL CNDGSLLL CNDGSLLL RYHKLRM DGGNYTCS
SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFPKGTS  LAEVWMDSYKKIFYRRNLQAAKMAQEKSFGDISERLI HNFSWYLHRVYPEMFVPDLIPTFYGAIKNLGTNQCLL GKPLIMYSCHGLGGUYFEYTTQRDLRHNIAKQLCLI LGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCLI MAPCNPSDPHQLWLFV  5577 3 1275 RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKL YSLSLNDLNVSPPELTVHVGDSALMGCVFQSTEDKC SPGEHAKDEYVLYYYSNLSVPIGRPQNRVHLMGDIL QDVQEADQGTYICEIRLKGESQVPKKAVVLHVLPEBL GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFI SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESI THLGNLVFKKTIVLHVSPBEPRTLVTPAALRPLVLGG GIVCATILLLPVLJLIVKKTCGNKSSVNSTVLVKNTI EKPCHPBRCEGEKHIYSPIIVREVIEEBEPSEKSEA	QLREQLHC DVGENNRG HVSKGALG TSQDKKPA  ILLPVLLD IFKIDWTL CNDGSLLL PKELMUHV RYYHKLRM DGGNYTCS
LAEVWMDSYKKIFYRRNIQAAKMAQBKSFGDISERI HNPSWYLHNVYPEMPVPDLTPTFYGAIKNIGTNQCLI GKPLIMYSCHGLGGNQYFRYTTQRDLRHNIAKQLCII LGSCHPTGKNSQVPKDEEWBLAQDQLIRNSGSGTCLI MAPCNPSDPHQLWLFV  5577 3 1275 RNSDCSCGRISVHCLPWVLFILDLKVBSSMFCPLKL YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKC SPGEHAKDBYVLYYYSNLSVPIGRPQNRVHLMGDIL QDVQBADQGTYICBIRLKGBSQVPKKAVVLHVLPBBI GGLIQMGCVFQSTBVKHVTKVBW IFSGRRAKBEIVFI SVBYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESI THLGNLVFKKTIVLHVSPBBPRTLVTPAALRPLVLGG GIVCATILLLPVLJLIVKKTCGNKSSVNSTVLVKNTI EKPCHPBRCEGEKHIYSPIIVREVIEBBEPSEKSBA	QLREQLHC DVGENNRG HVSKGALG TSQDKKPA  ILLPVLLD IFKIDWTL CNDGSLLL PKELMUHV RYYHKLRM DGGNYTCS
HNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNOCLI GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLI LGSCHPTGKNSQVPKDEWBLIAQDQLIRNSGSGTCL: MAPCNP3DPHQLWLFV  5577 3 1275 RNSDCSCGBISVHCLDWVLFILDLKVBSSMPCPLKLI YSLGINDLMVSPPRLTVHVGDSALMGCVFQSTEDKC SPGEHAKDBYVLYYYSNLSVPIGRPQNRVHLMGDIL QDVQEADQGTYICBIRLKGESQVPKKAVVLHVLPBBI GGLIQMGCVFQSTEVKHVTRVBWIFSGRRAKBBIVFI SVBYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRBSJ IHLGNLVFKKTIVLHVSPBBPRTLVTPAALRPLVLGG GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTI EKPCHPBRCEGEKHIYSPIIVREVIEBBEPSEKSAN	DVGENNRG HVSKGALG TSQDKKPA  ILLPVILD IFKIDWTL CNDGSLLL PKELWHV RYYHKLRM DGGNYTCS
GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLI LGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCL MAPCNPSDPHQLWLFV  5577 3 1275 RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPFKL YSLGINDLWSPPELTVHVGDSALMGCVFQSTEDKC SPGEHAKDEYVLYYYSNLSVPIGRPQNRVHLMGDIL QDVQEADQGTYICEIRLKGESQVPKKAVVLHVVLPBE GGLIQMGCVFQSTEVKHVTXVEWIFSGRAKREIVFI SVEYSQSWGHFQNRVHLVGDIFRNDGSIMLQGVRESI IHLGNLVFKKTIVLHVSPBEPRTLVTPAALRPLVLGG GIVCATILLLPVLLIVKKTCGNKSSVNSTVLVKNTI EKPCHPBRCEGEKHIYSPIIVREVIEEEEPSEKSEN	HVSKGALG TSQDKKPA ILLPVILD IFKIDWTL CNDGSLLL PKELMVHV RYYHKLRM DGGNYTCS
LGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCLI MAPCNPSDPHQLWLFV  5577 3 1275 RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKL. YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKC. SPGEHAKDEVVLYYYSNLSVPIGRPQNRVHLMGDILA QDVQEADQGTYLCEIRLKGESQVPKKAVVLHVLPBE. GGLIQMGCVFQSTEVKHVTKVEWIFSGRAKBEIVF. SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESI THLGNLVFKKTIVLHVSPBEPRTLVTPAALRPLVLGG GIVCATILLLPVLLIVKKTCGNKSSVNSTVLVKNTI EKPCHPBRCEGEKHIYSPIIVREVIEEEEPSEKSEA	TSQDKKPA  ILLPVILD  IFKIDWTL  CNDGSLLL  PKELMVHV  RYYHKLRM  DGGNYTCS
MAPCNPSDSHQLWLFV  5577 3 1275 RNSDCSCGRISVHCLPWVLFILDLKVESSMFCFLKL. YSLSLNDLMVSPPRLTVHVGDSALMGCVFQSTEDKC SPGEHAKDEXVLYYYSNLSVPIGRFQNRVHLMGDIL QDVQRADQGTYICEIRLKGESQVPKKAVVLHVLPBE. GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAREIVPI SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESI IHLGNLVFKKTIVLHVSPBEPRTLVTPAALRFLVLGG GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNT EKPCHPBRCEGEKHIYSPIIVREVIEEREPSEKSA	ILLPVILD IFKIDWTL CNDGSLLL PKELMVHV RYYHKLRM DGGNYTCS
5577 3 1275 RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKL. YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKC SPGEHAKDEXVLYYYSNLSVPIGRPQNRVHLMGDIL ODVQEADQCTYICEIRLKGESQVPKKAVVLHVLPBE. GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKBEIVPI SVEYSQSWGHPQNRVNLVGDIFRNDGSIMLQGVRESI THLGNLVFKKTTVLHVSPEBPRTLVTPAALRPLVLGG GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNT. EKPCHPBRCEGEKHIYSPIIVREVIEEREPSEKSEA	IFKIDWTL CNDGSLLL PKELMVHV RYYHKLRM DGGNYTCS
YSLSINDINVSPPELTVHVGDSALMGCVFQSTEDKC SPGEHAKDEYVLYYYSNLSVPIGRPQNRVHLMGDIL QDVQEADQGTYICEIRIKGESQVPKRAVVLHVIPBEI GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFI SVEYSQSWGHFQNRVNILVGDIFRNDGSIMLQGVRESI IHLGNLVFKKTIVIHVSPEBPRTLVTPAALRPILVLGI GIVCATILLILPVLILIVKKTCGNKSSVNSTVLVKNTI EKPCHPBRCEGEKHIYSPIIVREVIEEBEPSEKSEA	IFKIDWTL CNDGSLLL PKELMVHV RYYHKLRM DGGNYTCS
SPGEHAKDBYVLYYYSNLSVPIGRPQNRVHLMGDIL QDVQEADQGTYICBIRLKGESQVPKKAVVLHVLPBEI GGLIQMGCYFQSTBVKHVTKVEWIFSGRRAKBBIVFI SVBYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESI IHLGNLVFKKTIVLHVSPBEPRTLVTPAALRPLVLGG GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTI EKPCHPBRCEGEKHIYSPIIVREVIEEBEPSEKSEA	CNDGSLLL PKELMVHV RYYHKLRM DGGNYTCS
QDVQEADQGTYICBIRLKGESQVPKKAVVI.HVLPBE GGLIQMGCVFQSTEVKHVTKVEWIFSGRAKBEIVF SVEYSQSWGHFQNRVNI.VGDIFRNDGSIMLQGURESI IHLGNLVFKKTIVI.HVSPBEPRTLVTPAALRPI.VLG GIVCATILILIVKLTCGNKSSVNSTVLVKNT EKPCHPBRCEGEKHIYSPIIVREVIEEBEPSEKSEA	PKELMVHV RYYHKLRM DGGNYTCS
GGLIQMGCVFQSTBVKHVTKVEWIFSGRRAKBBIVFI SVBYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRBSI IHLGNLVFKKTIVLHVSPBBPRTLVTPAALRPLVLGG GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNT EKPCHPBRCEGEKHIYSPIIVREVIEEBEPSEKSEA	RYYHKLRM DGGNYTCS
SVBYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRBSI IHLGNLVFKKTIVLHVSPBBPRTLVTPAALRPLVLGG GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNT EKPCHPBRCEGEKHIYSPIIVREVIEEBEPSEKSEA	DGGNYTCS
IHLGNLVFKKTIVLHVSPEBPRTLVTPAALRPLVLG GIVCATILLLPVLJLIVKKTCGNKSSVNSTVLVKNT EKPCHPBRCEGEKHIYSPIIVREVIEEBEPSEKSEA	
GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNT EKPCHPBRCEGEKHIYSPIIVREVIEEBEPSEKSEA	コルグアハブエム
1 1 1	
WPSLRSDRUNSLEKKSGGCMPKTQQAF	TYMTMEPV
5578 3 763 AVESMAS PGACRAPPELPERNCGYREVEYWDQRYQG	AADSAPYD
wfgdfssfrallepelrpedrilvlgcgnsalsybl	PLGGPPNV
TSVDYSSVVVAAMQARYAHVPQLRNETMDVRKLDFP:	
EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRV	
SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGSHFHL	
LSVAQLALGAQILSPPRPPTSPCFLQDSDHRDFLSA	
5579 3 1540 RNSGLARGASALARHGGGLAGGVGNDCGACASRCQQ	
CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSI REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGC	
RAMEKLVRVIDQEMQAIGGQKVNMPSLSPARIMQATI	
BLLRIRDRHGKEYCLGPTHEFAITALIASQKKLSYK	
VTRKPRDBPRPRGLLRGREFYMKDMYTFDSSPEAA	
DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVI	
ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEV	
KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTR:LAAA;	IEVLSTED
CVRWPSLLAPYQACLIPPKKGSKBQAASELIGQLYDI	HITEAVPO
LHGEVILLDDRTHLTIGNRLKDANKFGYPFVIIAGKRI	ALKDPAHF
BVWCQNTGEVAFLTKDGVMDLLTPVQTV	
5580 1681 450 ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAA	
WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSM	
GPSRYVLGMQELFRCHSKTREFLAHSAKVHSVAWSCI	
SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPS	
ASGDKTIRIWDVRTTKCIATVNTKGRNINICWSPDG	
DDVVTFIDAKTHRSKARRQFKFEVNEISWNNDNNMFI	
INILSYPELKPYQSINAHPSNCICIKFDPMGKYFATY LWDVDBLVCVRCPSRLDWPVRTLSFSHDGKMLASASI	
EVETGDXLWEVOCESPTFTVAWHPKRPLLAFACDDKI	
RAGTVKLFGLPNDS	YCCTTY
5581 54 947 GGGSGPRAPSATILDTGESVAAVASGEDKGIAASAAI	AAAVPACQ
CSPDPOSSTMNPVYSPVOPGAPYGNPKNMAYTGYPTX	
YNPSLYPTNSPSYAPEPQPIHSAYATILMKQAWPONS	
TEHLEVOIGIENETYQASSAAFRYTAGTPYKVPPTQS	
SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYA	
TTVVQPNSIPSAIYPAPVAAPRTNGVANGNVAGTTNJ	
TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW	
5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMES	ROKRKADI
RKGLQFIQSTLPLKQEEYEAFLLKLVQNLFAEGNDL	
ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAAC	_
ekaledsekalgldsestralfrkaralnelgrhkei	
SLALPHDRSVTQLGQELAQKLGLRVRKAYKRPQKLKT	
TAAGVADQGTSNGLGSIDDIRTDCYVDPRGSPALLPS	
PHVLDLLAPLDSSRTLPSTDSLDDPSDGDVFGPRLDT	CLLDSLSL
VQGGLSGSGVPSELPQLIPVPPGGTPLLPPVVGGSI	QQ.TQ22VQ
ASPGLVMDPSKKLAASVLDALD9PGPTLDPLDLLPYS	

WO 01/53312

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DSFGSTRGSLDKPDSFMERTNSQDHRPPSGAQKPAPSPEPCMPN
1		1	TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK
	1		RDILLGRLRSSEDQTWKRIRPRPTKTSPVGSYYLCRDMINKQDC
[		j	KYGDNCTFAYHQEEIDVWTEERKGTLNRDLLFDPLGGVKRGSLT
{	{	1	IAKLLKBHQGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAK
l	)	1	HSPYNNKCLVHIVRSTSLKYSKIRQFQKHFQFDVCRHEVRYGCL
	}	Į.	REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAH
		ł	AGKASSSMGAPRTHGPSTYDLQMKFVCGQCWRNGQVVBPDKDLK
Ì	1		YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD
	1	ł	LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY
	<b>}</b>		DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL
	(	!	CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRPPMGEFR LCDRLQKGKAC?DGDKCRCAHGQEELNEWLDRREVLKQKLAKAR
1	}	1	KDMLLCPRDDDFGKYNFLLQEDGDLAGATPRAPAAATATTGE
5583	3	1265	SSGCROGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEH
2203	1 3	1203	IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
		1	QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
Ì	ţ	1	HOLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
ļ	Ì	j	CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCRSC
1		1	SGAKVIREKKII EVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
	ļ		IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGPKKTIKTLDNRI
l			LVITSKAGKVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
	į.	ľ	PEKHWLSLEKLPQLEALLP?RQKVRITDDMDQVELKRFCPNEQN
1			WROHREAYEEDEDGPQAGVQCQTA
5584	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEB
}		1	IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
			QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
	ł	l .	HOLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
!			CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIRBKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
t	1		IVLDOKDHSVFORRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
ļ		}	LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLRKGILLIQFLVIF
ĺ	, T		PEKHWLSLEKLPQLEALLPPRQKVRICDDMDQVELKEPCPWEQN
			WROHRRAYERDEDGPQAGVQCQTA
5585	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
		Į.	YHSLTYATILEMQAMMTFDPQDILLAGNMMKBAQMLCQRHRRKS
	1		SVTDSFSSLVNRPTLGQFTEEE IHAEVCYAKCLLQRAALTFLQD
l	1		RNMVSF1KGG1KVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
1	1	1	VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
			GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEBABKLLKPYLNR
l	1		YPKCAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
	Į.	- 20	CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
Í		1	SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
Į		}	RRYFSSNPISLPVPALEMMYINNGYAVIGKQPKLTDGILEIITX
1		1	AREMLEKGPENBYSVDDECLVKLLKGLCLKYLGRVQEAKENFRS
1	1	1	ISANBKKIKYDHYLIPNALLELALLIMEQDRNERAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSELENSSRSMVSSVSL
FFAR	762	015	NYKNYSMESKTHFRIQAATLQAKSSLENSSKSMV5SV5L LPAGTFESSLHFALDQCMTALDLFLTNQFSEALSYLKFRTKESM
5586	2619	915	YHSLTYATILEMQAMMTFDPQDILLAGNMMKBAQMLCQRHRRKS
1	1	1	SYTDSFSSLVNRPTLGQFTBEE I HABVCYAKCLLQRAALTFLQD
[	(	1	KNMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
1		Į.	VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
		1	GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEABKLLKPYLNR
1		ł	YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
		1	CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
l	1	ì	SMPGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
1		1	RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
[	Į.	1	AEEMLEKGPENEYSVDDRCLVKLLKGLCLKYLGRVQEAEENFRS
1	1	1	ISANEKKIKYDHYLIPNALLELALLIMEQDRNERAIKLLESAKQ
			NYKNYSMESRTHPRIQAATLQAKSSLENSSRSMVSSVSL
5587	1768	148	SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA
		<del></del>	

C OPA	Predicted	I Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	} -	\=possible nucleotide insertion)
	1		CVAVYKDGRAGVVANDAGDRVTPAVVAYSKNEBIVGLAAKOSRI
1	•		RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIBKNGKLRYE
j.	1	1	IDTGEETKFVNPEDVARLIFSKMKBTAHSVLGSDANDVVITVPF
1		1	
!		l	DFGBKQKNALGBAARAAGFNVLRLIHEPSAALLAYGIGQDSPTG
		Ì	Kanilveklegtalslsvmevnsgiyrvlsintddniggahfte
1	l .		TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAKVAKHSLSTLGS
1		l l	ANCPLDSLYEGODFDCNVSRARFELLCSPLFNKCIEAIRGLLDQ
l .			NGFTADDINKVVLCGGSSRIPKLQQLIKDLFPAVELLNSIPPDE
l	] .	}	VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
		1	SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYBSDGKNSAK
1	1	ļ.	EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET
l	1	1	
		l	GKCEAISIBIAS
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVN1RGK
1	I	1	LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
Į		i	VLAFPCNQFGQQEPDSNKBIESFARRTYSVSFPMFSKIAVTGTG
1	Ī	(	AHPAPKYLAQISGKEPTWNFWKYLVAPDGKVVGAWDPIVSVEEV
ì		1	RPQITALVRKLILLKREDL
5589	1884	553	LROAWHEGGIGOTDKERGAAALPGEEGDPTRGRSLGRASWESGS
] 3303	1001	}	PRRPRSPFSSFLPRPICLSLRARPCSIEDRRNWSLIGRPGAPAS
1			GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL
ŀ	1	ı	ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF
Į.		l .	RPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALM
i	i		The state of the s
			KEIEAAGEALQSVHAVPSAPAVPSGTGQTSAELEVQRRHSLVSF
1		1	VVRIVPSPDWFVGVDSLDLCDGDRWREQNALDLYPYDAGTDSG?
}			TFSSPNFATIPODTVTBITSSSPSHPANSFYYPRLKALPPIARV
I	ì		TLLRLRQSPRAFIPPAPVLPSRDNBIVDSASVPBTPLDCEVSLW
ı	1 .	Į.	SSWGLOGGHOGRLGTKSRTRYVRVQPANNGSPCPELEERABCVP
1		İ	DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
			EDAVKETSSVKOPWDHTTTTTNRPGTTRAPARPPGSGLDLADA
1	f	(	LDDODDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
) .			LADALDDRNDRDDGRRKPIAGGGGPSDKDLEDIVGGGEYKPDKG
1		l .	KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY
1	`	}	
l .		1	QQKKPCFSIQQGLNADYVKGENLEAVVCBBPQVKYSTLHTQSAB
L			PPPPPBPARI
5591	68	1494	AGSSRRAAABRILVSAGCRSLAGRASGVLLLPABLLPGBEEAMA
i		1	LRVTRNSKINAKNKAKINMAGAKRVPTAPAATSKPGLRPRTALG
1			DIGNKVSEQLQAKMPMKKRAKPSATGKVIDKKLPKPLEKVPMLV
i		1	PVPVSRPVPEPBPBPBPKPVKEEKLSPEPILVDTASPSPMETSG
J	1		CAPAREDLCQAFSDVILAVNDVDAEDGADPNLCSRYVKDIYAYL
1			ROLEEBOAVRPKYLLGREVTGMMRAILIDWLVQVQMKFRLLQET
1	{	1	MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPBI
			GDPAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS
1	ł		
1			KIGEVDVEQHTLAKYLMELTMLDYDMVHPPPSQIAAGAFCLALK
1		1	ILDNGEWTPTLQHYLSYTERSLLPVMQHLAKNAAMVNQGLTKHM
	L	<u> </u>	TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGBSKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
1	1		VGKSALVVRPLIKRFIWEYDPTLESTYRHQATIDDEVVSMEILD
1	1		TAGOEDTIQRECHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
1	1	Į.	IKKPKNVTLILVGNKADLDHSRQVSTEEGRKLATELACAFYECS
	1		ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK
1	l	Į.	
	ļ		MLTKISS
5593	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
	1		SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
			DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
i	]		8LDLYDNQIKKIKNLEALTELBILDISFNLLRNIEGVDKLTRLK
1	İ	}	KLPLVNNKISKIENLSNIHQLQMLEIGSNRIRAIENIDTLTNLB
			SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIPGLQNLVNLR
1		1	RLYLSHNGIBVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
1	ł	}	EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV
A	J	ì	PERMINDIAND SASDED TO THE WAS TELLA I THE WAS TO THE WAY A

SEO	Dwg 25-4-3	[ N	
	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S-Scrine, T-Threonine, V-Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Degacines	\=possible nucleotide insertion)
	sequence	<b> </b>	<del></del>
J			MLALPSVRQIDATFVRF
5594	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
	}	ł	SSGIVADLSEQSLKDGEERGBEDPBEEHBLPVDMETINLDRDAR
	į		DVDLNHYRIGKIEGFEVLKKVKTLCLRONLIKCIENLRBLOSLR
i			ELDLYDNQIKKIENLBALTELEILDISFNLLRNIEGVDKLTRLK
ł	1	ļ	KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
4	1		SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLONLVNLR
į.	1		RLYLSHNGIRVIEGLENNNKLTMLDIASNRIKKIENISHLTELO
1	ļ		
l .			EFWINDNLLESWSDLDELKGARSLETVYLBRNPLQKDPQYRRKV
			MLALPSVRQIDATFVRP
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE
1 .			PIALANSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK
Ì	1	1	LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
1	Į į		AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
	1		NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
1			NDGLVKRLEBLERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD
1			VFSVIGVRBPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
1	<b>i</b>		DINTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC
1	<b>J</b>		
1	j		IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL
ł	ł i		LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA
}	ł		HTTLAYGLNQEEFTDGREEEEREDTAAGEPSRDTRGAAGPLDKG
			GSWCDS
5596	698	219	GAVLAPSSLPAABLAAQGESQSLEDLSNTSRPTSEVYKISPIPP
			NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
			FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
	_		KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP
	·	, , , ,	VFVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIORPR
1			PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLYLRMHQTNNA
1			
1	i		RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG
· .			GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
			FEYTVTRABARNRQRKLGTKLQ
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
}			VPLIGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
			DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
1	Į l		EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEB
1			IKCALCSPHSQSLPHSPEREVLERDLVLPLLCKDYCKEFFYTCR
			GHIPGFLOTTADEFCFYYARKDGGLCFPDFPRKOVRGPASNYLD
1			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
[			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVOSGIKGGDERGLL
j !			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1	,		· · · · · · · · · · · · · · · · · · ·
1			NPHQVDLRTARVFLEVABLHRKHLGGQLLFGPDGFLYIILGDGM
1			ITLDDMREMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
1 1			TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
1	1		SARILQIIKGKDYESEPSLLBFKPFSNGPLVGGFVYRGCQSERL
1 1	Į		YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYPSG
1 1			HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
			CRATVQPAQTLTSECSRLCRMGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
		~270	VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGPPEG
1 1			
}	1		DAKFGERNEGSGARRRRCLINGNPPKRLKRRDRRMMSQLELLSGG
į (	ſ		EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
1 1	ì		IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
1 1	Į		GHIPGFLQTTADBFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
1 1	ĺ		QMEEYDKVEETSRKHKHNCFCIQEVVSGLRQFVGALHSGDGSQR
1 1	ł		LFILEKEGYVKILTPEGEIFKEPYLDIHKLVOSGIKGGDERGLL
1	1		SLAFHPNYKKNGKLYVSYTTNOBRWAIGPHDHILRVVBYTVSRK
( )	1	l	
] ]	}		NPHQVDLRTARVFLEVABLHRKHLGGQLLFGPDGFLYIILGDGM
] 1		Į	ITLDDMEEMDGLSDPTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
		· <u>-</u>	TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

	Predicted	Predicted end	I amino agid goment gentaining nimel montide
SEQ	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO	location		Glutamic Acid, F-Phenylalanine, G-Glycine,
1	2	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y≈Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	i	\=possible nucleotide insertion)
			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
i	i		YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
1		i '	HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
F		ì	CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQB
			EDMCPEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLRDPNGSF
1		1	SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
l .		1	FPNCKFARKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
1			AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTOCTRPDC
ľ	i		· · · · · · · · · · · · · · · · · · ·
5601	1022	2044	TPYHPTINVPPRHALKWIRPQTSB
2007	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
1.			EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
1	·	1	SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
1	:		FPNCKFARKCLFVHPNCKYDAKCTKPDCPFTHV\$RRIPVL\$PKP
			AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
			TFYHPTINVPPRHALKWIRPQTSB
5602	246	766	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK
			NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC
			AAALRLMKIPLVVYGCONERFGGCGSVLNIASADLPNTGRPFQC
L			IPGYRABBAVBMLKTFYKQENPNAPKSKVRKKBCQQILNMF
5603	1	565	PRGRTPISGGRRGCAQYPIPATPARSGENRTMPGAGDGGKAPAR
			WIGTGLIGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS
1			CFGFRDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI
i			TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLOHHA
			TIFLQVVDRRMQ
5604	1	1506	EDIFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG
i			GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ
		*	RLDGILSETIPIHGRGNFPTLBLQPSLIVKVVRRRLAEKRIGVR
1			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV
	'		VLDCLLDPLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
	1		
		1	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE
		2	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE
		4)	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTBTFHPTIIGESVYGDFQBAFDHLCNKIIATRNPBEIRGGG
			SLSNNSGKNVELKFYDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGESVYGDFQBAFDHLCNKIIATRNPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL
		4	SLSNNSGKNVELKFYDSLRROFEFSVDSFOIKLDSLILFYBCSE NPMTETFHPTIIGESVYGDFOBAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDBIKTLORYMCSRFFIDFSDIGEQORKL ESYLONHFVGLBORKYBYLMTLHGVVNBSTVCLMGHERROTLNL
5605	35	1821	SLSNNSGKNVELKFYDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGESVYGDFQBAFDHLCNKIIATRNPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLBDRKYBYLMTLHGVVNBSTVCLMGHBRRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV
5605	35	1821	SLSNNSGKNVELKFYDSLRRQFBFSVDSFQIKLDSLLLFYBCSE NPMTETFHEFTIGESVYGDFQBAFDHLCNKI IATRNPBEIRGGS LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFYGLBDRKYBYLMTLHGVVNBSTVCLMGHBRRQTLNL ITMLAIRVLADQNVIENVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGESVYGDFQBAFDHLCNKIIATRNPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKI ESYLQNHFVGLEDRKYBYLMTLHGVVNBSTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDBATRSRHRTRPVFQ
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTBTFHPTIIGESVYGDFQBAFDHLCNKIIATRNPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYBLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSFSSPAPPWARCSNPDSKTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDBATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDBRLQRHRTSG
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGESVYGDFQBAFDHLCNKIIATRNPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLBORKYBYLMTLHGVVNBSTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPR6F98FPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDBATRSRHRTRFVFQ KALRSLRRYPLPLRSGKBAKILQHFGDGLCRWLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTBTFHPTIIGESVYGDFQBAFDHLCNKIIATRNPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYBLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSFSSPAPPWARCSNPDSKTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDBATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDBRLQRHRTSG
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHEPTIGESVYGDFQEAFDHLCNKI IATRIPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLBORKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIDNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACFNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLKSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVQDSSMPVPAQPKAGGSGSYMP ARHSGARVILLVLYREHLNPNGRHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFR PASDBIKTLGRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYBYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKLIQHFGDGLCRWLDERLQRHRTSG GDHAPDSPSGENSPAPQRIAEVODSSMPVAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPAIRSLLHENLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGG LLKYCNLLVRGFR PASDBIKTLQRYMCSRFFIDFSDIGEQQRKI ESYLQNHFVGLEDRKYBYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYFLPLRSGKEAKILQHFGDGLCRWLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVODSSMPVAQVRAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPBGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GBYRVLLCVDIGETRGGGHRPBLLRELQRLHVTHTVRKLHVGDF
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTBTFHPTIIGESVYGDFQBAFDHLCNKIIATRNPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKI ESYLQNHFVGLEDRKYBYLMTLHGVVNBSTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACFNPLFVRWLTEWRDBATRSRHRTRPVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRWLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYRBHLNPNGHHFLTKBELLQRCAQKSPRVAP GGSARPWPALRSLLHRNLVLRTHQPARYSLTPBGLELAQKLAESB GLSLLNVGTGPKEPPGEETAVPGAASAELASBAGVQQQPLELRP GBYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGBLVLDHIVERKRLDDLCSSIDGRPREQ
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHETTIGESVYGDFQBAFDHLCNKI IATRNPBEIRGGS LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYBYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIENVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRMLTEWRDBATRSHRTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLIHRNLVLRTHQPARYSLTPBGLELAQKLAESE GLSLLNVGIGPKEPPGBETAVFGAASAELASEAGVQQQPLELRP GSYRVLLCVDIGETRGGGHRPBLLRELQRLHVTHTVRKLHVGDF VWVAQBTWPRDPANPGELVLDHIVERKRDDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPBSTLLQAVINTQVIDG
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHETTIGESVYGDFQEAFDHLCNKI IATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIENVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVQDSSMPVPAQPKAGGSGSWMP ARHSGARVILLVLYREHLNPNGHHFLTKBELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLERLQRLYHTVTKKLHVCDF VMVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRPREQ KFRLKRCGLERRVYLVBEHGSVHNLSLPESTLLQAVTNTQVLDG PFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHEPTI IGESVYGDFQEAFDHLCNKI IATRAPEEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLBORKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVI DNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACFNPLFVRWLITEWRBEATRSRHRTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDBELQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYMP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGTGPKEPPGEETAVPGAASAELASRAGVQQQPLELRP GFYRVLLCVDIGETRGGGHRPEILJRELQRHAVTHTVRKLHVCDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRPREQ KFRLKRCGLERRVYLVBEHGSVNNLSLPBSTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQCHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGG LLKYCNLLVRGFRPASDBIKTLGRYMCSRFJDFSDIGEQQRKL ESYLQNHFVGLBORKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIDNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAPPVRLGRKRPLPACENPLFVRWLTEWRDBATRSRHRTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGRHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GBYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVCDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSILDGRFREQ KFFLKRCGLERRYYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLESRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
		-	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLILFYBCSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDBIKTLGRYMCSRFFIDFSDIGEQQRKI ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSIRRYPLPLRSGKEAKILQHFGDGLCRMLDRRLQRHRTSG GDHAPDSPSGENSPAPQRIAEVQDSSMPVAQKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPAIRSLIHHNLVLRTHQPARYSLTPBGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GBYRVLLCVDIGETRGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQBTNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFPLKRCGLERRVYLVEBHGSVHNLSLPBSTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPB SGAMTSPNPLCSLLTTSDFNAGAIKNKAQSVREVPARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQBTLLSTIKCGRL
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPBEIRGG LLKYCNLLVRGFR PASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILDHFGDGLCRMLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVODSSMPVAQKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPBGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GBYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKCGLERRVYLVBEHGSVHNLSLPBSTLLQAVTNTQVIDG PFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTBASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT
		-	SLSNNSGKNVELKFVDSLRRQFBFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGSSVYGDFQBAFDHLCNK I IATRIPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLBORKYBYLMTLHGVVNESTVCLMGHBRRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPPACPNPLFVRULTEWRDBATRSHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVQDSSMPVPAQPKAGGSGSYMP ARHSGARVILLVLYRBHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPBGLELAQKLAESE CLSLLNVGIGPKEPPGBEETAVFGAASAELASBAGVQQQPLELRP GBYRVLLCVDIGETRGGGHRPBLLRELQRLHVTHTVRKLHVGDF VWVAQETNFRDPANFGELVLDHIVERKRLDDLCSSIIDGRFRRQ KFRLKRCGLERRVYLVBEHGSVHNLSLPBSTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPB SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
		-	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGSSVTGDFQBAFDHLCNK I IATRIPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLBORKYBYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVI PNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRBEATRSCHRTTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVQDSSMPVPAQPKAGGSGSYMP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESB GLSLLNVGIGPKEPPGEETAVPCAASAELASEAGVQQPLELRP GBYRVLLCVDIGETRGGGHRPELLRELQRLHYHTVKKLHVCDF VWVAQETNPRDPANPGBLVLDHIVERKRLDDLCSSIIDGRPREQ KFRLXRCGHERRVYLVBEHGSVINLSLPBSTLLQAVTNTQVIDG PFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRBRCPGPGARGGTMSPRSCLRSLRLLVFAVPSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVWDSVRRGAQLA IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA
		-	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGSSVTGDFQBAFDHLCNK I IATRIPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKI ESYLQNHFVGLBORKYBYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIDNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACFNPLFVRWLTEWRDBATRSRHRTRFVPQ KALRSLRRYPLPLRSGKEBKILQHFGDGLCRHLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGTGPKEPPGESTAVPGAASAELASEAGVQQPLELRP GFYRVLLCVDTGETRGGGHRPEILJRELQRHVHTTVRKLHVCDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSTIDGRPREQ KFRLKRCGGERRVYLVBEHGSVNNLSLPBSTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAVDACATPKBQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA LEECQYQFRNRRWNCSTLDSLFVFGKVVTQGTRRAAFVYALSSA GVAFAVTRACSSGBLEKCGCDRTVBGVSPQGFQWSGCSDNIAYG
		-	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGSSVIGDFQEAFDHLCNKI IATRIPEEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKI ESYLQNHFVGLBORKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIDNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACFNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GFYRVLLCVDIGETRGGGHRPELLJELQRHYTHTVRKLHVCDF VWVAQETNPRDPANPGELVLDHIJRELQRHYTHTVRKLHVCDF VWVAQETNPRDPANPGELVLDHIJRELQRUNTTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQCHTLRSRPWGTPGRPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFBARGGTMSPRSCLRSLIRLLVFAVFSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGQLA IBECQYQFRNRRWNCSTLDSLEVFGKVVTQGTRERAAFVYALSSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNILAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC
		-	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHETTIGESVYGDFQEAFDHLCNKI IATRNPEEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLBORKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIDNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACFNPLFVRWLTEWRDBATRSRHRTRFVPQ KALRSLRRYPLPLRSGKEBKILQHFGDGLCRMLDBELQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYMP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGTGPKEPPGEETAVPGAASAELASRAGVQQQPLELRP GFYRVLLCVDIGETRGGGHRPEILJRELQRLHVTHTVRKLHVCDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRPREQ KFRLKRCGGERRVYLVBEHGSVNNLSLPRSTILQAVTNTQVTDG FFVKRTADIKESAAYLALLTRGLQRLYQCHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSVGSISBEETCEKLKGLIQRQVQMCKRNLEVWDSVRRGAQLA LEECQYQFRNRRWNCSTLDSLFVFGKVVTQGTERRAFVYAISSA GVAFAVTRACSSGBLEKCGCDRTVHGVSPQGFQWSGCSDNIAYG
		-	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGSSVIGDFQEAFDHLCNKI IATRIPEEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKI ESYLQNHFVGLBORKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIDNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACFNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GFYRVLLCVDIGETRGGGHRPELLJELQRHYTHTVRKLHVCDF VWVAQETNPRDPANPGELVLDHIJRELQRHYTHTVRKLHVCDF VWVAQETNPRDPANPGELVLDHIJRELQRUNTTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQCHTLRSRPWGTPGRPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFBARGGTMSPRSCLRSLIRLLVFAVFSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGQLA IBECQYQFRNRRWNCSTLDSLEVFGKVVTQGTRERAAFVYALSSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNILAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC
		-	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGESVYGDFQEAFDHLCNK I IATRNPEEIRGGG LLKYCNLLVRGFR PASDBIKTLGRYMCSRFFIDFSDIGEQQRKI ESYLQNHFVGLBORKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIDNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACENPLFVRWLTEWRDBATRSRHRTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFEDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVODSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GFYRVLLCVDIGETRGGGHRPELLRELQRHVTHTVRKLHVCDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSILDGRFREQ KFRLKCGLERRVYLVBEHGSVHNLSLPBSTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPFGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IBECQYQFRNRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGBLBKCGCORTVHGVSPQGFQWSGCSDNLAYG VAFSQSFVDVRERSKGASSSRALMNLHNNRAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPPRQVCHALKEKFPGATEVEPRRVG
		-	SLSNNSGKNVELKFVDSLRRQFBFSVDSFQIKLDSLLLFYBCSE NPMTETFHPTIIGSSVYGDFQBAFDHLCNK I IATRIPBEIRGGG LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLBGRKYBYLMTLHGVVNESTVCLMGHBRRQTLINL ITMLAIRVLADQNVI PNVANVTCYYQPAPYVDANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSFBSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRNLTEWRDBATRSHRTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDBRLQRHRTSG GDHAPDSPSGENSPAPQGRIAEVQDSSMPVPAQPKAGGSGSYMP ARHSGARVILLVLYRBHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPBGLELAQKLAESB GLSLLNVGIGPKEPPGEETAVPGAASAELASEASVQQQPLELRP GBYRVLLCVDIGETRGGGHRPBLLRELQRLHVTHTVRKLHVGDF VWAQETNPRDPANPGBLVLDHIVERKRDDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVBEHGSVHNLSLPBSTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPB SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKBQBTLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSCCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA LBECQYQFRNRRWNCSTLDSLEVFGKVVTQGTRRAAFVYAISSA GVAFAVTRACSSGBLBKCGCDRTVHGVSPQGFGWSGCSDNIAYG VAFSQSFDDVRERSKGASSSRALMNLHNNEAGRRAILTHMRVEC KCHGVSGSCCKVKTCWRAVPPFRQVCHALKEKFDGATEVEPRRVG SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	Guidelidino T. Tanlandine, George ine,
	corresponding		H=Histidine, I=Isoleucine, K=Lysine,
Ĭ		to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	N-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
5607	521	141	PPVCNPARAMPSPGTVCSLLLLGMI.WLDLAMAGSSFLSPEHQRV
1	ł	1	QQRKBSKKPPAKLQPRALAGWLRPRDGGQAEGAEDELEVRFNAP
1	i	i	EDVICTIVI COVOVOQUANTA CONTRACTOR
5608	2		FDVGIKLSGVQYQQHSQALGKFLQDILWBEAKEAPADK
3608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
Į.	İ		RIQTEPKYTGIWHCVRDTYHRBRVWGFYRGLLLPVCTVSLVSSE
1		}	VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
1	1	1	SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPRP
1	i .		KYRGPLHCLATVARKEGLCGLYKGSSALVLRDGHSFATYFLSYA
1			VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
1			QADGQGQRRYRGLLHCMVTIVRREGPRVLFKGLVLNCCRAFPVN
	ł i		MVVFVAYBAVLRLARGLLT
5609	1628	304	
3003	1020	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSNRPRRMNHKSK
1	ł		KRIRBAKRSARPELKDSLDWIRHNYYESFSLSPAAVADNVERAD
ŀ			ALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY
1			RNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
1	ļ	\	EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS
1			GTGIHIDPLGTSAWNALVQGHKRWCLPPTSTPRELIKVTRDEGG
			NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFVPGG
			WWHVVLNLDTTLAITQNFA9STNFPVVWHKTVRGRPKLSRKWYR
1			ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSSDSD
1 :			SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
		/	R
5610	54	1196	LERTPASADMAWTKYQLPLAGIMLVTGSINTLSAKWADNFMAEG
	3.	1130	OCCUPATION OF THE PROPERTY OF
1			CGGSKEHSFQHPFLQAVGMFLGBFSCLAAFYLLRCRAAGQSDSS
1 1			VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA
			VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
1 1			DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
: 1			VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ
i l	i		VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
i l			TVVIWALSLALGWRAFHALQILGFLILLIGTALYNGLHRPLLGR
1			LSRGRPLAEESEQERLLGGTRTPINDAS
5611	2	577	FVLPNRLGIPGSTFRGPGACAESESLAASAKPGAGGSPALAMSG
1 [			ELSNRFQGGKAFGLLKARQERRLABINREFLCDQKYSDRENLPE
1			KLTAFKEKYMBFDLNNEGBIDLMSLKRMMEKLGVPKTHLKMKKM
1 1			ISEVTGGVSDTISYRDFVNMMLGKRSAV:kLvmmfegkanessp
i i			KPVGPPPERDIASLP
5612		721	
	*	121	ASRDGYMDATIAPHRIPPRMPQYGBENHIFRLMQAMWLCKHLNS
	į		SLLTLENLILNEFSYTATKARRLYLQRKTVPSALLVQLIQERLA
1 1	·		eedcikqgwildgipetreqalriqtlgitprhvivlsapdtvl
1 1	i	ı	IERNLGKRIDPQTGBIYHTTFDWPPBSBIQNRLMVPEDISBLBT
; l	1		AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
			NHRTNAPFTPRVLLLGPVGS
5613	115	1279	RGVDPALRRAEKMLPLSIKODEYKPPKFNLPGKISGWFRSILSD
Į į	i		KTSRNLFFFICLMLSFAFVBLLYGIWSNCLGLISDSFHMFFDST
	ŀ	1	ALLAGLAASVISKWRDNDAFSYGYVRAEVLAGPVNGLFLIFTAF
	[	1	FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
, !	1		GRSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
	Į.	}	AKCHCHPHCHDGDGI. PERWADORATI AMERICHANGAAHSHDH
	1	1	AHGHGHPHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI
} i	ſ	į	ASAIMMONFGLMIADPICSILIAILIVVSVIPLLRESVGILMOR
i 1	·		TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL
			IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5614	3	1268	LLSRNEHACPLOAGLGLTQRKPKAIRGREGRATNQGQGETQNER
	İ		APWGARQRLGVMABLQQLQBPBIPTGRBALRGNHSALLRVADYC
		1	EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD
l		}	
		I	LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG
			QKVIAPBNLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT
		ļ	LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS
i I	ľ	[	SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPAAVEVF
!	ł	i	QRPPTLEELSPPPPDEELPLPLDLPPPPPPLDGDELGLPPPPPGF
			GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY
			· · · · · · · · · · · · · · · · · · ·

	Dundintad	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			Hatistidine, I=Isoleucine, K=Lysine,
į.	location	corresponding	
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	]	\=possible nucleotide insertion)
<del></del>			SDGWCRGVSSEGTGFFPGNYVEPSC
5615	9	1558	ALGRERPGDPREMEAAATPAAAGAARREELDMDVMRPLINEONF
2012	, ,	1550	
ì	1		DGTSDREHEQELLPVQKHYQLDDQEGISFVQTLMHLLKGNIGTG
1	I		LIGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR
i	į.	Į.	FKKSTLGYSDTVSFAMEVSPWSCLQKQAAWGRSVVDFFLVITQL
1			GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVD
			LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIYQ
ì	}	)	YVVRNMPDPHNLPIVAGWKKYPLFFGTAVFAFEGIGVVLPLENQ
ļ	į.	Ì	MKESKRFPOALNIGMGIVITLYVTLATLGYMCFHDBIKGSITLN
Į.	ł	ł	LPQDVWLYQSVKILYSFGIFVTYSIQFYVPARITIPGITSKFHT
l	l .		KWKQICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA
1	}		LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGFLLGTYITV
1	1	1	
			REITYPTPKVVAGTPQSPPLNLNSTCLTSGLK
5616	1	719	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE
1		1	LKHLSSGDLLRDNMLRGTBIGVLAKAFIDQGKLIPDDVMTRLAL
	1	i	HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
<b>{</b>	1	<b>I</b>	IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDD
i	[	1	KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV
1	1	Ì	YAFLQTKVPQRSQKASVTP
5617	176	765	PWRGRGSRPRGAGAMAREQVNRSAGLAPDCEASATABTTVSSVG
2027			TCEAAGKSPEPKDYDSTCVFCRIAGRODPGTELLHCENEDLICF
Į.	1	Į.	KDIKPAATHHYLVVPKKHIGNCRTLRKDOVBLVENMVTVGKTIL
I	l		ERNNFTDFTNVRMGFHMPPFCSISHLHLHVLAPVDQLGFLSKLV
I			
			YRVNSYWFITADHLIBKLRT
5618	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES
1 .			LFLNSGGDSLKSIRLLSBIEKLVGTSVPGLLBIILSSSILEIYN
1	ì	-	HILQTVVPDEDVTFRKSCATKRKLSNINQBRASGTSLHQKAIMT
[	i	1	FTCHNBINAFVVLSRGSQILSLNSTRFLTKLGHCSSACPSDSVS
i	1		QTNIQNLKGLNSPVLIGKSKDPSCVAKVSEEGKPAIGTQKMELH
l .		} .	VRWRSDTGKCVDASPLVVIPTFDKSSTTVYIGSHSHRMKAVDFY
	i		SGKVKWEQILGDRIESSACVSKCGNFIVVGCYNGLVYVLKSNSG
1	ì	)	EKYMMFTTEDAVKSSATMDPTTGLIYIGSHDQHAYALDIYRKKC
l			VWKSKCGGTVFSSPCLNLIPHHLYFATLGGLLLAVNPATGNVIW
ļ	į .		KHSCGKPLFSSPQCCSQYICIGCVDGMLLCFTHFGEQVWQFSTS
	ł		GPIFSSPCTSPSEQKIFFGSHDCFIYCCNMKGHLQWKFETTSRV
			YATPPAFHNYNGSNEMILAAASTDGKVWILESQSGQLQSVYELP
1	1		
			GEVFSSPVVLRSMLIIGCRDNYVYCLDLLGGNQK
5619	2160	1477	DSPVLPTSGNVISTAQPAQPWSAVRAALRSLGSPPGAGRGCPCP
1	1	1	AGSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR
1	1	1	RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSPLGHCSVL
1	1	1	LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQPPLGP
1	1	1	TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA
	l .	1	ECSPPATP
5620	930	182	PLPPPTLAMPLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST .
-,,,,	1	]	AIGIOTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGCAMSG
1	1	1	LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLALQPG
I	1	1	REDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR
l	1	I	
1	[	1	AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEEKLNA
L			TNIELATVQPGQNFHMFTKRELEEVIKDI
5621	3	819	VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA
1	1		ENDLTWVLKHCERPLKOOQTSIKSSLLCLQGNYAGHDWFVSSLF
I	1	1	MIMLGDKEKTFOFLHOFSRLLTSAFLWLPRLHISSYLPNDTVES
1	]	1	GIHPVYFCSTHYIKMLLKARLPLVFSAFHMSGFAPSQICLQWIT
ł	I		OCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDILQ
ļ	Į.		HTOTODLOVFLKEBALHOPRVSDYPEYMEILEONYRTVLLRDMR
1	Į		
		<del></del>	NIRLOST
5622	1122	456	AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAMY
1	1		PGTFYFQFKNLWBANDRNETWLCFTVEGIKRRSVVSWKTGVFRN
1	Į.	1	QVDSETHCHAERCFLSWFCDDILSPNTKYQVTNYTSWSPCPDCA
ì	1		GEVARFLARHSNVNLTIFTARLYYFQYFCYQEGLRSLSQEGVAV
L			

<del> </del>			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
I	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
[	sequence		\-possible nucleotide insertion)
			EIMDYEDFRYCWENFVYNDNEPFRPWKGLKTNFRLLKRRLRESL
			Q
5623	3	954	FLPFFIRAPKISRNGQWLFTFTTPFPFANKALPGWEGIVPACFW
1	1		rkkiltpstgtmellqvtilfllpsicssnstgvlraannslvv
ŧ		ł	TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNBLLKMSLMST
ŀ	ł	1	ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS
l .	ì	l	SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT
1	1	Ì	SQSQVIGTEGGKNASTSATSRSYSSIILPVVIALIVITLSVFVL
1	1		VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH
ļ	<b>!</b>	<b>L</b>	SAQGKTKN
5624	159	898	PGVAAAAGALPOYHGPAPALVSCRRELSLSAGSLQLERKRRDFT
			SSGSRKLYFDTHALVCLLEDNGFATQQABIIVSALVKILEANMD
I	I	1 .	IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE
	I	f	NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKBLYSLN
1	1	1	EKKLLELRTBIVALHAQQDRALTQTDRKIETEVAGLKTMLBSHK
1			LDNIKYLAGSIFTCLTVALGFYRLWI
5625	1	1280	TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP
	l -		AGSLSRKKRLELDDNLDTERPVOKRARSGPOPRLPPCLLPLSPP
	Ì		TAPDRATAVATASRLGPYVLLEPBEGGRAYQALHCPTGTBYTCR
)			VYPVQRALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH
i			CDMHSLVRSRHRIPBPKAAVLFROMATALAHCHOHGLVLRDLKL
1	}	1	CREVEADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE
1		ĺ	ILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSRPVLLFGKI
į		l	RRGAYALPAGLSAPARCLVRCLLRREPABRLTATGILLHPWLRQ
			DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENOVLTPHVYWAQRHRELYLRVELSDVQNPAISI
1 3020	1		TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
ŀ			ITVOKKVSQWWBRLTKQRKRPLPLAPDFDRWLDESDAEMELRAK
1		į.	EEERLNKLRLESEGSPETLINLRKGYLFMYNLVQFLGFSWIFVN
1	l	ĺ	LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
ſ			SPVLPSLIQLLGRNFILPI1FGTMEEMQNKAVVFFVFYLWSAIE
1 '	77. 0		IPRYSFYMLTCIDMDWKVLTWLRYTLNIPLYPLGCLARAVSVIQ
		1	SIPIFNETGRESETLPYPVKIKVRFSFFLQIYLIMIFLGLYINF
1		<i>.</i>	RHLYKQRRRRYGQKKKKIH
5627	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPATSI
	{		TENVLHFKAQGHGAKGDNVYBFHLEFLDLVKPBPVYKLTQRQVN
1	1	ľ	ITVOKKVSQWWRRLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
1	I		BEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
1	1		LTVRFCILGKRSFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
1	}		SPVLPSLIQLLGRNFILFIIFGTMREMQNKAVVFFVFYLWSAIB
1	1		IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLABAVSVIQ
Ì	I		SIPIPNETGRESETLPYPVKIKVRESEFLQIYLIMIFLGLYINE
	1		RHLYKORRRYGOKKKKIH
5628	75	1455	VAGAMASKCLKAGPSSGSLKSPGGASGGSTRVSAMYSSSPCKLP
	1		SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG
1	j		GGNFGEGILTGNEKETMOSLNDRLAGYLEKVROLEQENASLESR
1			IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI
1	I		DNAKLAADDFRTKYBTEVSLRQLVESDINGLRRILDDLTLCKSD
1	1		LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV
i	l		DINRVLEEMRCQYETLYENNRRDAEDWIDTQSEEINQQVVSSSE
1			QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY
1	1		SSOLACMOCMITNVEAGLAEIRADLERQNQEYQVLLDVRARLEC
i	1		SSQLACACCATTAVEAQUAETRADESROAGETQVILLEVRARLECT
	1		
	7705	0.20	ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV
	I		PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVANAMA
j	1		NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLIQHLRPHWDP
1			QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR
1	[	<b>\</b>	DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN
	L	l	PAIFRLIARQLAKTHAIHAHNGWIPKSNLWLKNGKYPSLIPTGF

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l .	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
'	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid		Codon, /=possible nucleotide deletion,
		sequence	
	sequence		\=possible nucleotide insertion)
l .			ADEDINKRPLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL
l	Į.	1	LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFACVSDV
]		i	DYSLYPDRBLQSQWLRAYLEAYKEFKGFGTBVTEKEVEILFIQV
1			NOFALASHPFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP
i i	1	ì	BYTALKYPB
5630	1194	278	GFWAIAOTCAHHLPPGSPWLVPASPWRLPEMSSFGYRTLTVALF
3630	1199	} 2,0	TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG
Į.	į.		GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM
i		}	KSNVSVYQPPRQVILTLQPTLVAVGKSPTIBCRVPTVBPLDSLT
ļ	Į.		LFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGHRNFSC
1			LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL
l	1	1	LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP
5631	1053	290	SRVDDFVRPEPSRAEPSRSGRRRPARKAATMSVFGKLFGAGGGK
1	1		AGKGGPTPQEAIQRLRDTEEMLSKKQEPLEKKIEQELTAAKKHG
!	j.	1	TKNKRAALQALKRKKRYBKQLAQIDGTLSTIBFQREALBNANTN
1		ļ	TEVLKNMGYAAKAMKAAHDNMDIDKVDBLMQDIADQQELABBIS
l	ł	1	
i			TAISKPVGFGBEFDEDBLMARLEBLEQBELDKNLLEISGPBTVP
L	L	L	LPNVPSIALPSKPAKKKBBEDDDMKELENWAGSM
5632	3	952	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
i			SVRVARGRIGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
1	j	}	FTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY
}		ŀ	GWLLEVEDDDPEDNKPLLEBLDIDLKDIYYKIRCVLMPMPSLGF
1	į.	(	NROVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWIITIWIFGS
ł		1	LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFB
			VVSTLIKLFGVFWAAYSAASLLVGREFKTKKPLLIYPIFLLYIY
ł	1	Į.	FLSLYTGV
	0		OGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN
5633	771	460	
1	i	1	CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL
<b>{</b>			LLLLLSGHRPWGSSMV
5634	1446	855	PRATGRIRSRAAASRPRAGAGASGAEPRSGRERSRLSGRRAPAM
}	ţ		ARNTLSSRFRRVDIDEFDENKFVDEQBEAAAAAAEPGPDPSEVD
ł	}	Į.	GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK
1	(	Į.	SSBIBOAVOSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK
1	1		ALAVGGLGSIIRVLTARKTV
5635	3	• 943	DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL
	1	1	RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL
1	i	i	GVRRAVLOLPGLTQVRWSRYSPEPKDPLIDKEYYRKPVEELTEE
1	1		RKYVRELKKTOLIKAAPAGKTSSVFEDPVISKFINMMIGGNKV
ľ			
}	1	}	LARSIMIQTLEAVKRKQFEKYHAASABBQATIERNPYTIFHQAL
ł	1	1	KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRPLAMKWMITECRD
	l		KKHORTLMPEKLSHKLLEAFHNOGPVIKRKHOLHKMAKANRALA
			HYRWW
5636	2253	1143	LEDTICQHPPAEKKLYLYHRKLREVKRNGIPRLPKDVPMDTHQG
1			LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI
I	1		ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK
	1		
}	}	}	
			YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGPD
			ALLHEIQEIRETQARLEESYETLKEHYORDYSLIMOTLQEERYR
			ALLHBIQEIRBTQARLBESYBTLKEHYQRDYSLIMQTLQEERYR CERLBEQLNDLTBLHQNEILNLKQBLASMBEKIAYQSYBRARDI
			ALLHBIQEIRBTQARLBESYBTLKEHYQRDYSLIMQTLQEERYR CERLBEQLNDLTBLHQNBILNLKQBLASMBBKIAYQSYBRARDI QBALBACQTRISKMBLQQQQQQVVQLBGLKNATARNLLGKLINI
			ALLHBIQEIRBTQARLBESYBTLKEHYQRDYSLIMQTLQEERYR CERLBEQLNDLTBLHQNEILNLKQBLASMBEKIAYQSYBRARDI
			ALLHBIQEIRBTQARLBESYBTLKEHYQRDYSLIMQTLQEERYR CERLBEQLNDLTBLHQNBILNLKQBLASMBBKIAYQSYBRARDI QBALBACQTRISKMBLQQQQQQVVQLBGLKNATARNLLGKLINI
5637	948	2532	ALLHBIQEIRBTQARLBESYBTLKEHYQRDYSLIMQTLQEERYR CERLBEQLNDLTBLHQNBILINLKQBLASMBEKIAYQSYBRARDI QBALBACQTRISKMBLQQQQQQVVQLBGLBNATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK
5637	948	2532	ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFUSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR
5637	948	2532	ALLHEIQEIRETQARLEESYETLKEHYQRDYSLIMQTLQEERYR CERLEBQLNDLTBLHQNEILINLKQELASMBEKTAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVPUSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR MSFCGARANAKMANYNGGTSAAAAGHHHHHHHLPHLPPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAMLNFG
5637	948	2532	ALLHEIQEIRETQARLEESPETLKEHYQRDYSLIMQTLQEERYR CERLEEQLINDLTELHQNEILINLKQELASMBEKIAYQSYERARDI QEALEACQTRISKMELQQQQQQVVQLEGLEMATARNLLGKLINI LLAVMAVLLVFUSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR MSFCGARANAKMMANYNGGTSAAAAGHHHHHHHHLPHLPPPPHLH HHHHPQHHLHFGSAAAVHPVQQHTSSAAAAAAAAAAAMLNPG QQQYYFPSPAPGQAPGPAAAAPAQVQAAAATVKAHHHQHSHHP
5637	948	2532	ALLHEIQEIRETQARLEESPETLKEHYQRDYSLIMQTLQEERYR CERLEEQLINDLTELHQNEILINLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLUFUSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHLPHLPPPPHLH HHHHPQHHLHPGSAAAVHFVQQHTSSAAAAAAAAAAAANLNPG QQQYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL
5637	948	2532	ALLIBIQEIRBTQARLEESYBTLKEHYQRDYSLIMQTLQEERYR CERLBEQLNDLTBLHQNEILNLKQBLASMBEKIAYQSYBRARDI QBALBACQTRISKMBLQQQQQQVVQLEGLBNATARNLLGKLINI ILAVMAVILUFYSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHTLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAMLNPG QQQYYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCPFKHDNVLSALDILQPPHIDYFEBIYVVTE
5637	948	2532	ALLIBIQEIRBTQARLEESPETLKEHYQRDYSLIMQTLQEERYR CERLBEQLNDLTRLHQNEILNLKQELASMEEKIAYQSYERARDI QBALBACQTRISKMBLQQQQQQVVQLEGLBNATARNLLGKLINI LLAVMAVLLVFYSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHTLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAMLNPG QQQYYFPSPAPGQAPGPAAAAPAQVQDAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCPFKHDNVLSALDILQPPHIDYFEBIYVVTB LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD
5637	948	2532	ALLHEIQEIRETQARLEESPETLKEHYQRDYSLIMQTLQEERYR CERLEBQLNDLTBLHQNEILINLKQBLASMBEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVPUSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR MSFCSARANAKMMANYNGGTSAAAAGHHHHHHHHLPHLPPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAMLNPG QQQYYFPSPAFGQAPGPABAAPAQVQAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCPPKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVJPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPCNLLVNSNCVLKICDPGLARVEELDESRHMTQEVVTQYYRA
5637	948	2532	ALLIBIQEIRBTQARLEESPETLKEHYQRDYSLIMQTLQEERYR CERLBEQLNDLTRLHQNEILNLKQELASMEEKIAYQSYERARDI QBALBACQTRISKMBLQQQQQQVVQLEGLBNATARNLLGKLINI LLAVMAVLLVFYSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHTLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAMLNPG QQQYYFPSPAPGQAPGPAAAAPAQVQDAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCPFKHDNVLSALDILQPPHIDYFEBIYVVTB LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD
5637	948	2532	ALLHEIQEIRETQARLEESPETLKEHYQRDYSLIMQTLQEERYR CERLEBQLNDLTBLHQNEILINLKQBLASMBEKIAYQSYERARDI QEALEACQTRISKMELQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVPUSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR MSFCSARANAKMMANYNGGTSAAAAGHHHHHHHHLPHLPPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAMLNPG QQQYYFPSPAFGQAPGPABAAPAQVQAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVFRELKMLCPPKHDNVLSALDILQPPHIDYFEBIYVVTE LMQSDLHKIIVJPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPCNLLVNSNCVLKICDPGLARVEELDESRHMTQEVVTQYYRA

Deginning   location	SBO	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   location   corresponding   to first   maino acid   residue of amino acid   residue of amino acid   residue of amino acid   sequence   P-Pcoline, O-Giutamine, R-Anglaine,   P-Pcoline, O-Giutamine, R-Anglaine,   P-Pcoline, O-Giutamine, R-Anglaine,   P-Pcoline,   P-Pcoline, O-Giutamine, R-Anglaine,   P-Pcoline,   P-Pcoline, O-Giutamine, R-Anglaine,   P-Pcoline,				(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
Cocation   Contesponding   Cofirst   Samina acid   Antina acid   Antina acid   Antina acid   Antina acid   Antina acid   Antina acid   Sequence   Section   Tendencine   New York   New York   Sequence   Section   Tendencine   New York   New York   Sequence   Section   Tendencine   New York   New York   Sequence   Section   Tendencine   New York   Sequence   Section   Tendencine   New York   Sequence   Section   New York   Sequence   Section   New York   Sequence   Section   New York   Sequence   Section   New York   Sequence   Seque				Glutamic Acid. F=Phenylalanine, G=Glycine,
Cottret	2.0.			
to first amino acid residue of amino acid residue of amino acid sequence  #TEXPUTORINE, VETYCOSINE, X-EURINOOM, *=SEQ Codon, /-possible nucleotide deletion, \[ -possible nucleo				
amino acid residue of amino acid sequence sequence codon, /-possible nucleotide deletion,				
residue of amino acid sequence				
amino acid sequence  Codon, /-possible nucleotide deletion, -possible nucleotide insertion)  THEAMHALERHUFPFYRTISANDALAHFILDERGRAPHTSCHO COCSTSTGAVTTOBERFYTNSFEDDIEGERLSSWORGENET THEAMHALERHUFPFYRTISANDALAHFILDERGRAPHTSCHO LEGOGNINGVILCHPGSAARRSFISSTVAGESBEPGSFUNDE SERMSELDGERGERSKORGENETERSSWORGENETER THEAMHALERSHUPPTAREST STANDALAHFILDERGRAPHTSCHON LEGOGNINGSTANDALAHFILDERGRAPHTSCHOOL LYSSGDUKKLITHES THEAMHALERSHUPPTARESTHALTCHOOL CONTROL LYSSGDUKKLITHES ROWNERSCHALTSHOOL CANADAL THE SERVER CONTROL LYSSGDUKKLITHES GOOTTFTCHTROUMSISLADTHLFYSGACDASAKUDVERS CREPTORISESTHALTCH YMMENTOSICHATCHOPACHWARLARD WITSENDILICUTTSVSTSKSGERIALAGTUPPACHWARLARD GUAMHANISCLGYTDERMANTASTBARCHLORSACDAKLITHES THAVHALFLESSWOMTCAYARSSON VACCGLUBACTUPPACHWARLARD GUAMHANISCLGYTDERMANTASTBARCHLORSACDAKLITHES THAVHALFLESSWOMTCAYARSSON VACCGLUBACTUPPACHWARLARD GOOTTFTCHTTOUNSISLADDTELLVSGACDASAKUDVERS CREPTORISESTHALTCH CORPORATATISCORGACACHUMANTASTBARCH CONTROL				
Sequence			1	
THEAUHILERHUVEDPYRRISAKOALAHEYLDSGRERHTHYONG CCESTGGRYTTSDEPTYRREPOTRERISAYONGVERT HIS LLOQUKUNRUPLCTBOGSAARKSPISSTVAQGSEMBESEPLVIRK TURKURITERISAKTIANHIGTUSALLVSAGODGKLI TURS RIQMETERITLERGIHARI TVAHHIGTUSALLVSAGODGKLI TURS RIQMETERITLERGIHARI TVAHHIGTUSALLVSAGODGKLI TURS TYNKURATERILERGIHARI TVAHHIGTUSALLVSAGODGKLI TURS GOOTTETICHTGOVARSISLLAPOTREPUSGACONSAKUMOVRAS CREPTOHISSONING ICEP PRINCAPATSOSDATICALDILARDOR GOOTTETICHTGOVARSISLLAPOTREPUSGACONSAKUMOVRAS CREPTOHISSONING ICEP PRINCAPATSOSDATICALDILARDOR GVIA-MENDRIVICATURE PRINCAPATSOSDATICALDILARDOR GVIA-MENDRIVICATURE PRINCAPATSOSDATICALDILARDOR GVIA-MENDRIVICATURE PRINCAPATSOSDATICALDILARDOR GVIA-MENDRIVICATURE PRINCAPATSOSDATICALDICALDILARDOR GVIA-MENDRIVICATURE PRINCAPATSOSDATICALDICALDILARDOR GOOTTETICHTGOVARSISLAPOTREPUSGACONALITING ECHVEVERRILARITY SILCEPERIODIO TUVISGOTICALDICAL GOOTTETICHTGOVARIALITA TURBUTALITA ECHVEVERRILARITY SILCEPERIODIO TUVISGOTICALDICAL GOOTTETICHTGOVARIALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA ECHVEVERRILARITY SILCEPERIODIO TURBUTALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA TURBUTALITA GOOTTETICHTGOVARIALITA TURBUTALITA TURBUTALITA GOOTTETICATURA GOOTTETICHTGOVARIALITA TURBUTALITA TURBUTALITA TURBUTALITA TURBUTALITA LATERICATICA TURBUTALITA TURBUTATI TURBUTATI TURBUTATI TURBUTATI TURBUTATI TURBUTATI TURBUTA TURBUTATI TURBUTATI TURBUTATI TURBUTATI TURBUTATI TURBUTATI TURBUTA TURBUTA TURBUTA TURBUTATI TURBUTA TURBUTA TURBUTA TURBUTA TU			sequence	
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125. 1155 DREMSELJOLAGEAROLENGTERDAKACADATLSGITNNIDEV RIQMETRETLEGHAKIYAMHMOTTSELLUSASJOGKLIJUS TITKVHAI PLESSWOMTGATASSGNIVAGGGLONICSIYNLKT EGNVKVSRELAGHTSYLSCCRFLIDNOGVTSSGNITTCAMDLE GQQTTFTFGHTSDWASILALAFDTRIPVSGCDASAKMDVRES CRGTTFTGHESDINALCEFPHKORAFATGSDDATGRIPOLKRADGE WITSEDNILGGTISVSTSKESKILLAGHTOKWODALAND GVLAGHDNRVSCLGVTDDGHAVATGSDDATGRIPOLKRADGE WITSEDNILGGTISVSTSKESKILLAGHTOKWODALAND GVLAGHDNRVSCLGVTDDGHAVATGSDDATGRIPOLKKO GVAGHLNRVSCLGVTDDGHAVATGSNDSTLATUN GVAGHLNRVSCLGVTDDGHAVATGSNDSTLATUN GVAGHLNRVSCLGVTDDGHAVATGSNDSTLATUN GVAGHLNRVSCLGVTDDGHAVATGSNDSTLATUN GVAGHLNRVSCLGVTDDGHAVATGSNDSTLATUN GVAGHLNRVSCLGVTDDGHAVATGSNDSTLATUN GVAGHLNRVSCLGVTDDGHAVATGSNDSTLATUN GVAGHLNRVSCLGVTDDGHAVATGSNDSTLATUN GVAGPLKEIT PERFETT TAVE KYTQSPWAG INSPENDIL LFFPBGKABLPDYRSFRRVATPFGGFERASRAVKKVEVDFELL LFFPBGKABLPDYRSFRRVATPFGGFERASRAVKKVEVDFELL LFFPBGKABLPDYRSFRRVATPFGGFERASRAVKKVEVDFELL LFFPBGKABLPDYRSFRRVATPFGGFERASRAVKKVEVDFELL LFFPBGKABLPDYRSFRRVATPFGGFERASRAVKKVEVDFELL LFFPBGKABLPDYRSFRRVATDFGGFERASRAVKKVEVDFELL LFFPBGKABLPDYRSFRRVATDFGGFERASRAVKKVEVDFELL LFFPBGKABLPDYRSFRRVATDFGGFERASRAVKKVEVDFELL LFFPBGKABLPDYRSFRRVATBATTGVATTGVATTGVATTGVATTGVATTGVATTGVA		}		
RIGMETRETLEGHLAKITYAMIMGTDERLLIVASDORGLIITUNG TITMIYHAT PLESSNAWITCAYAPSGOTYYACGGIDNICS ITMIKTHE ECNYRYGRELAGHTGYLS CCRPLIDINQI VTSSGITTCALWD IE GOQTTTFTGHTGDVMSLSLAPDTELFVSGACDASARIMWYRES CROTTEGHESDINAL CEPPHORABRAGSDDATCRLEPLARDGE WITSHDNII GGITSVSFSKSGELLLAGYDDPHCWWDALKARR GYLAGHDRWGVSLGSVIDGMAVATGSIDSFLKING  5640 280 1092 OGENKYTHLSHINKQARLPKMRQRKDKYTFENFQYQSRAQ MISLAMQNGKVDGSNLEGGSOQAPLITPTFTTPDRSPPNPDRIA GYSGPLKEIPPEKNTTAVPKYYQSPHEQALSHDPELBRALVE LYPPSKARLD WITSHNAYPKYYQSPHEQALSHDPELBRALVE LYPPSKARLD WITSHNAYPKYYQSPHEQALSHDPELBRALVE LYPPSKARLD WITSHNAYPKYYQSPHEQALSHDPELBRALVE LYPPSKARLD WITSHNAYPKYYQSPHEQALSHDPELBRALVE LYPPSKARLD WITSHNAYPKYYQSPHEQALSHDPELBRALVE LYPPSKARLD WITSHNAYPKYYQSPHEQALSHDPELBRALVE LYPPSKARLD WITSHNAYPKYYQSPHEQALSHDRELBRALVE LYPPSKARLD WITSHNAYPKYYGSPHEQALSHDRELBRALVE LYPPSKARLD WITSHNAYPKYYGSPHEQALSHDRELBRALVE LYPPSKARLD WITSHNAYPKYYGSPHEQALSHDRELBRALVE LYPPSKARLD WITSHNAYPKYYGSPHEQALSHDRELBRALVE S642 199 1247 ITPERNDPLAYFLYLASVIMGILVLICVCSKTHELKGLARGGA MGBSYLLAHUTHT IVLHLUCVGSKTHELKGLARGGS WIRSPHHLOWNING ICAMNISYFLIYULTITASAATVALVSTI LYPHCYOCOBLELSHAYLLIPPTHINFTIVLHLUCOMYTE TWENGYOCOBLELSHAYLLIPPTHINFTIVLHLUCOMYTE LYGHULVWBSDLYQGTYYLDDLGHLHWDTVPLLQYLEFTFRITVY LYGHULVWBSDLYQGTYYLDDLGHLHWDTVPLLQYLEFTFRITVY LYGHULVWBSDLYQGTYYLDDLGHLHWDTVPLLQYLEFTFRITVY LYGHULVWBSDLYQGTYYLDDLGHLHWDTVPLLQYLEFTFRITVY LYGHULVWBSDLYQGTYYLDGAARGPROWERSARCHGSTRINDP RYQFDWCATTGOPLASGKSFMSBMIGTGOPYYBLGYQTIRV RYGFRYLDPLAGYLLFYLDFYLDYLLAGARGAGCHERKRGB TRAGSGYQUTTAGAARGPROWINGERGAGAATAKKIAAR YKRRGTYLLABDQLAQMSKQLDMFKINLBEFASKHAQETRINDP RYQFDWCATTGOPLASGKSFMSBMIGTGOPYYBLGYQTIRV RYGFRYDLAYGCYLLAGARGAGCHERKRGBTRINDP TOLYSQETTABERARALD TOLYSQETTABERARALD  5644 83 1138 PREMESWYQLTAGSGORGHOTHERGGGAAACHARMINITY VALBOKDMQQKRQOPREMPLKEPPQITRKIQGS ELIRUYIAN LABRIRGGITTIBELHQOLAAGA GLGJASATAGTASSTURYTYTTSABLTAGSRATAGTSTOLLEAR RYGFRYOVETLARGAPTKINLSPTTAGSRATAGREPTATIGSKATOGRELIA RYYDTNOVETLARGAPTKINLSPTAGRAGAGERGPTAGSSGORGHOTHERINGSKAG GLGJASATAGTASSTURGFROWTHAGAGCHERMINITHINGSKAGA GLGJASATAGTASSTURGFROWGTHAGAGFROWTHAGAGC		136	1155	
TTMANDA PLESSWAMTCAVAPSCNYVACCGLDNICSIYALTE  REMYRYSRELAGHTGYIS.CCRPLDDNQIVTSGDTTCALMOTE  GQQTTTPTGHTGDVMSLSLAPDTELFVSGACDASAKLMOVREG  CRCTPTGHESDINALCPPNCMRFAGSDDATCHEPLRAPORE  MYSSIDNICGTISVSFSKSGELLLAGYDDOPHCNWDDALKADR  GVLAGHDMRVSCLSVTDCMAVANGSNDSFLEIUM  S640 280 1092 QGNKKYMLSHYMMKQRKQQATAIMKZYGGDDVGHDLCKKV  IPDD.TM.EELSHLSHKGRALFRMQQRATAIMKZYGGDVGHDLCKKV  IPDD.TM.EELSHLSHKGRALFRMQQRATAIMKZYGGDVGHDLCKKV  IPDD.TM.EELSHLSHKGRALFRMQQRATAIMKZYGGDVGHDLCKKV  IPDD.TM.EELSHLSHKGRALFRMQRRSKYTFENFQYQSRAQ  MISSIAMQMGKVDGSNLEGGSQQABLTPPHYTEDPRSPPNEDIA  GYSGPIKERIPPERKNITAPFKGGFSKASRWKKKVDFELL  LTDPRRMSFVAPELSGRSFNRTPKGWISENIPTYTTEPTDDT  VPESEDL  5641 27 332 CRINCHGDVKLLSNQMDKLFAFHLDFLGSIQKLIQ  LTDPRRMSFVAPELSGRSFNRTPKGWISENIPTYTTEPTDDT  VPESEDL  5642 199 1247 ITDCRMBFDLVFLGFYLASVLMGLULICVCSKYHSLKGLARGGA  IFSCILPBCLQRAMIGLLHYLFFTRNHTFIVIHLVLQGMVYTE  KARSLLFHLYVSEDISWMPFKNKCSTCDLKRARSKICSVCSW  WHRPDHCVWVNNCIGAMMIRYFLIYVLTITASAATVATVSTT  LUGHLVWRGDVJOSTTYTDLGHLHAUDVLLQTAFLFFPETVV  LGFUVVLSPLLGGYLLFULJAANNQTTNEWYGCDWAWCDGCC  VMPPSAEPQUHRNIHSHGLRSNLGEIFLPAPPCHERKKQB  TRAGGGACATIGUDELAGKGKGFMSEMICSVGFYWLGDVGIKK  ALGTGFGIIPVGGTYLLGSVLARDLGHTFLPAPPCHERKKGB  RVGFQDACATIGUDELAGKGKGFMSEMICSVGFYWLGVOITKV  LALKHRNGGLTTLGELHQQVLKGGKRADOWSODDLTRATKKL  ALGTGFGIIPVGGTYLLGSVLARDLDAPCGBAIKNLGAR  RVGFQDACATIGUDELAGKGKGFMSEMICQSIERKRGYTELTY  TRIVSGCTABEDQATKLRGCKGFMSEMICQSIERKRGYTELTY  KKVSPVHLKILLTSDEAMKFPVRVAGEPPRINKIQSIERLRVLAN  TOLYSQCTABERBALD  TOLYSQCTABERBALD  FRANGSWQUTENTSHCOSTILSVIGWHLAPFTAGLSISTTAGG  GLGIASATAGTASSIVENTYTTRSAELTAGRLTATSTQLEARR  LIEUTPRMLSFALDDDATKHANDVIGSFILBRINGFRILVDING  RVVPTNVVETLRTRGAPTRILVKVARNLGKARSGVUVLDVW  VQDSUDLIKKGKSSSAELLRQMQELEBRIMELTHHIGSLKAG  GLGIASATAGTASSIVENTTYTRABELTAGRLTATSTQLEARR  ILBUTTPRUS-GFALDFARMLSPTTPOEDATKHANDVIGGSIERDFARMSRICHIAVSIS  TLCIQNSILGHSSWGDARTMELVQISQRIRARRGRGRFALDGLAGRAGGAG  AGYGFSPHLLFTMLLSCLFPANVTKARAPPPINGSLTATTDQLEARR  AGYGFCRYTTILIRASIPATRASFLSSFIKMFPELEYILG  LSLLKKHHVUNSVSAICHERGREDVTCPINGASSGQUVVLDVW  VQDSUDLIKGEKSSSAELLRQMARMELVQISQRIRARRGRUFLIAVSLITAD  AGRAPACRY	7072	143,	1133	
BCRVRYSRILAGITGYLSCRPLDDMQIVTSGUTTCAMDIE   GQQTTTFTGHESDINALCPPRICHDMQIVTSGUTTCAMDIE   GQQTTTFTGHESDINALCPPRICHPUSACADASKLMDVREG   CRQTTFTGHESDINALCPPRICHPUSACADASKLMDVREG   CRQTTFTGHESDINALCPPRICHPUSACAGASKLMDVREG   GVIAGHDRIVGSGUSACHGANGUSCHLAGYDDPHCDWRDALKARR   GVIAGHDRIVGSGUSACHGANGUSCHLAGYDDPHCDWRDALKARR   GVIAGHDRIVGSGUSACHGANGUSCHLAGGSQOALTPRITPPRSPPRIPDIS   GYSGPLKEIPPEKRITTAVPKYYGSPHEQALSINDPELIBALVE   LFERBSKARLEDTRISTRIVATPKYGSPHEQALSINDPELIBALVE   LFERBSKARLEDTRISTRIVATPKYGSPHEQALSINDPELIBALVE   LFERBSKARLEDTRISTRIVATPKYGSPHEQALSINDPELIBALVE   LFERBSKARLEDTRISTRIVATPKYGSPHEQALSINDPELIBALVE   LFERBSKARLEDTRISTRIVATPKYGSPHEQALSINDPELIBALVE   LFERBSKARLEDTRISTRIVATPKYGSPHEQALSINDPELIBALVE   LFERBSKARLEDTRISTRIVATPKYGSPHEQALSINDPELIBALVE   LFERBSKALLEDTRISTRIVATPKYGSTESILISTICSA   MCSSPYLLSINUTG   CRINCGEDVKLLSNQMDKLFAFHLFTFHELLEDLGSIQKLQ   EILLSDINSSLIVLENNFLFKVKSKQFTHLLIKKKJESIQKLQ   RILSDINSTLIVLENNFLFKVKSKQFTHLLIKKKJESIGKLGU   RGSSPYLLSINUTG   STEVERTYCORELISLISLLEPTLLGVULFFFFTLICGTNRGII   KARKLLFLHYZEDDEWMPEKNVCSTCDLRKRARSKICSUCSM   VHRPDHHCVWONCICGAMIRYPLIVALAGANYTE   LGSUVVLSPILGSYLLFVLIJAATNQTTNEWNCORMACQREG   LGSUVVLSPILGSYLLFVLIJAATNQTTNEWNCORMACQREG   LGSUVVLSPILGSYLLFVLIJAATNQTTNEWNCORMACQREG   LGSUVVLSPILGSYLLFVLIJAATNQTTNEWNCORMACQREG   LGSUVVLSPILGSYLLFVLIJAATNQTTNEWNCORMACQREG   LGSUVVLSPILGSYLLFVLIJAATNQTTNEWNCORMACQREG   SGOVEDVETRIGSGSAAAGGPVWHERGSVGGAATAKKKARS   VKREGTVLAEQQILAGKSCFMSBMIRGVOTY   KRINGTVLAEQQILAGKSCFMSBMIRGVOTY   RIKASLKANGSTSTAAGATASTACKKKARS   RKVPQDMCATIGOPLASKGFMSBMIRGVOTYPTLICAGNIVALDAL   TOLYSQEITAEEAREALP   LALKHRINGGLTTLEBLHQQVLLKGRKPAQDVOQDLIRAIKKI   ALKTGFGIIPVGGTYLLGVABALNDLQAFGBAHYMLPAL   TOLYSQEITAEEAREALP   SGOVEDVETRIGSGSTGALTURGVGSIBLISITAAG   GLGLASATAGTASSIVENTYTRABELTASRLTATSTOQLEAR   KKVSPVHLKILLISDBAWKFVRVAGELPERAVSICSITENING   LGUTRAVLSFALDDRINGSFMILGREGUSALDLAGRANGELPILAVSIC   LGUTRAVLSFALDDRINGSFMILGREGUSALDLAGRANGELPILAVSIC   LGUTRAVLSFALDDRINGSFMILGRAGASGUVVLIDUW   VQUSLDLIKKGRKSSAELLRONAQELFENINGELPILAVSIC   SGOVED   SGOVEDLIKTLSPYTDPGGSGA		]	1	
GQQTTTPTGHTGDVMSLSLAPDTRLFVSGACDASAKIMVDVRSS CRQTPTGHTSDVMSLSLAPDTRLFVSGACDASAKIMVDVRSS CRQTPTGHTSDVMSLCYPPHONAPATGSDDATCRLFDLRADOR MTYSEDNICTTSVSSKSGRLLLAGGYDDDMAVATGSMDSFLKIM GVLAGHDMRVSCLGVTDDGMAVATGSMDSFLKIMD GVGGNKKTHGSHTMMKDGRQATAINKGDDVGGHDLGKKV IPDD_MLERLSHLSHNGGARLFKMGDRVSGDVGGHDLGKKV IPDD_MLERLSHLSHNGGARLFKMGDRVSGDVGGHDLGKKV IPDD_MLERLSHLSHNGGARLFKMGDRVSGDVGGHDLGKKV IPDD_MLERLSHLSHNGGARLFKMGDRVSGDVGGHDLGKKV IPDS_MLERLSHLSHNGGARLFKMGDRVSGDVGGHDLGKKV IPDS_MLERLSHLSHNGGARLFKMGDRVSDVTFERPTDVTS LTDPRFMSFVMPLGGRFSJNNLFGGTSKASRUKVEDPELL LTDPRFMSFVMPLGGRFSJNNLFGGTSKASRUKVEDPELL LTDPRFMSFVMPLGGRFSJNNLFFGGTSKASRUKVEDPELL LTDPRFMSFVMPLGGRFSJNNLFFGGTSKASRUKVEDPELL LTDPRFMSFVMPLGGRFSJNNLFFGGTSKASRUKVEDPELL LTDPRFMSFVMPLGGFVKKSKGFTHLIARKFYLSTITVSA NGBSPVLSMITTG  5642  199  1247  1322  CRHNCGDVKLLSNQMDKLFAFHLDFTFGLLHPLDGSLQKLI FSCLIPSCLJRAMIGLLHYLFYRRHTFIVLHLVLLGMYTF TWEVFGYCOKLELSHYLLLPYLLLGVNLFFFTLTOGTNIGLI KARHLFHHYSEDISVMFFKNNCSTCDLGKDARSKHCSVCNN WHRPHHCVWVNNCIGAMMIRYFLITVLITAGASATVALVSTT LUGHLVWMSDJVGTTYTIDDLGHLHMDVTLQTYLFLTFPFILV LGFUVVLSPLLGGYLLFVUTILAANOTTNEWYGCDAMCGRCF VAMPPSAEPQWHRITHSLRSHLGSHJGTLGYTLFYLTTGFRHVV LGFUVVLSPLLGGYLLFVUTILAANOTTNEWYGCDAMCGRCF VAMPPSAEPQWHRITHSLRSHLGSHJGTLGYTLFYLTLGTFRHVRCDAMCGRCF VAMPPSAEPQWHRITHSLRSHLGSHJGTLGYTLFYLTLGTLHLGYLLKGGLAWLDLAGAGARAKKKLAEA YKRGTVLAEDQLAGMSKQLDMFTINLBEFASKHKDSITRMSF RVGFQDMCATTGGDPLAGKGFWSHGTGGTGFTYBLGVGTUTL LALKHRINGGLTTLEELHQQVLLGGGKFRADDVSDDLTRATKKL ALGTGFGIIPVGGTYLLQSVPARLIMBGTRGVTY RIFAGLKWSTERRARDLP FRIMGSWQLTSVGYQOMHECMTVAGQFQEKKRFTEEVIEY KXVSPVHLKTLLTSDEAMKRFVRVAGLFRERDALTSLLSLITAG GLGLASATAGTASSIVENTTTRSAELTAGSRLTATSTQLEARIK RVFTRGCVIANVUSSTSILSVIGWHLAPFTAGLSISITAG GLGLASATAGTASSIVENTTTRSAELTAGSRLTATSTQLEARIK RVFTRGCVIANVUSSTSILSVIGWHLAPFTAGRLTATHGRKATVGRFLIA RVVPTNVVETLGTRGAPTTIVKARNLCKATSGVIVVLDUVM VQDSLDLHKKGKSSASLLLRQNAQELEENLINGLTHLUGLKGG SAGAS 5645 537 799 VGSVRDLKRLSPTDFFGDSGRRDVTRGLYGATGSRIFKTEPLIVSSITTAG AGRAPCRVTLTILLGRSIPATRASFLSSFIKMFPBELEFILG LSLLKKHHVHUSVVSAICHEQKSGGRBNTSFTCTPELEPRLQTH		1		
CROTPTGHESDINALCFFPREAGAGEAGSDATCRLEPLEADAGE MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCWWDALKADR GUAGHDRINGSCLGVTDDGHAWATGSWDSFLKIWN 5640  280  1092  QGCNKCTMISHNTWMKQRKQQATAIMKZWEGNDVDGKDLKAGA NHSIAMQNGKVDGSNLEGGSQOAPLTPPNTEDPRSPPNPEND GYSGPLIKEIPPEKRNTTAVPKYYQSPWGAISNDEFLEBALYP LYPEBGKARLEDYBSFRWATPFGGFBKASHWKFKVPDFBLL LTDPRFMSFVYPLSGRSFWRTPKGWISENIPIVITTEPTDD VPSSBL  5641  27  332  CHINCNGDVKLLSNQMDKLFAFHLPTFHGLIHPLDGSIQKLIQ EIILSDNSSIDVLENNFLFKVKSKGFIHLIAKKFY1SITIVSA NGSFYLSHIVTG NGSFYLSHIVTG  FESCLORAMIGLIHVILFTHRHTFIVIHLIALGANGGA NGSFYLSHIVTGFFFTHAGAMAGALHYLFFFTHITGTNPGII KARELLFHIVYEFPEWFFKNVRCSTCOLGRABSKHCSVCRW VHEPDHHCWWNNCLGAWNTYFLITVUTITAGSATAVATUSTI LVFILVWSDLYGSYLLDGVALFATROFTHAWATGTSCHRRKKGR VHEPDHHCWWNNCLGAWNTYFLITVUTITAGSATAVATUSTI LVFILVWSDLYGSYLLDGVALFARBSKHCSVCRW VHEPDHHCWWNNCLGAWNTYFLITVUTITAGSATAVATUSTI LVFILVWSDLYGSYLLDGVALFARBSKHCSVCRW VHEPDHHCWWNNCLGAWNTYFLITVUTITAGSATAVATUSTI LVFILVWSDLYGSYLLDGVALFARBSKHCSVCRW VARPPSAEPQVHRI HISHGLRBLUEFILPAPPCHRRKGG  5643  1  847  PSGGVRUVETRGGSRAARGPRVVMERREVGAGAIAKKGARG ALKHHRIGGITTLEEHQQVILKERASKHCDBVRND RVQFQDMCATIGVDPLASGKGFMSEMLEVGDPYYBLGVOILBK LALKHHRIGGITTLEEHQQVILKERASHKUGDBRIRND RVQFQDMCATIGVDPLASGKGFMSEMLEVGDPYYBLGVOILBK LALKHHRIGGITTLEEHQQVILKERASHKUGDBRIRND FRWGSWQLITSIGVOONPEGWTVAGQFGEKKRFTEEVIEYF KKVSPVHLKILLTSDRAWKRPVEVAELPREAGADALYKALKINDI TOLYSQEITABEARBALP  5644  83  1138  PRIMGSWQCKGOPREWFLKEFPQIRWKTGSSIBLISTTAAG GLGIASATAGTASSIVENTITSABLTASRLTATSTOQLEALB LIEDITPRWLSFALDPDEATRHLANDUTTLRRSKATVGRPLA RYVPINVVETLATRGAPTRIVRVARANLGKATSGALVJUCALAL RYVPINVVETLATRGAPTRIVRVARANLGKATSGALVJUCALAL RYVPINVVETLATRGAPTRIVRVARANLGKATSGALVJUCAL RYVPINVVETLATRGAPTRIVRVARANLGKATSGALVJUCALAL RYVPINVVETLATRGAPTRIVRVARANLGKATSGALVJUCALAL RYVPINVVETLATRGAPTRIVRVARANLGKATSGALVJUCALAL RYVPINVVETLATRGAPTRIVRVARANLGKATSGALVJUCALAL RYVPINVVETLATRGSGAPARMELYQISGRIBARGLPRILAVBO VODSLDLIKGEKSESBALLAGNAGERIMHELTHINGSLKAG ALGGGRQ  5645  3745  3328  AEQUGSSPHLLFMILASGCLPPANVTKAAPSPLUCALSJUTALTA		į.		
MTYSHONIICGITSVSPSKSGRILLGAGYDDEFNAWMALKADR  GVLAGHDNRVSCLGVTDDGMAVATGSMDSFLKIWN  5640  280  1092  QCRNKTMISHNYMKQRKQQATAIMKZVHONDVDGMDLGKKV IPRDIMLERLSRLSNRGARIFKMRQRESDKYTFENRGYGSRAG MISLAMQNCKVOGSINLEGGGOOAPLTPPNTTDPRSSPPNPINTA GYSGPLKEIPPEKPNTTAVPKYYQSPWEQAISNDPELLBALYF LYRPBGKARLDDYRSYMRVALTPFGGFEKASMWKFKVPDFELL LITDPRRMSSVPNLSGRRSYMTPKGWISENIPIVITEPTDDT VPRSEDL  5641  27  332  CRHNCNGDVKLLSNQMDKLFAFHLPTFHGLLHPLDGSIQKLIQ EILLSDNSSILVLENNPLFKVKSKQFIHLIAKKFYISITIVSA NGBSPVLSMIVTG  SGSPVLSMIVTG  1PPCI PRCLQRAMHGLLHYLLGVALFFTLITGTMGFIL KABKLLFHUYEFDEVMFPKNVRSCTGOLRRPARSKRESVCIW VHRPDHHCWWWNCIGAWNTRYFLIYVLTLYASAATVALVSTI LUHLVVMSDLYQETYIDDLGHLHWMDTVFLIQVLLFTPRIVF LUFVUVLSFLLGGVLLEVLYLANTAQTINEFYLGOMAWCQRCP VAMPPSAEPQWERNIHSHGLIRANGIFILAPPCHRKRQB  5643  1 847  PSGGVEDVETROGGSRAARGFRVMLWERGVGAGALAKKLARF RVQFQDMCATIGVDPLASKGFWSEMLGVGGDYYBLGVQIIEK LAKKHRNGGLTTLSELLIQVLLKGRGFAQDVSODDLTRATKKI ALGTGFGIIPVGGTYLLQSVPAELINDHTUVLQLARENGVTV BIKASLKWBTERRAQVLEHLIKEGLANLDLQARGARHYWLFAI ALGTGFGIIPVGGTYLLQSVPAELINDHTUVLQLARENGVTV BIKASLKWBTERRAQVLEHLIKEGLANLDLQARGARHYWLFAI  5644  83  1136  PREMGSWYQLITSVGVOONIBCHTVAGQOGSKKRFTEEVIETK KKVSPVHLKYLLTSDEAWKRFVRVAELPREEADALYEALKNIJT VVAIRBOKDMQQKRGQFREWFLKRFPGIRWKTGESIERLEVIAN IEKVHRGCUTANVVSGSTGILSVIGYMLAPFTAGLSISTTAAG GLGASATAGIASSIVENTYTRSAELTSAELTAGHTATSDLJEALKI TRYVINVVETERTRABTITTVRVARANLGKATSGAULVIAN RYVINVVETERTRABTITTVRVARANLGKATSGAULVIAN RYVINVVETERTRABTITTVRVARANLGKATSGAULVIAN RYVINVVETERTRABTITRATSDLJEALKHLINGSKAG  5645  537  799  VGSVRDLKRGENSSRALLRONAGENIAMLHHINGSKAG AGGGSPALLDFUNLASCGCPPADVYTKARPPPLINKSLFHINGSKAG AGGGSPALLDFUNLASCGCPPADVYTKARPPPLINKSLFHINGSKAG AGGGSPALLDFUNLASCGCPPADVYTKARPPPLINKSLFHINGSKAG AGGGSPALLDFUNLASCGCPPADVYTKARPPPLINKSLFHINGSLFAL AGKPAPCRVTITILRASIPATRASFLSSFIKMPPBBLEVILG LISLKRHYBVSVYSAICHPQKRSTGNRSFTCTPELPPRLQTH		1	1.	
GVLAGHDRRVSCLGYTDDGHAVATGSWDSFLEIUN  5640  280  1092  QGRKKTMLSHITMIKQRKQQATAIMKSVUKINDVDGMDLCKKV IPRDLMLEELSHLSHNRGARLFKMRQRRGDKTFERNFQYGSRAQ NHSLAMQNISVUGGSNLEGGSQOAPLTPPNTTDPRSPPNPINTA GYSGPLAKETPERKENTTAVP KYVQSPWEGATSINDE ELIBALVE LYKPBGKAELPDYRSPRIVATPFGGFEKASRMVKFKVPDFELL LITDPRIMSFYPLSGRRSPRATTAVP KYVQSPWEGATSINDE ELIBALVE LYKPBGKAELPDYRSPRIVATPFGGFEKASRMVKFKVPDFELL LITDPRIMSFYPLSGRRSPRATTAVP KYVQSPWEGATSINDE ELIBALVE LYKPBGKAELPDYRSPRIVATPFGGFEKASRMVKFKVPDFELL LITDPRIMSFYPLSGRRSPRATTAVP KYVQSPWEGATSINDE ELIBALVE LYPWISTPLAVEN APHILTYFIGLIHPLDGSIQKLIV PESSEL  5641  27  332  CRINCRGDVKLLSSQMKLFAPHLTYFIGLIHPLDGSIQKLIV EILLSDNISSILVLENNINFLFKVKSKQFIHLIAKKFYISTIVSA NGSSFYLEMIVTG  1FSCL TPRECAPANHGLIAHTPHTRHTFYLHLIAKKFYISTVSA NGSSFYLEMIVTG  TWEYFGYCOELELSLHYLLLDYLLGAVNLFP FILTOGTNPG II KARELLPHIVLEFDEWMFPKNVRCSTCOLRKPARSKHCSVCNW VHEPDHHCWWINNCIGAWNITYFLIYVLTLANAATVAIVSTI LUSHVVMSDLYGETYIDDLGHHAVHDTVPLIQVIAFLSFRRIVE ULSHVVMSDLYGETYIDDLGHHAVHDTVPLIQVIAFLSFRRIVE LUSHVVMSDLYGETYIDDLGHHAVHDTVPLIQVIAFLSFRRIVE LUSHVVMSDLYGETYIDDLGHHAVHDTVPLIQVIAFLSFRRIVE VAMPPSAEPQVHRNIHSHKLRSNLQEIFLAPAPCHERKQB  5643  1 847  PSGGVEDVETREGSRRARGFRVWHERRGVGAGAIAKKKLARE RVQFQDMCATIGVPLASGKGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGKGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGKGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGKGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGKGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGKGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGKFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGKFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGRGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGRGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGRGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGRGFWSKMLGVGDFYYELGVOITE RVQFQDMCATIGVPLASGRGFWSKMLGVGAGAIAKKLARE RVQFQDMCATIGVPLASGRARARDFYVLAGLRRGABAIYMLPAI TDLYSGCETAMAVGGGTGILSVIGGMLAAFTFAGLISISTAMA LEGURAGATAGIASSIVENTYTRABELTASRLTATSTQLGEAL LIEDLTTRVLSFARGFTRANGLYTITARSKATVGRVLIV VANGBLAMAGATAGIASSIVENTYTRABELTASGLAVIANULTARSKATVGRPLA RVQFILDLRGEKSSBALLRGNAGENIMELTHIUGUKAG GLASATAGIASSIVENTATSTOQLGEAL RVQFDLAKKTANTATSGCFPANALTAGANTATVALTYLGAT		}	1	
1092   QGNKKYMLSHTMMKQRGALTAIMKZVESNDVDGKDLEKKV   IPRD_MLEBLSHLSNGAR_FKMRQRRSDKYTPENFQYQSRAQ   MBIAMQNGKVDGSNLEGGSQADALTPPNTTPDPRSPPNPINL   GYSGPLKEIPPEKPTTAVPKYYQSPMGQALSDDBILBBLYP   LYKPEGKAELPPYRSPNRVAIPFGGPEKASRMVKPKVDPBELL   LTDPRRMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDT   VPESEDL   CRINCGEDWALLSNGMDKLFAPHLPTFHGLISHFLOGSIQKLIQ   EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSA   NGESFYLSHIVAS    NGESFYLSHIVAS   NGESFYLSHIVAS    NGESFYLSHIVAS    NGESFYLSHIVAS    NGESFYLSHIVAS			<b>[</b>	
IPRDIMLERIJSRIGARGARLFKMRQRRSDKYTFENROYOGSRAQ NIBI IAMQNGKVDGSNILEGGSQOAPLTPPNTPDPRSPSPNDNIA GYSGPILKETPPEKFMTTAVPKYYGSPMEQAISHDPELLBALVE LFKPEGKABLPDYRSFNRVATPFGGFEKASRMVKFKVPDPELL LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDT VPRSEDL  5641 27 332 CRINCGGDVKLLSNQMDKLFAFHLFTFGLLHFLDGSIQKLQ EIILSDNSSIULLENNFLFFVLKSKQFIHLIAKKFYISITIVSA NGESFVLSMIVTG  5642 199 1247 ITPCRMDFLVFLLSVHGLVLICVCKKTHSLKGLARGSA IFSCI JPECLGRAMIGLLHYLPFYRNHTFYVLHLVLAGMVYTK WEVFGYCOBLELSHYLLLPYLLGVNLFFFTLTCGTNPGII KARKLLFLHVIFFDEVMFPKNVRCSTCDLKKPARSKHCSVCNW VHRPDHCWWNNCGSTOLLKKPARSKHCSVCNW VHRPDHCWWNNCGSMNIKPFLIYVLTUTAGARATVALVSTI LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIQYLFLFFFRIVF LSFVVVLSFLLGGYLLFVLYLAAINQTTNEWYRCDWAMCQRCF VAMPPSAEPQVIRMINISHGLANDLGEIFLEAPCHERKRQB  FORGOMCATIGOPPLAGSGGFMSMIGVGDFYYBLGVDIIK ALKHRNGGLTFLEBLHQQVLKGRGKFAQDVSQDDLIRAKKIARA RVFGPGIPVCGTYLLQSVPAELNMDHTVVLQLAEKMYVTV BIKASLKWBTERARQVLEHILKEGLANIDLQARGRAHYMLPAL TDLYSGETTAEEARRALP  5644 83 1138 PREMGSWQCLTSVGVQCNHPGWTVAGQFQBKKRFTEEVIEYF KKVSPWHLKILLISDEAWKRYVRVAELPREEADALTEAKHNI YVAIBOKDMQQKQQFREMFLKEFPQIRWKIQSSIBRLKRVIAN IEKVHRGCVIANVVSGSTGILSVIGWALAPFTAGLSISITAAG GLGIASATAGLISSIVENTYTRSAELTASRLITATSTQLEALR ILHDITPNVLSFALDFDERTKMIANDWITTLRRSKATVGRPLIA RVYPINVVETLETRGAPTRIVRKVARRIGKATSGVIVVULDVN VOOSLDLHRGEKSSSBELLRQNAQGELEENILNELTHINGSLKAG 5645 537 799 VGSWRDLKRISPTDPFGDSGRRDWTREDFYTGPIAGASSQVFT YLCLQKSLIGHSSVEDARATMELYQISQRIRARRRGLFRLAVSD 5646 3745 3328 AEQGGTSPHLLFPMLSSCLPPARVTKAATSFDLVSLTALAS LILLERTHYNSVYSAICHFQKEGTGNSRSPTCTPELFPRLQTH LSLLKKHPURUSVYSAICHFQKEGTGNSRSPTCTPELFPRLQTH LSLLKKHPURUSVYSAICHFQKEGTGNSRSPTCTPELFPRLQTH				
MISIAMONGKUDGSALEGGSQQAPLTPPNTPDRSPPNEDNIA GYSGPLKEIPPEKRYTTAVPKYYQSPMEQAISNDPELLBALYE LYRPBGKARLEPPYRSPNEVATPGGPEKASRMYKPKVPDFELL LITDPRMSFYNPLSGRRSFNRTPKGWISENIPIVITTEPTDDT VPESEDL  5641 27 332 CRINCRGDVKLLSNQMDKLFAFHLFTFHGLLHPLDGSIQKLIQ EIILSDNSSILVLENNPLFKVKSKQFIHLIAKKFYISITIVSA MGRSPVLSMIVTG  5642 199 1247 ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGA IFSCI_PECLQRAMHGLLHYLFHYRNITYTVLHLVLQGWYTE TWEVFGYCQELEISHYLLLPYTLYLLHGVNLFFFTINTGTTHPGII KANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSUCW WHRPDHHCWWNNCIGAWNIRYFLITVULTITASANTVAIVSTT LUBILVVMSDLYQETYIDLIGHHWDTVPLIQUFLFTFRIXVP LUBIVVMSDLYQETYIDLIGHHWDTVPLIQUFLFTFRIXVP LUBIVVMSDLYQETYIDLIGHHWDTVPLIQUFLFTRKKQB  5643 1 847 PSGGWEDVETKGGSTARARGFRVWHEREGVGAGAIAKKKLAER RVQFQDMCATIGVDPLASGKGFWSEMIGVGDFYBLGVGIIXW ALGTGGGIIPVGGTYLLGUJKKGRGKPAQDVSQDDLIRAIKKI ALGTGGGIIPVGGTYLLGUJKKGRGKPAQDVSQDDLIRAIKKI ALGTGGGIIPVGGTYLLGUJKKGRGKPAQDVSQDDLIRAIKKI ALGTGGGIIPVGGTYLLGUVLKGRGKPAQDVSQDDLIRAIKKI ALGTGGGIIPVGGTYLLGUVLKGRGKPAQDVSQDDLIRAIKKI ALGTGGGIIPVGGTYLLGUVLKGRGKPAQDVSQDDLIRAIKKI ALGTGGGIIPVGGTYLLGUSVAREINMDHTVVLQLAEKNGVYTV BIKASLKWBTERARQVLEHLLKEGLAWIDLQAPGERHYWLPAI TDLYSQEITAEEAREALP FREMGSWVQLTTSVGVQQNHEGWTVAGQFQEKKRFTEEVIEYF KVSYPULKTILLTSPAWKRFWYVAGELPFREADALVRAIKNTI VAIBDKDMQQKSQOFREWFIKEPPQIRWKIQES IBELRUJAN IEKVHGCVTANVVGSGTGILSVIGWHAEPTAGLISI TTAGG GLGIASATAGIASS UVBTYTTSAELTASRILTATSTQDLEARR ILHDITPNVLSPALDPDEATKMIANDVITTRGSFXTDQLEARR ILHDITPNVLSPALDPDEATKMIANDVITTRGSFXTUVVLUVVN VONSLUHRIGEKSSAELLRONAGELEENILNKEITHHGGIKAG GLGIASATAGIASS SAELLRONAGELEENILNKEITHHGGIKAG TYVFINVVETLETRGAPTRIVKVARNLIGKTSGVLVVLUVVN VONSLUHRIGERSSAELLRONAGELEENILNKEITHHGGIKAG SGKPAPCRYTITLIRAS IPATRASFI,SSFIRMPFRELEYILG LISLKKHHUNGVYSAICHFQKEGTGNSRSPCUTPELPPRLQTH LISLLKKHHUNGVYSAICHFQKEGTGNSRSPCUTPELPPRLQTH	5640	280	1092	
GYSGPLKEEIPPEKPNYTAVPKYYQSPWBQAISNDEPLLBALVE LFTPBGKABLPDYRSFNRVATPFGGFFKASRWVKPKVPDFELL LFTPBGKABLPDYRSFNRVATPFGGFFKASRWVKPKVPDFELL LTDPBFMSFVNPISGRRSFWRTPKGWISENIPIVTTTEPTDDT VPBSBDI.  5641 27 332 CHRICINGDVKLLSNQMDKLFAFHLPTFHGLLHFLDGSIQKLIQ EIILSINSSILVLENNFLFRVKSKQFIHLIAKKFYISITIVSA NGBSPVLSMIVTG  5642 199 1247 ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGA IFSCI_PECLGRAMKGLLHYLEPHTRHHTFIVLHLVLAGMVYTE KANELLFLHVYEFDEVMFPKNVCSTCDLRKPARSKHCSVCNW VHRPDHHCWWNNCIGAWNIRYFLIIVVLTIASAATVALVSTI LVHLVWMSDLYGETYIDDLGHLHVHDTVFLIQYLFLTFPRIVY LGPVVVLSPILGGYLLFVLJVLANHDTVFLIGYLFFFRING 1 847 PSGGVRDVETRGGGSRAARGPRVVMERGUBAMCQRCP VAMPPSAEPQVERNIHSHGLRSNLGEIFLAFAFCHBRKQB FRUGFODMCATIGVDFLASGKGFWSEMIGVGDFYYELGVQIIEV LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKI ALGTGFGI IPVGGTYLIQS PASLINNDHTVULJALBKNGVYVY BIKASLKWBTERRRQVLEHILKEGLAWLDLQAFGBAHYWLPAL TDLYSQBITAEEARBALP FREMGSWVQLTTSVGVQQMPDGWTVAGQFOEKKRFTEEVIEYF KKYSPVHLKTLLTSDBAWKFPVRVARGLFRERGBALFKALRIAT FRANGSWVQLTTSVGVQQMPDGWTVAGGFOEKKRPTEEVIEYF KKYSPVHLKTLLTSDBAWKFPVRVARGLFRERGBALFTAGSLSTTAAG GLGLASATAGLASSIVENTYTRSAELTASRLTATSTDQLEALB LIENTTPNVLSFALDFDEATKMIANDUTTLRESKATVQRPLIA FRYPINVVETLRTRGAPTRIVKVARNLIGKATSGVLVVLJDVW VQDSLDLHRGEKSESAELLRQWAQELEBHINKLTHIHGSLKAG GLGLASATAGLASSIVENTYTRRAELTASRCTATSTDQLEALB LIENTTRVLSFALDFDEATKMIANDUTTRRSKATVQRPLIA FRYPINVVETLRTRGAPTRIVKVARNLIGKATSGVLVVLJDVW VQDSLDLHRGEKSESAELLRQWAQELEBHINKLTHIHGSLKAG GLGLASATAGLASSIVENTYTRRAELTASRCTATSTDQLEALB LIENTTRVLSFALDFDEATKMIANDUTTRRSKATVQRPLIA FRYPINVVETLRTRGAPTRIVKVARNLIGKATSGVLVVLJDVW VQDSLDLHRGEKSESAELLRQWAQELEBHINKLTHIHGSLKAG GLGLASATAGLASSIVENTYTRRAELTASRCTARGLPRLAVSD VGSKDLKRILSPTDPFGDGSGNRDVTREDPVTGPLARSSGVQT FGLLQMSLLGHSSVBDARATMELYQISQRIRARRGLPRLAVSD AGKPAPCRVTLTLLRASIPATRASSILSFIRMFFBELEYILG AGKPAPCRVTLTLLRASIPATRASSILSFIRMFFBELEYILG LISLIKHHVHVSVYSAICHPQKEGTGNSRSFTCTPELPPRLQTH		(	Į.	
LYKPEGKARLPDYRSPNRVATPFGGPEKASRMVKFKVPDPELL LITDPRTMSTVINPLSGRRSPNRTPKGWISENIPIVITTEPTDIT VPESEDI.  5641 27 332 CRENCNGDVKLLSNQMDKLFAFHLPTFHGLLHFLDGSIQKLIQ EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSA NGESPYLSMUTG  5642 199 1247 ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGA IFSCI:PBCLQRAMKGLLHYLPHTHRHHTFIVLHLVLQGWYTH TWEVFGYCOELESLHYLLLDYLLFYLLGVNLFFF PTLTCGTNPGII KARKLLFLHVYEPDEVMFPKNVRCSTCDLRKPARSKHCSVCNW WHRPDHHCWWNNCIGAWNIRYELIVJUTITASAATVATVSTI LVHLVVMSDLJQDSTYIDDLGHLHVMDTVFLIQVLFFFRIVG LGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRCDWAWCQRCF VAMPESAEPQVHRNIHSHGLRSNLGEIFLPAFPCHERKRQB VAMPESAEPQVHRNIHSHGLRSNLGEIFLPAFPCHERKRQB FKRGGTVLAEDQLAQMSKQLDMFKINLBEFASKHQDEIRNIPB RVQFQDMCATIGUDPLASCKGFWSMLGVGDFYYELGVIIKV ALGTGGIIPVGGTYLLGGVLBHLKKGGKPAQDVSQDDLIRAIKKL ALGTGGIIPVGGTYLLGGVLBHLKKGGKPAQDVSQDDLIRAIKKL ALGTGGIIPVGGTYLLGGVPARLMDHTVULQLARKNGVTV BIKASLKBTERRAQULEHLLKEGIAWLDLQAFGBAHYWLPAI TDLYSQEITAEEARBALP S644 83 1138 PRRMSSWOLTISVGVQOMHPGWTVAGQFQEKKRFTEEVIEYF KKVSPVHLKILLTSDRAWKRPVRVABLPRERADALYRALKNIT YVAIEBKDMQQKRQOFREWFLKEPQIIRWIQESIERLRVIAN LEKWHRGCVITANVSGSTGILSVIGWALAPFTAGISLSITTAG GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALR LIHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVORPLIK RYVPINVTETLEFTRRGAPTEIVTRVARNICKATSGYLIVUDVN VQDSLDLHKGEKSESAELLRQWAQELFENLNBLTHHQSLKAG  5645 537 799 VGSWRDLKRISPTDPFGGGSGRRDVTRAATREDPVTCPLASSASQUT TCLQNSLLGHSSVEDARTMELVQISQERRARGGPRLAVSD 5646 3745 3328 AEGYGTSPHLLPTMLISSCLPPANVTTKAATPPPLVLSLTTAL AGKRAPCRVTLITLRASIEPTRRASFLSSFIKMFPRELEYIGG LSLLKFHVVHVSVYSAICHPQKEGTGNSRFTCTPELFPRLQTH RASSGAQ				
LITDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDT VPBSRDI.  CRINCNGDVKLLSNQMDKLFAFHLPTFHGLHELDGSIQKLQ EIILSNNSSILVLENNFLFRVKSKQFIHLIAKKFYISITIVSA NGBSFVLSMIVTG  5642  199  1247  ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGA IFSCI_PECLGRAMMGLLHYLFHTRNHTFIVLHLVLCGMVYTE KARKLLFLHVYEFDEVMFPKNVKSTCDLKKPARSKHCSVCNW WHRPDHHCWWNNCIGAWN RYFLITVLTIASAATVALVSTI LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIQYLFLFPRIVF LSFUVVLSFLLGGYLLFVLYLAATMQTTMEWRRGDWAMCQRCF VAMPPSAEPQVHRNIHSHGLRSNLOBIFLPAPPCHERKRQB  5643  1  847  PSGGVRDVETRÖPGSRAARGPRVVMERRGVGAGATAKKKLAEA RVQFQDMCATIGVDPLASGKGFWSRMLGVGDPYYBLGVOLIEV LAKKHRNGGLITLEELHQQVLKGRGKFAQDUSQDDLIRAIKKL ALGTGFGIIPUGGTYLLQSVPASLANDHTUVLQLARKNGVYTV EIKASLKMETERARQVLEHLLKGELAWLDLQAFGBAHYWLPAI TDLYSQEITAEEARRALP  5644  83  1138  PRRMGSWVQLITSVGVQOMPECWTVAGQFOEKKRFTEEVIEYF KKVSPVHLKILLISDEAWKRPVRVAELPRERAIALYKALKNINT VVAIEDKDMQNGQPERBFIKSPPQIRRKIGSIBRLRVIAN IEKVHRGCVIANUVSGSTGILSVIGVMLAPFTAGLSLSITAAG GLGIASATAGIASSIVENTTTRSAELTASRLTATSTQLEAAR ILHDITPNVLSFALDFDEATMILADVHTLRRSKATVGRPLIA RYVPINVETLRTRGAPTRIVKRVARNLGKATSGVLVVLDUVN VQDSLDLHKGEKSBSAELLRQNAQELFEBILNKLITHHGSLKAG  5645  537  799  VQSVRDLKRLSPTDPFGDSGRRANTMELVOISQRIRARRGLPRLAVSD  5646  3745  3328  AEQYGTSPHLLPTMLSSCLPPANVITKAATPPPLVLSLTTAD AGKRAPCRVTLTILRASIPATKRASSLSSFIKMFPRELEYILG LISLLKPHVVNVSYSAICHPQKEGTGNSRSFTCTPELFPRLQTH RASSGAQ			į	
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YLCIQNSILGHSSVEDARATMELYQISQRIRARRGIPRIAVSD 5646 3745 3328 AEQYCTSPHILDTMILSSCIPPANVTTKAATPPPIVISLTTAD AGKPAPCRVTLTLIRASIPATKRASFISSFIKMPPEBLEYIIG LSLIKFHVHVSVYSAICHPQKEGTGNSRSPTCTPELFPRLQTH RAEGGAQ	5645	537	799	VOSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL
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RAEGGAQ		1	}	AGRAPCRATETERRASTEATERRASTERSOFTARE EBBELLING
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5647 288 800 GVIMATSKLSCEVSERNCERREAFWARWADDTLSTREAGGCSL	5647	288	800	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPBEGCSLH
EESTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQBYQLP		1	l	EEDTORHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	1	to first	L=Leucine, M=Methionine, N=Asparagine,
I	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
<b>5</b>			S=Serine, T=Threonine, V=Valine,
į.	amino acid	residue of	
l .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence		\=possible nucleotide insertion)
			QRVLPLPIPTPAKMGATKEEREDTPIQLQELLALBTALGGQCVD
l	1	·	RQEVAEITKQLPPVVPVSKPGALRRSLSRSMSQEAQRG
5648	7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLQQAGNTDWSLTM
	l		APOSLPSSRMAPLGMLLGLLMAACFTFCLSHONLKEFALTNPEK
}	1	1	SSTKETERKETKAEEELDAEVLEVFHPTHEWQALQPGQAVPAGS
l	1		HVRLNLOTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS
1	İ	ì	ALAKFKEGABMESSKEDKARQAEVKRLFRPIEBLKKDFDBLNVV
ł			IRTDMOIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQD
1	1		LLSPGGLQVVINGLNSTEPLVKEYAAFVLGAAFSSNPKVQVEAI
l	I	j	EGGALOKLLVILATEOPLTAKKKVLFALCSLLRHFPYAORQFLK
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1	194	l	LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFAEKEAELT
1		<b>{</b>	QEMSPEKLQQYRQVHLLPGLWEQGNCEITVHLLALPRHDAREKV
١.	1	I	LOTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLBLQDGE
			DEGYPORLLGSVNSLLKELR
5649	1172	3006	MIQEQLDAINEEIRMIQEEKESTELRAEBIBTRVTSGSMEALNL
}	j	}	KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
1	1	1	MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
i	1	Į.	TLRLEKLGHPALSQEBGKSALEDQGSNPSSSNSSQDSLHKGAKR
}		Į.	KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
		i	VPAKLGTQAKKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
ŀ			ELWVGMPAWYVAACRANVKSGAIMSALSDTBIQRBIGISNALHR
ł			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
}	}	1	TDSREGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
1	l .	ĺ	DARMLDHLTKKOLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
<b>\</b>	*		LEKRREESQHBIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
		1	HGALLALDENFOHNTLALILQIPTONTQARQVMEREFNNLLALG
ļ	Į.	ļ	TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASABTLPA
			GFRVSTLGTLOPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQLDAINERIRMIQEEKESTELRAERIETRVTSGSMEALNL
3030			KOLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
l		}	MGVMTLPSDLRKHRRKLLSPVSRBENREDKATIKCETSPPSSPR
i .		Ì	TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
Į	}	l	KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
l			V?AKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
ĺ			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
1			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVNVTHBEMETLETSTK
		1	TDSEBGSWAOTLAYGDMNHBWIGNEWLPSLGLPQYRSYFMBCLV
1	1	1	DARMIDHITKKOLRVHIKMVDSFHRTSLQYGIMCLKRINYDRKE
1			
1	}	1	LEXRRESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTONTOARQVMERBFNNLLALG
		1	
1		1	TDRKLDDCDDKVFRRAPSWRKRFRPRHHHGRGGMLSASAETLPA
	ļ		GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL
	1	]	AWGEGAGIR+ASCLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP
l		l	WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP
1	l	1	ADP+LPGHSSQSPPRG+RWGRSRSAPAPAHPEHPAPAGSASASQ
			QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS
1			PAGSNAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA
1	1	1	PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA
1	1		GWRAGISPBLLGAAGLSDNWARCPGPGPAR*GGQPGCRTIPASA
[	1		CMPSPPVEGSLGLSRKGHGDLPSQAR+GWHECRRARHLVPLPRL
1	j.	1	LGPRGRTGRPSSPS
5652	735	343	HHKKYOHTHOKSPSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI
1 2002	,33	, ,,,,	CEPCARSPRISSNLVIHRRIHIGEKPLQCEICGFTCRQKASLNW
1		1	
	·	I	HQRKHABTVAALRFPCBFCGKRFBKPDSVAAHRSKSHPALLLA
5653	66	1401	RGRLQSRGRLTLGLVLLLDILGARQHGQRVSHGWKGGFLTAPL
1	İ		CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL
	1		COMEQUELECGOTFWOTALDNCQDLFLLDPPRPNLTSHPDGSED
1		1	Leplaggspeatspoutetknsplmedffeegfsqei/srdviq
1	]		GWLLBLQFRRSLYRGHLVR+FARRSRKSSEV+YCHQRGKSHGMQ
	<del></del>		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	I 1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
			ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF
ı	1		SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK
1	1	•	PTVHQECEQGFDRKASHSGYPKTHTGYKFYVCNEYGTPFSQSTY
1	]		
1			LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN
i .			ECGKAFTRIFHLTRHQKIHTRKRYBCSKCQATFNLRKHLIQHQK
			THAANV .
5654	3	598	TLPLFPGRRFRGNRRCGAVAARKNSTGGNVSINQRRDSVRMSAL
1	[		NWKPFVYGGLASITABCGTFPIDLTKTRFQ1QGQTNDAKFKB1I
j	1		YRGMLHALVRIGRERGLKALYSG*VGLHAFLCHCSLFHMGIDFR
			PRLHRSQVKSLRCV+KEQIA++/MFSLLISTLISKYIYYAADVL
	1	ļ	EKLFYYIQVQTDWNKKICLFKNI
5655	2	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP
	I -	[	PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGGDPELC
1	I	]	
	1		ATDEMIPFKDEGDPQ\REKIFARIVNPEEEGDLADIKSSLVNES
			EIIPASNGHEVARQAQTSQBPYHDKAREHPDDGKHPDGGLYNKG
I	I		PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH
	İ	1	AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI
			PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
		ļ	LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLK
l			PSNMNAFMENLKKNIHLRTSYSELVGFNSVBFGGRTNKVPHIWK
1	1		YDNPPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP
i	į		WSKLQKPPKRGVYELAVFQMKPGGPALWGDAPERATNAHVNLGY
			TKVVGVFHTEYGELNRVHVLWWNRSADSRAAVRHKSHEDPISWG
ŀ	<b>l</b> .	*	GVRESVNYL\VSQQNM
5657	105	1052	GQRLQSPRVQMPVQPPSKDTEEMEAEGDSAABMNGEEBESEBER
]		~~~~	SGSQTESEESSEMDDEDYERRRSECVSEMLDLKKQFSELKEXL
i			
1 .			FRERLSQLRLRLEEVGABRAPEYTEPLGGLQRSLKIRIQVAGIY
	ļ .		KGFCLDVIRNKYBCELQGAKQHLESEKLLLYDTLQGELQBRIQR
1	ļ		LEEDROSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
1	i i		PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
1			GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL
			ALVWTPPL
5658	2346	3541	TERRVYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK
			NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY
1			RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE
1			RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA
<b>(</b>			LKVIFYLDSYHPSKLPSRLBGGASLRLHTALFTKVLENVEGLPS
			PGSQAAEDLQQDINAQSLBKVQQYYRKLRAFYLERSNLPTDAST
1			TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS
1 1			SELCYRLGACOMVMCGTGMORSTLSVSLRQAAILARSHGLLPKC
	•		IMOATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCOPKMN
1 .			
ECEO		CE C	GDL
5659		696	WKRSGEVSPKGELGAWRGNSGRPKIIGRAABAENEDRTLGRLLP
			GNERSQPRSPLRLLAPQLKARAAADKGLAPVPPPFSSGHSGPC\
			EREGRGQRGRGRSRRGAHLBLKPSPGLRAGAPTDRGRGGPAEVA
1			AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG
1 1			EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
			FRRLQKWELNTYL
5660	229	853	PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
[ ]			CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE
į l		•	QRKAFPHHRPVALIGALLAICCMIFLGFADDVLNLRWRHKLILLP
i l			
<u> </u>	· ]		TAASLPLLMVYFINFGNTTIVVPKPFRPILGLHLDLGR*SYHCC
<u> </u>			PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAAALGASFLAKAPLPVTVRGSGL
			AGMAVTCDPXAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK
j i			ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP
J 1			SLAVHMHERGMDMDGEQKWQYRGRT
5662	2	1318	LRKEGRCRRGSNRGVWAAPAEGLGGRGNLGVRCLLRSVRPCSSA
) I			PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLP
			TANA CALIFORNIA CONTRACTOR AND AND AND AND AND AND AND AND AND AND

_ <del>                                     </del>	1 5 32 - 5 - 3	1 8 12 14 14 14 14	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
	bedanie	<del></del>	LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR
	1		MANDOSSIDESIQV VADSGEDSKELT PGSSVEVQGQLI KSPSKR
	l		QNVELKAEKIKVIGNCDAKDFPIKYKERHPLEYLRQYPHFRCRT
l i	l		NVLGSILRIRSEATAAIHSFFKDSGFVHIHTPIITSNDSEGAGE
1		•	LFQLEPSGKLKVPRKNPFNVPAFLTVSGQLHLEVMSGAFTQVFT
1	J	j.	FGPTFRAENSQSRRHLAEFYMIRAEISFVDSLQDLMQVIBELFK
1		ľ	ATTMMVLSKCPEDVELCHKFIAPGQKDRL+HMLKNNFLIISYTE
1		f	AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIPVFVINY
1			PLTLKPFYMRDNEDGPQELEGSVA+HSLGLMILLSIVVIGQP
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL
			VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLRNYR
1			NLVFLGIALTKPDLITCLEQGKBPWNIKRHEMVAKPPVICSHFP
1 1			QDLWAEQDIKDSPQEAILKKYGKYGHANFQLQKGCKSVDECKVH
1 1			
5664	410	F 77	KEHDNKLNQCLIPKKKK
P00C	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG
i			GPPPGWDAAPPERGCEIFIGKLPRDLFEDKLIPLCEKIGKIYEM
1 1			RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYBIRNGRLLGV
			CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE
1 1			etevkgkrkrgrpgrppstnkkprkspgeksrieagirgagrgr
1 1			ANGHPQQNGEGEPVTLPEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFII
1			GLPVNITALWVPSCTTKKRTTVTIYMMNVALVDLIFIMTLPFRM
1 1			FYYAKDEWPFGEYFCQILGA
5667	<del>- 1</del>	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP
5007	-	0,55	SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
	• *	•	
1 . 1			VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
	·		ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
1			PTPLTHHNTGLSEALBILABAAGFBGSEGRLLTFCRAASVLKAL
			PSPVTTLSQLQ
5668	691	894	CSFLFCIPDLFLQFLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ
			VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	1 :	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD
1 1			ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFFPK
}			ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL
1 1		•	NSQ
5670	3	373	SSECLTMAWIPLLIPLLILCTVSVASYRLAQPSSVSVSPGOTAK
			ITCSGDVLAKKYARWFQQKPGQAPVLVIYKDTERPSGIPERFSG
1 1			STSGTTVTLTISGAQVEDRADYFCYSATDNFLWVP
5671	280	524	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE
]		-4-A	PKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
5672	2	557	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPAKDITGS
20/2		100	
į į			SDPYCIVKVDNEPIIRTATVWKTLCPFNGEEYQVHLPPTFHAVA
1	Į.		FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSP
[			WPPSHSETSPLGSVWSPAQCKPFLLSPEAGATFCTPGLCSAACS
<u>l</u>			QAWLLLPLP
5673	327	696	ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV
ļ i	i		KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC
			DVMIVARDVETEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMEGESTSAVLSGPVLGALAFOHLNTDSDTEGFLLGEVEGE
		-	AKNSITDSQMDDVEVVYTIDIQKYIPCYQLFSFYNSSGEVNEQA
1			LKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQ
1 1			
1			DLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLG
1 1	}		MSEQLGYKTVSGSCMSTGFSRAVQTHSSKPFEEDGSLKEVHKIN
į l	]		EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIERRRGA
			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
1			MFLKVAVTTTTISM
5675	80 ·	753	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG
			KSGVPVSAPGSDGKWWBERPGMFSLMASCCGWFKRWREPVRKVT
	1		
			LLMVGLDWAGKTATAKGIQGEYPEDVAPTVGFSKINLRQGKFEV TIFDLGGGIRIRGIWKNYYABSYGVIFVVDSSDERRMEETKRAM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	corresponding to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible mucleotide deletion,
}	sequence		\=possible nucleotide insertion)
		†	SEMLRHPRISGKPILVLANKODKEGALGEADVIECLSLEKLVNE
			HKCL
5676	2	930	FVSSPPPRPVQPARPGGFGLSGRRSLLCQVASTPAHVGVMRSPV
			RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
			PFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
			HNQTGKKYQWDAETQGNILGSFFYGYIITQIPGGYVASKIGGKM
			LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
			MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
	i	i	WTYVFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS
			L
5677	1	1028	PPRDGFLBLRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
İ			VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLNLIHH
ĺ			RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIONSKRKGPEF
1		1	TREFESVLVDAFSHVARRADEGCKKPLERLLNIWOERSVYGGEF
1		1	IQQLKLSMEDSKSFPPKATREKKSLKRTFQQIQBEBDDDYPGSY.
		1	SPODPSAGPLLTERLIKALODLENAASGDATVROKIASLPOEVO
			DVSLLEKITDKBAABRLSKTVDBACLRNRGPGTS
5678	3	593	SSSPPSSTPSLPLPFYLLLGQLRLQLLMGTAHLSGAGKAAPCPG
	[		GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIER
		+	SLAEFTEOFNOLHNRRNENLOLGPLGRDPPORCSTFSPTDSGRB
			PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
			AAALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDBDYYGSAABWGDEADGGQQBDDSGEGR
ļ	1	1	DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYPQAGGSPENVIQL
	. 7	1	LSENYTAVAQTVNILIAEWLIQTGVEPVQVQETVENHLKSLLIKH FDPRKADSIFTEEGETPAWLBQMIAHTTWRDLFYKLABAHPDCL
			MINFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLONRNSHTPLESLIHPOPSYKGFGIMFGKKKKKIE
3005	250	33"	ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
			DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA
			RQTRPQRLRKRAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL
			FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP
		<b>1</b> .	PASCVFSQVMNMAAFLALVVAVLRFIQLKPKVLNPWLNISGLVA
	•	<b>1</b> .	LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWIQAAL
			TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
5700	30		QGFVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL OKINGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGL
		1	PFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYO
			GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
		1	LRHRSPGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA
	1		HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS
			ATYCTYCSKKPASPNAYENHLKSRRHVBLEKKAVQAVNRKVEMM
	1		NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK
			BARNVVAVGTGGRGTHDRDPSEKPPRLQWFECQAKKLAKHSEDD
	ļ	1	SEDEEHDLC
5684	195	677	TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT
		1	AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY
	}	1	QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGEREFARSET
	Ī	<b></b>	LDQLPLTNPEHFOTPVIGKKTNRGRRYE
5685	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
			VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPRIKKPLNAFMLYMK
			EMRANUVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
			ROLHMOLYPGWSARDNYVSPSSIPVALHS
5686	128	1181	CTHWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
		1	VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
Ĺ <u> </u>	<u> L</u>	L	PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
140:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K*Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u> </u>	\=possible mucleotide insertion)
			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGMP
}	Ì	Ì	RMDYLINSSSGVVVTTTELDRERIAEYQLRVVASDAGTPTKSST
	ļ	l	STLTIHVLDVNDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN
1		ĺ	NDVGLNABLSYFITGGNVDGKPSVGYRDAVVRTVVGLDRETTAA
	<u> </u>		YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIILQSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA
[		ļ	QGDGGAAAVGHVLVVPAVGPVRVNPGLQTPVPRPBLLPGP\SSS
1	1	i	LHSDSSYPPDAGLSDDEKPPDASLPPDPPPLTVP/ADA/PMPVT
1	ì		SGCRMPSTSASE/AAGCQGACTHAKGSETPPPASPQTSEPAPSP
1	)	1	LPPHLTCGPGMYSSEAKLPNSFSCLGLAGTGAGI*GTASAHGTG
1			PPVLPHVCTPSLANPQP\AVGPBASSLPLGVSGIGMSA/SAPIS
1	1	1	SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP
			VLDI
5688	1	420	LTKMDLFGRCYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLFF
l		1	+SHMIIRSLL+KVIDDSLGQLPLLRELLL++LNVIDRCIILAYV
Í	1	}	LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID
F600			DGY1PAVF
5689	1504	3	HBLSGKHISMVSGNTCNWHPGGHSPGGGCQGEITSKDRGEIPAL
			IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPFQPCEGPRSTSRG
1	1	}	GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEGGAH GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQFWDQHPHS
			PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ
}	<b>§</b>		KLPRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\
ļ			POTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGGH
1		١.	GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLQCPCSK
			EL*RVPPGSIGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF
	1	- 1	GOELKGPLDAGRLNPGAPSASSSHR*GG*ERARAGAGHRGST*A
	1		SSKIEGGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P
			GSPPPA*ASAGRKGTVSTLGGGLL
5690	1424	58	PSPPAGVCAAPAPLPLLALARRDRRPCSPGARAAPWQTGGPAID
			GAWRTSVSALRRGATG/APCSPGARAAPWQTGGPAIDG\DGELP
1		ľ	*VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGQGRQQDPEP
{	į.		DGLRHROHGAASHARHRLORLRPGHHONRHVRRDPQAPPGGPAP
i		ļ	GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERARPRH
1		ļ	PTPOGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA*GNPQLE
l			KAPRSDRNPSQGLRTRIRRPBTPDCGPPSPAGSSASASTFRCTS
ł		1	SLSLLGP/PGAHNLDTAPQDR+HGP+GDKRGAPGVAGEDPRPP+
1	1		CNFVR+LLLMP/GVA+RHGTSPFLGPSLGENGCQWDSGNLFGTP
<b>[</b>	1		kg*shpaftkst*smeaeksywnhphr\drgrqgvrinclrvge
	1		semwgpysaprpgtvfl&splspaskeh\pegsssfntpfppag
L			PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMDVSFSG-LSFIED
ļ	1		VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S
1	1		GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG
L			GVGVYVLLRSVPLSYS
5692	1193	548	TQAWTRAEKDRKGSVRALRLHLRRGPPT*RGSHPL\QSVPCIQK
1	ł.	ļ	PSIPSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL
ľ	1	l	TSRSVPPGRGALPPDSLSTRRGLPRPSTAGHRVRESGHKVPVSQ
	Į.	l	RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLQS
			VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVBTMGNGVD
5693	1258	1330	ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSQNTEPQAP
1	1		*QAGPPSSLRPP\SRRR*APEWPKRATGSRCRGLSAPPWPWPAA
(	1	l	RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS
1	J	<u> </u>	PEAIVWRSSRFPLWFPLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKRPARSLHRRGSGHKSSAGKNGSVTLSTAGALG*KQLHQ*WT
1	1		QRCL\NNLSSBEFNASSSLNSLPSTPTASRRNSTIVLRTDSBKR
İ		[	SLAESGLSWESESEBKAPKKLEYDSGSLKMEPGTSKWRRERPES
ŀ	1	1	CDDSSKEGELKKPISLGHPGSLEKGKTPFVAVTSPITHTAQSAL
}	1	l	KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
]		]	IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
			<u> </u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	Intermine, 1=1801eucine, K=Lysine,
	to first	1	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
•	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence		\=possible nucleotide insertion)
			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
	ļ		VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
i	į.	j	PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1	1		PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
1	i		DTTOCI
5695	3	1330	
3093	3	1338	GSKBPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
i	l		SLARSGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPRS
1	l	•	CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
	1		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
[			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
!			PTATKLABLPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
1			DITOCI
5696	3	1220	
3036	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
			QRCL\nnlssebfnassslnslpstptasrrnstivlrtdsekr
i .			SLAESGLSWYSESEKKAPKKLEYDSGSLKMEPGTSKWRRERPES
1 i			CDDSSKGGBLKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
1			KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1 1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
l i			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1	ì		PTATKLAKLPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
1 1			DTTQCI
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA
		••	OCDAMIOCUPDEUDODO ODCET POMMON PORTUGA VA
1 1			QGPATVQSVBDFVPDDRLDRSFLBDTTPARDBKKVGAKAAQQDS
1 1			DSDGEALGGNPMVAGYQDDVDLEDQPRGSPPLPAGPVPSQDITL
1 1			SSBEEARVAAPTKGPAPAPQQCSBPRTKWSSIPASKPRRGTAPT
f 1	j	•	RTAAPPNPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP
1 1	i		EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE
1 1	· '		DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEBAGPKESSERGK
ł i	1		EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR
1			RRQQRPPRSRERTAA
5698	2	666	GAKAABPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT
}	i		QREWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ
į i			GREPWIVEGRPLLQSYPDEVWQTDDLIERIQERENKPSRQTVPI
[ [	1		ETLI*R/ERGNVPGNTFDVETNPVPSRKLAYTHSLCNSCER\GF
1 1	i		NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDOAYE
1	1		FNO
5699	2	1448	
	*	73.70	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
1 1	i		EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA
1	ļ		RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS
ļ ļ	,		DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
1 1	ł		TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT
[	Į.		WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQY9NN
1	1	į	VPILFONPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP
1 1			VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA*
i	i		GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA
] }		ŀ	GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA
j 1	ł		HDANDDGCADDMAN COMMANDAG MANDER & CONTRACTOR AND THE TOPPLEA
	ŀ		HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL
5700			FPPGRG
3700	923	597	NGHKGVWEINIY*RRSNIHKNSKSBSHLNQDHSPPPPTPNSARS
!			KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD
			E*CSIASSLIKAILRVSVLSB
5701	59	410	IFEKICSDTORFISPKINPOICSWLIFDKGAK/NHATGKDSLFN
			KWSWKNWLSTCR+MRPGPYFTPYTKINSK+IK/DANIRCETVKL
1		l	LEENTGENLHDTGLGNVFLDMTPKTOPTKOK

Predicted   Pred				
Molectice   Corresponding to first and no actd residue of anno actd residue of anno actd residue of anno actd residue of anno actd gequence   Sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Costion   Coffee				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first antno acid residue of antno acid sequence  5702  3 1517  1517	I NO:			H-Wishiding T-Tepleveine, V-Ivedee
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence  5702  3 1517  1517  1517  1517  1517  1517  1517  1517  1517  1517  1517  1517  1517  1517  1517  1518  1517  1517  1517  1517  1517  1517  1517  1517  1517  1518  1518  1518  1518  1518  1519	1			Teleucine M-Mathionine N-Assaurating
amino acid				
residue of anino acid sequence  5702  3 1517  15	l			
amino acid sequence  5702  3 1517  REPUDESQUORTESDESSENSUITESTASSESSASSICENTUTES STORE  1518  REPUDESQUORTESDESSENSUITESTASSESSASSICENTUTES SASSASSICENTUTESTASSESSASSASSICENTUTESTASSESSASSASSICENTUTESTASSESSASSASSICENTUTESTASSESSASSASSASSICENTUTESTASSESSASSASSASSASSASSASSASSASSASSASSASSA	ł			
Sequence	1			
STO2   3   1517   RITPUPEGOGSTESSHEVITTSRASESSASSIGEHPUTTSRASESSASSIGEHPUTTSRASESSASSIGEHPUTTSRASESSASSIGEHPUTTSRASESSASSIGEHPUTTSRASESSASSIGEHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSIGHPUTTSRASESSASSASSIGHPUTTSRASESSASSASSIGHPUTTSRASESSASSASSASSASSASSASSASSASSASSASSASSAS	ł	sequence	•	
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TRYINGSITEIRTTSSIPARADULIPTERVASSISTEDPAST   BERVARADHITEVISSARITISTALTSSARITISTSTAPARADULIPTERVASIA   BERVARADHITEVISPARISTASSYSTSYRVAVGASIA   PUS IRMASINAVETTSPARISTASSYSTSSERALAMPTPESTLINDI   TTKOPPPTSRDPLDSVPPTTINSSKTINSTLAKITTSAKTTINKP   PTATPTTARTETTIA = VUVURIEVISSIGO = VMLIPRKTISLIPERI   KG	1	[		SSDGPHPVITPSRASESSASSDGPHPVTTPSRASESSASSDGLH
BSTEARGHITEVTRARATISTAGTTESARPITVOTELPINAS REPUTAROATISCALUTVISRIPUERTSALSYSTEYVAVGGA PVSIERGSAVGKTTSFAGGUSKTISTAALTTEKE PVSIERGSAVGKTTSFAGGUSKTISTAALTTEKE PVSIERGSAVGKTTSFAGGUSKTISTAALTTEKE PVSIERGSAVGKTTSFAGGUSKTISTAALTTEKE PTATPTTARETVTTA VOUVKNEVSSGG*VHLPRKTSLTPENG KG*CSSSTGNSTPTELTSRSPYCVSGGRANG*PSAGARHUFVAKT GCCP*FGPPTDCSCVTUKETGYCVPMKGSSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSKPLITDVAKTERG CCCP*FGPPTDCSCVTUKETGYCVPMKGSSKPLITDVAKTERG PKAGGIGTKAKPSSEILKLIHPCM*SLDRGGGGSAVPTAREV ALPTGPKCM**PARPT*PKRRIPESSERTHILIGYCRYCK**SVSL ALPTGPKCM**PARPT*PKRRIPESSERTHILIGYCRYCK**SVSL ALPTGPKCM**PARPT*PKRRIPESSERTHILIGYCRYCK**SVSL ALPTGPKCM**PARPT*PKRRIPESSERTHILIGYCRYCK**SVSL ALPTGPKCM**PARPT*PKRRIPESSERTHTILIGYCRYCKY**CSC ACCRGGGGC*HPPWWYSSSGSVCCSGR**HAGPLISAARPRA AGRAGLEAGGUCCOCOACITEMPASSUSSGGAAGGGAAAAAACATSAAAGGTSAAAAGATSAAAACATSAAAAAAAAAA				PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTN
REBUTAPICATITISCALUTUSENPILESTERALSUSTESSY PROVIDED PURE REMAGNING TYPE AGGINGS TO SERGALANIPT SETTEM DI TEKEPPYTER PAGGINGS TESSERALANIPT SETTEM DI TEKEPPYTER PAGGINGS TESSERALANIPT SETTEM DI TEKEPPYTER PAGGING TO SETTEM TO SETTEM TO THE SETTEM TO SETTEM TO SETTEM THE SETTEM TO SETTEM THE SETTEM TO SERGIO SETTEM THE SETTEM THE SETTEM TO SERGIO SETTEM THE SETTE	1			IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
FVSIEMGSAVGKTTSFAGSASSISSISSALAINNFTPSETLTINKE PTATFITARTRYTTA VOUVINEWSSIGG-WILIPEKTSLIPSEN RG *CSSIGNSTPELSTSBYVOYKOSSAMI, PPARTSTITARTTYKE PTATFITARTRYTTA *VOUVINEWSSIGG-WILIPEKTSLIPSEKT RG *CSSIGNSTPELSTSBYVOYKOSBAMI, PPARTSTITARTY REGORD *CCC+*PGDPPDCSCVYVLIKGTQKUPMKGSMSKPLTPDVATGES LITSTGYVYKGCASPVPRGVLGUTARTQKUPMKGSMSKPLTPDVATGES LITSTGYVYKGCASPVPRGVLGUTARTQKUPMKGSMSKPLTPDVATGES RILIKME*HTARAF*PERRILISSBYRTHLIGVLYKSPKEVGKS**VSL DPSCRERELETC**YGKRSVASSISRPPGGGGASVPFAREVS ALPTEPRCM**APRERTROPCIMPELSSPHATLATGTGHCISSE GSWETARGS**WCPHL**ARMINIMETASGASGLGRADDRESMI RUNGLLENGGLIVER H**TAGARAVUSSGGGASVPFAREVS ALPTEPRCM**APRERTROPCIMPELSSPHATLANGECPLISPS GSWETARGS**WCPHL**ARMINIMETASGASGLGRADDRESMI RUNGLLENGGLIVER H**TAGARAVUSSGGGATESPACCHOQ ACCREGESC*HPPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPPMPVPSBSBVVVCPSGR**HLRGPLISPACCHOQ ACCREGESC*HPMPVPSBSBVVCPGCPACCHOQ ACCREGESC*HPMPVPSBSBVVCPGCPACCHOQ ACCREGESC*HPMPVBSSBVECQCQACLLAV HUNGHEGUECCHOOPPHCLOCHTOCGGALD DYVANTONCLIADURCCERRYCAPHNGSVECQCQACLLAV HOVERHINGELRENSHMARKALLRVHIHMLIHTETFYFLLCSI LFF!IFLF  5707 28 609 GSPATTGGFBRFGGFFFSGTFRHGGRASSSILDFRSSSPPACC TPEGGAPDDULPSBVAQ ACCREGESCHHOPPHCAPTUSCHCHOCACHOCOCHOCACHO ACCREGESCHHOPPHCAPTUSCHCHOCACHOCACHOCACHOCACHOCACHOCACHOCACH	1		•	
TRIOPPPTISSEDILPSUPPTTTINSKGITISTAKITTSAKTITIKE PTATPTTARTPTTAN-TOWKSVASSCG-VALIPPRISTLEPBIN  G*CSSSTGINSTPTELTSRSPYCYGGERING / PSAAARHUYZAKR GCCP+PGPPTDCSCVTVLIGTGKVPMKGSMSKYLPYGATGPS LTSTGVYWGCASPVERGVLGITLAHVLCFSKECT  5703  14  1117  HHKDBISGGLPRTQECARPELERFLLCFRAIMPVTRGYRCPWQA PKAGLGTTAKPSSEIMLKIHEOWESLDRGGERTGTGTHCGOS RILMHIP+HTAAR*PRERRIPSSIEMTHHGVLRVQDKS*-VSL DPSCPRFILETC*+ YGMRSVASSSSPPPCHGERJAPVTRGYRCPWQA ALPTGPRCW*APRGRTTQPCGMPSLISSPHATADMCGOCCIJESPS GSWETAPGS**WCFWL*APRGTTQPCGMPSLISSPHATADMCGOCCIJESPS GSWETAPGS**WCFWL*APRGTTQPCGMPSLISSPHATADMCGOCCIJESPS GSWETAPGS**WCFWL*APRGTMGTAGAPASUGAGADEPSAMA REVAGLIDGGGLTVRR**H**TAGAPASVRSSQQATREPARCOCOC ACCRGGGSC**HDPFWPWVSPSSPVCPGGR**HLRGFLASARPRA AGMPRISHDTQTPEB  5704  23  562  GDVEPPDSFYWDDISQAARDLVTRLMEVGDQRITAREATSHEWI SGNAASDRNIKDGVCAQIERNPARAKWKAVRVTTLMKRLRAPP QSSTAAAQASAATUTATTGAAGGATAAAASGATSAPEGBAARAA KSDNVAPRRP**LPPQPGMEWPPQPLMAVSFGOPMEASILQPIMGE SPQP  5705  23  562  GDVEPPDSFYWDDISQAARDLVTRLMEVGDQRITAREATSHEWI SGNAASDRNIKDGVCAQIERNPARAKWKAVRVTTLMKRLRAPP GSTAAAQASAATUTATTGAAGGATAAAASGATSAPEGGAARAA KSDNVAPRRP**LPPQPGMEWPPQPLMAVSFGOPMEASILQPIMGE SPQP  5706  1161  610  OGREPARADTVATREAMCATAAAASGATSAPEGGAARAA KSDNVAPRRP**LPPQPGMEWPPQPLMAVSFGOPMEASILQPIMGE SPQP  5707  28  609  GSPAPTGBFRRPGRSTPSPGTRHQGRAPPAPAPABRACHAM KSDNVAPRRP**LPPQPGMEWPPQPLMAVSFGOPMEASILQPIMGE SPQP  5708  44  1925  SSPAPTGBFRRPGRSTPSPGTRHQGRAPPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPA		}		
### PTATPITARTEPITA*****PUNKREVSSSG4**PULPPRISLIPPEND  ### CSSSTGMENTPILITSRES**PUTOGGRAND**PUTANAR**  ### CSSSTGMENTPILITSRES**PUTOGGRAND**PUTANGPS**    1117	ŀ	į.		
GCCCP+GGPDPTPDCSCUTULEGECTIXUPMKGGMSKDLTPDVATGES   CCCP+GGPDPTPDCSCUTULEGECTIXUPMKGGMSKDLTPDVATGES   LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKERCT				
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5707  28  609  GSPAPTPGFRRPGRGTPSPGTRHHQGRAEPEPDAPERAPLRR* MFAIQPGLAEGGQPIGDPPPGLCQPELQPDSNSMFMASAKDANR NWHGMPGRVBPILRSSSESPBDNQAFQAPGSPEEGVRSPPEGA EIPGAEPBKMGGAGTVCSPLEDNGYASSSLSIDGRSSSPBPACG TTRGPGPPDPLLPSVAQA  5708  44  1925  GSPAMETISPCFPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP PRCPFTAMESPRTKQRVRNKVCLLIAITRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSPSLGAPGAPSPL RVSPASGGPRKGRQCSGG*AGGGQP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSGAMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGSGETGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*TTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GKAPA PPPPRPEPPPPPARRP  5709  2 2031  ITLCPLPQTEKCLWVVTEAATPLGTYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPK/NALSFLVNDCS	i			WQVBKHKQELRENESNWAYKALLRVKHLMLLHYEIFVFLLLCSI
MFAIQPGLARGGQFLGDPPPGLCQPELQPDSNSMFMASAKDANE NWHGMPGRVEPILRRSSSESPEDNQAPGSPEEGVRSPPEGA EIPGAEPRKMGAGTVCSPLEDNGYASSLSIDGRSSSPBPACG TPRGPGPPDPLLPSVAQA  5708 44 1925 SPSWETISPCPPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHEDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP PRCPFTAMPSPRTKQKVRNKVCLLIAITRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSPSLGAPGAPSPL RVSPASGGPRKEGCQCSG*AGCGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSG-AGCGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSG-MAVARSPSRCSRW*RQSGR*RG*S SRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSGSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGSGFTGAGRSHTLK AARSRLSPRPGSGSRGSY*SINDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGPAASCSCSCRAPAKPASS/GBAPA PPPRPEPPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVIEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCMGVMAPPAPK/NALSFLVNDCS				
NWHGMPGRVEPILRRSSSESPENQAPGSPEEGVRSPPEGA  BIPGAEPRINGGAGTVCSPLEDNGYASSLSIDGRSSSPBPACG  TPRGPGPPDPLLPSVAQA  1925  SPEWETISPCFPKMPAEPWHLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHEDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP PRCPFTAMPSPRTKQKVRNKVCLLIATRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSPSLGAPGAPSPL RVSPASGGPRKEGCQCSG*AGCGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSG-AGCGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSG-MAVARSPSRCSRW*RQSGR*RG*S SRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSGSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGSGBTGAGRSHTLK AARSRLSPRPGSGSRGSY*SINDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GKAPA PPPRPEPPPPPARRP  5709 2 2031  ITLCPLPQTEKCLNVVIEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCMGVMAPPAPK/NALSFLVNDCS	5707	28	609	
BIPGAEPEKMGGAGTVCSPLEDNGYASSLSIDSRSSSPEPACG TPRGPGPPDPLLPSVAQA  5708 44 1925 SPSWEETISPCPPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA+GEAVSLSLSSGDVCGHTDGGAGSDPQAKPKP PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA GNPHDRSSTAA+LHRRAGAGSLCLSASLLPPSFSLGAPCAPSPL RVSPASGGPRKEGRQGSG+AGGGGP\ARTHADLPCVGFVCSPP LLK+SDSPVKQLPA\SGQGSGASMPPVGSSDTLRPRPTSVGTG RAAG+CSWQPAACCTPRSQ+WAVARSPSRCSRM*RQSGR*RG+S SRRRGP+AAGRSTPAVP+PCS+GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA+*SRLGGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGSGSTGGRSHTLK AARSRLSPRPGSGSRGSY*SINDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPRLPAAS/SGGASGSPAASCSCSCRAPAKPASS/GKAPA PPPRPEPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCMGVMAPPAPN/NALSFLVNDCS				
TPRGPGPPDLLPSVAQA  5708 44 1925 SPSWETTISPCFPKMPAEPWHLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTIGGGAGSDPQARPKP PRCPFTAMPSPRTKQRVRNKVCLLIAIRYSDIPSDVSKAP\GPA GRPHDRSSTAA*LHRRAGAGSLCLSASLLPPSPSLGAPGAPSPL RVSPASGGPRKEGQGSG*AGGGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSGAMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACCTTPRQ*WAVARSPSRCSR*RQSG*RG*S SRRRGGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGSGSTGGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GKAPA PPPRPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GKAPA 1TTLCPLPQTEKCLWVVTEAATPLGTYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPK/NALSFLVNDCS			•	· · ·
5708  44  1925  SPSWEETISPCPPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQARPKP PRCPFTAMPSPRTKQRVRNKVCLLIAITRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSPSLGAPGAPSPL RVSPASGGPRKGRQCSGG*AGCGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSGASMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGSGETGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GKAPA PPFPREPPPPPARRP  5709  2  2031  ITLCPLPQTEKCLWVVTEAATPLGTYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPK/NALSFLVNDCS				
QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQARPKP PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSPSLGAPGAPSPL RVSPASGGFRKBGRQCSGG*AGGGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SQQGSGAMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRGP*AAGRSTTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GGGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGBTGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GBAPA PPPRPPPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVIEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCMGVMAPPAPK/NALSFLVNDCS	8700	44	1025	
PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSPSLGAPGAPSPL RVSPASGGFRKBGRQCSGG*AGCGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SQQGSGAMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRGP*AAGRSTPAVP*PCS*CGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPCGSGFTGAGRSHTLK AARSILSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGPAASCSCSCRAPAKPASS/GBAPA PPPRPEPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCMGVMAPFAPK/NALSFLVNDCS	3/08	72.72	1723	1
GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAPGAPSPL RVSPASGGPRKEGROGSG*AGGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSGAMPPVGSSDTLRPRPTSVSGTG RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA*SRLGGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGSGSTGAGRSHTLK AARSRLSPRPGSGSRGSY*SINDNWGTWPAPPPAGAGHLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GBAPA PPPRPPPPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVIEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCMGVMAPPAPK/NALSFLVNDCS				
RVSPASGGPRKEGRQGSGG+AGGGGP\ARTHADLPCVGFVCSPP LLK+SDSPVKQLPA\SGQGSGAMPPVGSSDILRPRPTSVSGTG RAAG+CSWQPAACCTPRSQ+WAVARSPSRCSRM*RQSGR*RG+S SRRRGP+AAGRSTPAVP+PCS+GGAGRRAYACRTGWGYAPSR+ LEPSGPTSGSAL+TWASHSTGA+*SRLGGTAGTGPLCSQSSRS+ AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGSGETGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPRLPAAS/SGGASGSPAASCSCSCRAPAKPASS/GKAPA PPPRPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCMGVMAPPAPK/NALSFLVNDCS				
LLK*SDSPVKQLPA\SGQGSGASMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACCTPRSQ*Mavarspsrcsrm*rqsgr*rg*s SRRRRGP*AAGRSTPAVP*PCS*GAGGRAYACRTGWGYAPSR* LEPSGPT*GSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGSGETGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GKAPA PPPPRPPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLWVVTEAATPLGTYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPK/NALSFLVNDCS				
RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSRBGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGPLCPGIPLSGASPGSGSETGARRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA PPPRPEPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPK/NALSFLVNDCS		l	i	
SRRRGP+AAGRSTPAVP+PCS+GGAGRRAYACRTGWGYAPSR+ LEPSGPTSGSAL+TWASHSTGA+*SRLCGTAGTGPLCSQSSRS+ AG*RCCCTAASPCGGGGPSFBGSPSAHCLSWGGGRTQPRAPSAH GRGRAMGSRCVCTCTGPCPGIPLSGASPGGSGETGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH+YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA PPPRPEPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCMGVMAPFAPK/NALSFLVNDCS				
Lepsgptsgsal+twashstga+*srlcgtagtgplcsqssrs+ AG*rcctaaspcggsgpshpgspsahclswsggrtqprapsah Gagramgsrcvctctglpcpgiplsgaspggsgesetgagrshtlk Aarsrlsprpgsgsgsy*shndnwgtwpapppaghllvgg*ns Qrtssdh*ytgtrrpwagpgtrcstapsraappvsrcrppppp pprpprlpaaas/sggasgspaascscscrapakpass/gkapa ppprpppppppparrp  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGTYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCMGVMAPFAPK/NALSFLVNDCS				
AG*RCCCTAASPCGGGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGBTGAGRSHTLK AARSRLSPRPGSGSRGSY*SINDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GBAPA PPPRPPPPPPPPPPPRRP  5709 2 2031 ITLCPLPQTEKCLNVVIEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPPAPN/NALSFLVNDCS				
AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GBAPA PPPRPEPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGTYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRC%GVMAPFAPR/NALSFLVNDCS				
ORTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GRAPA PPPRPEPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGTYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRC%GVMAPFAPR/NALSFLVNDCS				
PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GRAPA PPPRPEPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGTYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS				AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
PPPRPEPPPPPARRP  5709 2 2031 ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS				QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPPP
5709 2 2031 ITLCPLPQTBKCLNVVIBAATPLGIYLKARVEAGGLKBLEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS				·
LHQIVVRWGAVVMRAGMGGCRC#GVMAPFAPR/NALSFLVNDCS				
	5709	2	2031	
LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE				
	L	<u> </u>	<u> </u>	LIHNNVCMAAVEVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE

		14712	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /-possible nucleotide deletion,
L	sequence		\⇒possible nucleotide insertion)
			LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA
į.			ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFM
1		•	SNRFVETNLFLEEIQIKEPAEKQKPFQELSKSLDAPPEDFCRHK
			VLPQLLTAPEFGNAGAVVLTPLFKVGKFLSAREYQQKIIPVVVK
l	1		MFSSTDRAMRIRLLQQMBQFIQYLDEPTVNTQIFPHVVHGFLDT
			NPAIREQTVKSMLLLAPKLNBANLNVBLMKHFARLQAKDBQGPI
			RCNTTVCLGRIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV
l			LGFAATHNLYSMNDCAQKILPVLCGLTVDPBKSVRDQAFKAIRS.
l	ľ		FLSKLESVSKDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG
	Į.		VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT
1	1		TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAQQD
1	i		DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA
	L		CAKLPGATS+RYTAGQRV
5710	1	562	IPGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK
	1	·	VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
	1		\LNGHDYMRNIVHLPVFLNSRGL/RQ/LQENFS*LQQQMETFHA
	1		QILQGYRKYLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV
L			CIAIQFNTNKDDAT
5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFYPDSAQPFIVKSESS
1	İ		SQIAKAVLSQQRPSLFHECAFHFFS*SLQRHTINLDQGIF+LLM
İ			LSEBROHLFESS/IWTTPHNLK*/FBIHEHLGSHBGHWTLFFLL
L			ΔIΓ
5712	3	1391	GRKLFQSLDISERLKFLLTLDCVDDTLIVLAERHGCLDIIKELP
1	}		BTVIDLINKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA
1			SLFSSSLRCADLTLPRDISQLCKDINNDYLAERSIEEVYYLWCL
1			AGGDLEKELVNKBIIRSKPPICTLPNFLFEDGESFGQGRDRSS/
	ĺ	1	TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN
1			NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK
	1	•	EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI
1	,	.v.	EVDIPRCHQYDBLLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD
i	Í		SLCAPFLYINFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL
			HKIFHLW\DTILLGEFLFPILYWE
5713	734	284	PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH
5/13	634	404	TACRCSRRGAQVQHLPREDIRAAB*DPHLREVWPGLPTSSATSP
Į.	i		*RAVLTSPCSHLGSADAASSHWLCGVSPH
5714	212	613	WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSSGPKAGAAD
2/14		913	KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS
	}		HYSSFGSSGGSGMMGGESADKATAAAAAASLLANGHDLAAA
	1	ł	MA
5715	131	1979	ESASOOKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQB
3,12	1	,,,,,	QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
l .	1		GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVRNN
1			DSTCHKHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS
]		İ	PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS
	1		QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR
ľ	i .		TOAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL
	1		YPKTPKQRRWRRPL/LLGPSQ+GSRQSTC+EV\GALGEPVRIPG
[			L*PDLSCILENGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
			PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
1	1		VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE
1			EGPLRLPGODRGAOPCSHCPGRAAGOPEPGAGAPCRE/GG*DPT
Ī			GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E
	I		ROE/VGAGASSGVGLSRGRAGGPSSAWKVAAMLLLLRHGSHSEL
	1		TDLTEAQTSQH
5716	1711	1370	RVFSLLCEGPGHCYOGAVCREACAAASPGLDSAAEPHRLCEHTD
2/16	1711	1370	*LPK*GPGYIOHFHCDSNILCILYNISFNLFSYSF*GVARYAC*
ŀ	1		RCPLVL*SGFFTIIVGGYSCCMPLKT
5717	<del> </del>	1489	LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD
3/1/	44	1403	EGPGALVLESDILLGQDLEFEREEEEEFGDGNSDQLMGFERDSB
L	I	<u> </u>	EGLOUPARSONINGATURE PREFERENCIAMONOTALIA BROSE

[ GDO	There are a second	1 8 32 25 2 3 2 5 5	
SBQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=bysine,
į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	} "	\=possible nucleotide insertion)
			GDSLGARPGLPYGLSDDESGGGRALSABSEVEEPARGPGEARGE
i			RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFV
l		ĺ	SHYSSHLKRHMQTHSGEKPPRCGRCPYASAQLVNLTRHTRTHTG
1	İ		EKPYRCPHCPFACSSLGNLRRHORTHAGPPTPPCPTCGFRCCTP
İ			RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
i			Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGQKLEEGEGSRLG
			AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYPNHLA
1		į	RHMKTHSGEKPFRCARCPYASAHLDNLKRHORVHTGKKPYKCPL
L			CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
5718	120	284	VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT
		400	S**STADPLHL
5719	48	428	BLNINGPFOMPLCNGGNLAVTGSWADRSPLHRAASQGRLLALRTL
			LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
5720	1	1051	IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRAKKLSTDLK
3/20	1 1	TAST	LQAFKNASEVPMVLVGTQDAISAA\NPKVYRKTSKARKLSTDLK   \RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
ľ			GPCK\SLPN\SP8H\SAVSAASIPARAPINOGHE/SGGGSAFSD
			Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
			RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
}			EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG
1			KRLPRATPATAPGTSPRANGLSVERSNTOLGGGTGAPHSASSAS
			LHSERPLSSSAVAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
<b>I</b> .	'		QHPASG
5721	97	492	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
i			VFYATAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
L			SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
5722	88	1043	VALDVLAGSSPGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
1			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
1			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPAPA
			PPPPPHLGALTAGSGEERQSQPRABTLRLGRGAPLP\PRAERGG
1			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
		,	KSSTREIPEMI
5723	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGTRAVLRVARGGVOAPGAP
		•	GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPREPRFP
1			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
	i		GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
]			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA
			PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRABRGG
	ľ		RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
			KSSTREIPEMI
5724	3	1841	FINEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLINFK
			KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVAERAADLDGEID
			LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI MKHVHPTTAPDVTSSLPKEKNKSSCSFETCPRPTEKOKAKLGEP
			DPEQKRSRARE\RRREGRSKTFDWAEFRPIQOALAOERVGGVGP
	l		DPBQRKSKARE\RRKEGRSKTFDWAEFRPIQQALAQERVGGVGP ADTH\DPWRPEARHGELERERARRREERRKRFGMLDATDGPGTR
			DAALRMEVDRSPGLPMSDLKTHNVHVETEQRWHQVETTPLREEK
			QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSQKEASDLLEQ
			NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMKETHQKKIE
			DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME
	İ		RELEKSQRSQISSVNSDVEALRROYLERLQSVORELEVLSEOYS
	1		QKCLENAHLAQALEABRQALRQCQRENQBLNAHNQBLNNRLAAB
	j		ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTOLC
			TOEPOGSAAWPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEQ
5725	3	1049	VNGHSKETSQSPNRTEPHDSDCSVDLGISKSTEDLSPOKSGPVG
		-	SVVKSHSITNMRIGGLKIYDILSDN\DLSSHLQPLK/PTSAVDG
			KNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN
L [			PB/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA

SEQ	Predicted	Predicted end	I hmino pold possession
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
í	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ı	sequence	sequence	\=possible nucleotide insertion)
	Joquence	<u> </u>	LQTKSPNRPCQF5SSAPS/VDQRAQ/INQSYAKHSANMNFSNHN
\		ì	DOLASPARPOGESSAPS/VDQRAQ/LAQSYAKHSANMAPSNHN
	i		NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS
		*	SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG
i		Ì	SQRPLSARTYSIDGPNASRPQSARPSINBIPERTMSVSDFNYSR TSP
5726	2	486	
3/20		400	SRSLSMWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP
l .	1		TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG
ı	}	<b>j</b>	QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT
			GLIPHLCQARTPPYLQLQVTEKQVLLRADDG
5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDQASCEVI:TVKKK
C200			AGAVTSTPNRNSSKRRSSL?NGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG
1			NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPCAPDPPAVE
!	}		GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ
1			GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDWIPGPQGLWL
1	1		HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED
	ļ		BPPQVPEAGEEDAVPAEEGPGGTPETQADQVRERPEAHLAEGGA
5729		1505	KGSPRRLADPQDLPAGQMSLAPPFPPVAAVIRSNK
5/29	1	1525	AGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKEPPGEL
ĺ	ĺ.		CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKREGGLYRDK
i	[		QLDAAIAWQGKLTTHKBBLYPKNPYLQDFLSAEGVLSSDGVWRV
			KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI
1			CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE
1	Į	•	CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLP
			GPYHRGEAQRNIYRLINTAFGLVHLTAHSSLVCPLSLGGSLGLR
ļ			PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLCSSPVS
() ·			MVHL\ADMLSFCGKKVVTAGAIIPFPLAPGQSLPDSLMQFGGAT
1			PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA
i i			LHACTTGERILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS
5730	1258	1713	SCSPPGMVLDGSPKGAAVESVPVFG
ا 3،30	1236	1713	KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT
İ			KIETEGFWERPRNFENGGRPLKSPGGEDCPSC*GGCPGSNY*AQ
			GSSSREKGGQASWNPKLRVA
5731	122	443	RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI
3,31	122	443	BPSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK
!			KPGRGRGKQRRQEWFFLRVY
5732	226	772	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF
مدرر	Oaa	112	
			PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA
[			QVSTNLLDFEVTALHTVYEETCREAQELSLFVVGSQLVGLVPLK
			ALLDAA
5733	1	460	PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES
	_	400	
[			MRTACSPDGLCSDGNGLELKCPPTSRDFMKFRLGGFEAIKSAYM
			AQVQYSMWVTRKNANYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM
5734	3	968	
513%	٠	900	RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIF?IVFTVI
			GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFBVLS
			SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY
	]		GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG
			HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC
			VFIVYYLLEMLLRVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS
			TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP
			SMKPMAVVASTVLGL
5735	2	540	FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL
			atprqlyk/ssnmtqrwqrreisnfeylmplntlagrtyndlnq
	<b>]</b>		YPVFPWVLTNYESBELDL/TLPGNFRDLSKPIGALNPKRAVFYAE
			RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY
			LKILT
5736	1	382	GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
J	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	ведиелсе		\=possible nucleotide insertion)
			TARLSVIPPNLLPTVSFPQPDLPDNPVYSTTTRKLASDLRANKN
1		1	QES**ILPDSGIFIP*T*TSYLQSTTHLRRAKLPQLLRR
5737	290	1041	KACLHLLSSFLTSNFLFNPLLPDSLYSVEARSQRANLGPCRRKR
1		İ	LQTLMRLAAGFQYSSHKDPSLSAKEKETDYHNEARGPWPGWVG*
1		]	RTADGSCGRGPDGAHHPGPKSSSWRASRLLPGLGGSHHLDAYVG
1			RDLECGTPAPLQLEIPPQPRGHPAPIPTGQAGPRDSGPGASP*V
1			ETRPLTDGRR*PGVRPVGWTPAHPAGTLRPRGAVEPSVSACGKW
1			APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
5738	8	460	DTLSINCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTYSNEV
1			VTLWYRPPDILIGSTDYSTQIDMN*GQVEVWQGPCGKGGGLVTT
1		İ	ATQPAAFLFTVPSLPRGVGCIFYEMATGRPLFPGSTVBEOLHFI
1			FRILSERAWALCAVETHR
5739	1	1222	SFORRGIRWNVHTLHPHPRAVWAGIGRGHGS+ALLGRARAPALC
	~		PPTLLEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEV
l		[	SAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI
	ŀ	l	LOCOGFYQLCGVHORDVIYLALPLYHMSGSLLGIVGCMGIGATV
1	l		VLKSKPSAGOPWEDCOOHRVTVFOYIGELCRYLVNOPPSKAKEG
1	j		HKVRLAVGSGLRPDTWERFVRRFGPLOVLETYGLTEGNVATINY
1			TGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATS
ł			
]			PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVAEVFRALDF
1			LORVNYGVTV
5740	265	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A
3,40	403	231	YVYERVYN*NISRMVHALEQKRHPAGLSSSMALQLNPCLGMLMA
			LQSELHKLYDBETQSWVSGSACGGYP
5741	1	650	
3/41	*	630	PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD
3/41		630	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE
3/41		650	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT
3/41	*	650	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV
			YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK
5742	2	362	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNITDKDGNTALMIASKEGHTEIVQDLLDAG
			YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE GGKRHTISRRRVIPLPQWKANPBTDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKRGHTBIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK
5742	2	362	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTBIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG
			YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMYRDILQCNPDTEICTKDG GKTPEGIDAIEEIBIDLEETEREISPQENGLEEVKPLGEMQTDL
5742	2	362	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEB
5742	2	362	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPOWKANPETDPEALFOKEQLVLALYPOT TCYYRALIHAPPORPODDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGODSRGRAGIKHIPPLKKK TOSVKEILKRNPNVNLTDKDGNTAIMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLOXYADIDIRGODNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEBIBIDLEETEREISPOENGLEEVKPLGEMOTDL KATGREISPRETPEVIDATEBIDKDLETGRREISPEENGPEB VKPVDEMETDLKTTGREGSSRBKTREVIDAABVIETDLEETERE
5742 5743	2	362 415	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTISRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDILDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPRETPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE
5742	2	362	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE  GKERHTLSRRRVIPLPQWKANPBTDPEALFQKEQLVLALYPQT  TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKOGNTALMIASKEGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK  TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIKEIBIDLEFTEREISPQENGLEVKPLGEMQTDL  KATGREISPRETPEVIDATEEIDKDLEFTGRREISPEENGPEE  VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA
5742 5743	2	362 415	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTBIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIBIDLBETERKISPQENGLBEVKPLGEMQTDL KATGREISPRETPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEKATGLLTPEPSKEGPILTAESETVLP
5742 5743	2	362 415	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPBTDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLFBDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSSGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIKEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEBIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLGLTPSTLPERATGLLTPEPSRRGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMMKTSDSVSS
5742 5743	2	362 415	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTISRRVIPLPQWKANPETDPEALFQKEQLVIALYPQT TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQXYADIDIRGQDNK TALWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIBIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEKATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLITSKESKVMDLPSTSHVSMMKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLIMITAP
5742 5743	2	362 415	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTISRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDILDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQXYADIDIRGQDNK TALWAVEKGNATMVRDILQCNPPTEICTKDG GKTPEGIDAIEEIBIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPRENTPEVIDATERIDKDLEETGREISPEENGPEB UKDVDEMETDLKTTGREGSSREKTREVIDABKVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEKATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLIMIIAP SLGFVLFALFVAFLLFCKLMETYCSQKHTRLDYIGDSKNVLNDV
5742 5743 5744	2	362 415 703	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE  GKERHTISRRVIPLPQWKANPBTDPEALFQKEQLVLALYPQT  TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASREGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK  TALYWAVEKGNATMVRDILQCNPDTBICTKDG  GKTFEGIDAIEBIDLEFTEREISPQENGLEEVKPLGEMQTDL  KATGREISPREKTPEVIDATEBIDKDLEFTGREISPEENGPEB  UKPVDEMETDLKTTGREGSSRBKTREVIDABVIETDLEETERE  LSPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKRGPILTAESETVLP  SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMKKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP  SLGFVLFALFVAFLLRGKIMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL
5742 5743	2	362 415	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE  GKERHTLSRRVIPLPOWKANPETDPEALFOKEQLVLALYPOT  TCYYRALIHAPPORPODDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKOGNTALMIASKEGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK  TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEBIBIDLEFTEREISPQENGLEVKPLGEMQTDL  KATGREISPRETPEVIDATEEIDKDLEFTGREISPEENGPEE  UKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP  SOSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKKTSDSVSS  POPGASDTAVPEQNKTTKTGQNDGIPMSMKNEMPISQLIMIIAP  SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL  GKSRFVNLMKHSKRTYDSFQDELEDYIKVQKARGLEPKTCFRKM
5742 5743 5744	2	362 415 703	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPBTDPEALFQKEQLVLALYPQT TCYTRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTBIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLBETEREISPQENGLBEVKPLGEMQTDL KATGREISPRETPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEKATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMWKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLIMITAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKERFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTTPRSCNIPQT
5742 5743 5744	2	362 415 703	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTISRRVIPLPQWKANPETDPEALFQKEQLVIALYPQT TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQXYADIDIRGQDNK TALWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIBIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPRESTPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLISKESKVWDLPSTSHVSMMKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLIMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDBEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE
5742 5743 5744	2	362 415 703	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE  EGKERHTISRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT  TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDILDAG  TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQXYADIDIRGQDNK  TALWAVEKGNATMVRDILQCNPPTEICTKDG  GKTPEGIDAIEEIBIDLEETEREISPQENGLEEVKPLGEMQTDL  KATGREISPRENTPEVIDATERIDKDLEKTGRREISPENGPEB  VKPVDEMETDLKTTGREGSSREKTREVIDABVIETDLEETERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKRGPILTAESETVLP  SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP  SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QEGREDEDELFTL  GKSRFVNLMRHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT  VERNLPQWLPAHDSRLRLDSLSXCQFTRDCFSEKFVPLNFNQQE  YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR
5742 5743 5744	2	362 415 703	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE  GKERHTISRRVIPLPQWKANPBTDPEALFQKEQLVIALYPQT  TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK  TALWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEEIBIDLEFTEREISPQENGLEEVKPLGEMQTDL  KATGREISPRETPEVIDATEEIDKDLEFTGREISPEBRGPEB  VKPVDEMETDLKTTGREGSSREKTREVIDAAFVIETDLEFTERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKRGPILTAESETVLP  SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKTSDSVSS  PQDGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP  SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL  GKERFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPESTIQTTPRSCNIPQT  VENNLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE  YICGSHGVERRVYKHFSSDNSTSTHQASIKQIHORKKRHPBEGR  EKSERBRSKHKRKKSCEEIDLDKHKSIQRKKTEVBIETVHYSTE
5742 5743 5744	2	362 415 703	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE  GKERHTISRRVIPLPOWKANPBTDPEALFOKEQLVIALYPOT  TCYYRALIHAPPORPODDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASREGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGODNK  TALYWAVEKGNATMVRDILQCNPDTBICTKDG  GKTPEGIDAIEBIDLEFTEREISPQENGLEEVKPLGEMQTDL  KATGREISPREKTPEVIDATEBIDKDLEFTGREISPEENGPEB  UKPVDEMETDLKTTGREGSSRBKTREVIDABAVIETDLEETERE  LSPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP  SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSKNEMPISQLLMIIAP  SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL  GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTTYPRSCNIPQT  VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE  ZKSEBERSKHKRKKSCEBEIDLDKHKSIQRKKTEVEIETVHVSTR  KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI
5742 5743 5744	2 3 3	362 415 703	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE  GKERHTISRRVIPLPQWKANPBTDPEALFQKEQLVIALYPQT  TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK  TALWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEEIBIDLEFTEREISPQENGLEEVKPLGEMQTDL  KATGREISPRETPEVIDATEEIDKDLEFTGREISPEBRGPEB  VKPVDEMETDLKTTGREGSSREKTREVIDAAFVIETDLEFTERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKRGPILTAESETVLP  SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKTSDSVSS  PQDGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP  SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL  GKERFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPESTIQTTPRSCNIPQT  VENNLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE  YICGSHGVERRVYKHFSSDNSTSTHQASIKQIHORKKRHPBEGR  EKSERBRSKHKRKKSCEEIDLDKHKSIQRKKTEVBIETVHYSTE
5742 5743 5744	2	362 415 703	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE  GKERHTISRRVIPLPOWKANPBTDPEALFOKEQLVIALYPOT  TCYYRALIHAPPORPODDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASREGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGODNK  TALYWAVEKGNATMVRDILQCNPDTBICTKDG  GKTPEGIDAIEBIDLEFTEREISPQENGLEEVKPLGEMQTDL  KATGREISPREKTPEVIDATEBIDKDLEFTGREISPEENGPEB  UKPVDEMETDLKTTGREGSSRBKTREVIDABAVIETDLEETERE  LSPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP  SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSKNEMPISQLLMIIAP  SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL  GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTTYPRSCNIPQT  VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE  ZKSEBERSKHKRKKSCEBEIDLDKHKSIQRKKTEVEIETVHVSTR  KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI
5742 5743 5744	2 3 3	362 415 703	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE  GKERHTLSRRVIPLPQWKANPBTDPEALFOKEQLVLALYPQT  TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK  TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIKEIEIDLEFTEREISPQENGLEEVKPLGEMQTDL  KATGREISPRETPEVIDATEEIDKDLEFTGREISPEENGPEE  UKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE  LSPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP  SDEWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP  SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL  GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT  VENRLPQWLPAHDSRLRUDSLSYCQFTRDCFSEKEVPLINFNQQE  YICGSHGVEHRVYKHFSSINSTSTHQASHKQIHQKRKHPBEGR  EKSEEBRSKHKRKKSCBEIDLDKHKSIQRKKTEVEIETVHVSTE  KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEKEMLWDQSI  LGF
5742 5743 5744	2 3 3	362 415 703	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE  GKERHTLSRRVIPLPQWKANPBTDPEALFOKEQLVLALYPQT  TCYYRALIHAPPORPODDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK  TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEBIBIDLEFTEREISPQENGLEEVKPLGEMQTDL  KATGREISPRETPEVIDATEEIDKDLEFTGREISPEENGPEB  VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLOMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP  SOSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMMKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLIMIIAP  GKGRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT  VERRLPOWLPAHDSRLRLDSLSYCOFTRDCFSEKPVPLNFNQQE  YICGSHGVHENVYKHPSSDNSTSTHQASHKQIHQKRKRHPEEGR  EKSEBERSKHKRKKSCBEIDLDKHKSIQRKKTEVEIETVHVSTE  KLKNRKEKKSRDVVSKKEERKTYKKKKEQGQERTEEEMLWDQSI  LGF  SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES
5742 5743 5744	2 3 3	362 415 703	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTISRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQXYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIBIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPRERTPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEKATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLISKESKVWDLPSTSHVSMWKTSDSVSS POPGASDTAVPEQNKTTKTGQMEGIPMSMENEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDBOGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGSVUSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKEVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEBERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGGERTEEEMLWDQSI LGF SFASGRLTFSSPAFDGELDLORYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE
5742 5743 5744	2 3 3	362 415 703	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE  EGKERHTISRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT  TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDILDAG  TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQXYADIDIRGQDNK  TALWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL  KATGRBISPREBTPEVIDATEBIDKDLEETGRREISPEENGPEB  VKPVDEMETDLKTTGREGSSREKTREVIDABVIETDLEETERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPEHATGLLTPEPSKEGPILTAESETVLP  SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLIMIIAP  SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDELFTL  GKSRFVNLMRHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT  VENRLPQWLPAHDSRLRLDSLSVCQFTRDCFSEKPVPLNFNQQB  YICGSHGVEHKVYKHPSSDNSTSTHQASHKQIHQKRKHPBEGR  EKSEBERSKHKRKKSCEBIDLDKHKSIQRKKTEVBIETVHVSTE  KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEREMLWDQSI  LGF  SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLCMGAVSWSES  RAGERFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE  LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP
5742 5743 5744	2 3 3	362 415 703	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE  GKERHTISRRVIPLPOWKANPETDPEALFOKEQLVIALYPOT  TCYYRALIHAPPORPODDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASREGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGODNK  TALYWAVEKGNATMVRDILQCNPDTBICTKDG  GKTPEGIDAIEBIDLEFTEREISPQENGLEEVKPLGEMQTDL  KATGREISPREKTPEVIDATEBIDKDLEFTGREISPEENGPEB  UKPVDEMETDLKTTGREGSSREKTREVIDAARVIETDLEETERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKRGPILTAESETVLP  SDSWSSASETSADTVLLITSKESKVWDLPSTSHVSMMKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP  SLGFVLFALFVAFLLRGKIMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL  GKSRPVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCPRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTTYPRSCNIPQT  VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQOE  YICGSHGVEHRVYKHPSSDNSTSTHQASHKQIHQKKRHPBEGR  EKSEEBRSKHKKKSGEBEIDLDKHKSIQRKKTEVBIETVHYSTR  KLKNRKEKKSRDVVSKKEERKRTKKKKEQGERTEEEMLWDQSI  LGF  SFAGGRLTPSSPAFDGELDLORYSNGPAVSAMSLGMGAVSWSES  RAGERFPCPVCGKRFRFNSILALHLRTHQPERPRSPARRLLLE  LEERALLREARLGRARSSGMQATPATEGLARPQAPSSSAPRCP  YCKGKPTSAERERHIHILHENPKCGLCSFGSSQKEELLHHSLT  AHGAPERPLAATSAAPPPQPQPPPPPPPRSVPQPEPPPPER
5742 5743 5744	2 3 3	362 415 703	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE  GKERHTLSRRVIPLPQWKANPBTDPEALFOKEQLVLALYPQT  TCYYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG  TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK  TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIKEIEIDLKETEREISPQENGLKEVKPLGEMQTDL  KATGREISPRETPEVLDATEEIDKDLEETGREISPEENGPEE  UKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP  SOSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP  SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL  GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT  VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKEVPLINFNQQE  YICGSHGVEHRVYKHFSSINSTSTHQASHKQIHQKRKHPBEGR  EKSEBERSKHKRKSCGEIDLDKHKSIQRKKTEVEIETVHVSTR  KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI  LGF  SFASGRLTPSSPAFDGELDLQRYSNGPAVSAMSLGMGAVSWSES  RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPSPAARLLLE  LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP  YCKGKFRTSAKERHIHILHLRPNKCGLCSFGSSQBEELLHHSLT  AHGAPERPLAATSAAPPPQPQPPPPPEPRSVPLKGHMRKHKA
5742 5743 5744	2 3 3	362 415 703 599	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTISRRVIPLPQWKANPETDPEALFOKEQLVIALYPQT TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNITDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQXYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIBIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEKATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLISKESKVWDLPSTSHVSMWKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDBOELFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGGVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKFVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGRETEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLORYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPOAPSSSAPRCP YCKGKFRTSAERERHLHILHRPMKCGLCSFGSGREELLHHSLT AHGAPERPLAATSAAPPPPQPQPPPPPEPRSPPARPLERE EATPTTPAPAAPBERPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV
5742 5743 5744 5746	2 3 3 3 3	362 415 703	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE  EGKERHTISRRVIPLPQWKANPETDPEALFQKEQLVIALYPQT  TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV  ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDILDAG  TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQXYADIDIRGQDNK  TALWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL  KATGREISPRETPEVIDATEEIDKDLEETEREISPEENGPEB  VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE  ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA  VFTTANTCLSLTPSTLPEKATGLLTPEPSKEGPILITAESETVLP  SOSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMKTSDSVSS  POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLIMIIAP  SLGFVLFALFVAFYLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV  QHGREDEDGLFTL  GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM  KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT  VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKEVPLNFNQQB  YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKHPBEGR  EKSEBERSKHKRKKSCEBIDLDKHKSIQRKKTEVBIETVHVSTE  KLKNRKEKKSRDVVSKKEERKRTKKKKEQGERTEEEMLWDQSI  LGF  SFASGRLTPSSPAFDGELDLORYSNGPAVSAMSLGMGAVSMSES  RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE  LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP  YCKGKFRTSAERERHLHILHRPWKCGLCSFGSQEELLHHSLT  AHGAPERPLAATSAAPPPQPQPPPPPPREPRSPAPGRKHKA  SFDHACPV  DRHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG
5742 5743 5744 5746	2 3 3 3 3	362 415 703 599	YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE EGKERHTISRRVIPLPQWKANPETDPEALFOKEQLVIALYPQT TCYYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNITDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQXYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIBIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEKATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLISKESKVWDLPSTSHVSMWKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDBOELFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGGVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKFVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGRETEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLORYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPOAPSSSAPRCP YCKGKFRTSAERERHLHILHRPMKCGLCSFGSGREELLHHSLT AHGAPERPLAATSAAPPPPQPQPPPPPEPRSPPARPLERE EATPTTPAPAAPBERPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV

PCT/US00/34263

		1 - 10 - 1 - 2	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K≈Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l .	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į.	sequence	Sequence	\=possible nucleotide insertion)
	Bequence		
1		İ	SDNGDINYDYVHELSLEMKRQKIQRBLMKLEQENMEKREETIIK
ı	1		KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
l	ľ	į.	AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKE
1		ļ	KYKVKDRIEEKTRDGKDRGRDFBRQREKRDKPRSTSPAGQHHSP
l .		1	ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYQRTLTPPLRRS
	1		ASPYPSHSLS8PQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH
l	•		ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
			RK
5748	934	473	SEGPOVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEG
3740	7,74	1,3	KKNENLONLLOGSGAGVISKTLTYPLDLFKKRLQVGGPRHARAA
ł	į.	ł	1
			FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSILKAALSTGFM
			FFSYEPFCNVFHCMNRTASQR
5749	552	1	GFPVDPRVRGSTLSLARRPKGMIRSGSFRDPTDDVHGSVLSLAS
1		I	SASSTYSSAERRMQSEQIRKLRRELESSQRKVATLTSQLSANAN
1	1	Ī	LVAAFEQSLVNMTSRLRHLAETABEKDTELLDLRETIDFLKKKN
			SRAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI
			GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIQF
1		1	HLEWAYVFLYYYBYRKAKDQLDIAKDISQLQIDLTGALGKRTRF
1		1	QENYVAQLILDVRREGDVLSNCEFTPAPTPQEHLTKNLELNDDT
			ILNDIKLADCEQFOMPDLCABBLAIILGICTNFQKNNPVHTLTB
i .		İ	
l			VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ
1	1		TOALADQPEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
	<u> </u>		GCTSSALQIFEKLEMWE
5751	3	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA
	ł	1	FAAGETFLVLERSSAHWWLAARARSGETGYVFPAYLRRLQGLEQ
1	Ì		DVLQAIDRAIBAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
		1	RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
ļ	l	į.	SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPVKRRDREA
i			LMASGSGGHNTMPSGGNSVSSGSSVSSCI
5752	3	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGARLPCLSGAAT
		1	veremelrhknemlrvetbararakaerenadiireqirlkase
1		i	HRQTVLESIRTAGT_FGEGFRAFVTDRDKVTATVN1F1KQGWQV
			AEROHVGASWSPRSCPCRLCTAL
		402	
5753	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
l		I	GOEAFKKINYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK
I		1	PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
1			TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEFAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
	1	1	ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
			WPTPATPSPLTAPFSMB
5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI
	[	]	WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
1		1	PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQBIQ
1		<b>.</b> .	RVLENDENVERGNEREDLEEDIPKRKNRTRGRARGSAGGRRRHD
Ī	1		AASOEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDBAO
1		1	
1	1	[	DOETRSPPNHRNKNHRPOKGPDGTVTPNNYCDFCLGGSNMNKKS
	L	<u> </u>	GRPEELVSCADCGRSAHLGGEGRKEKEAAA
5756	3	621	SSKLQALFAHPLYNVPERPPLLGABDSLLASQEALRYYRRKVAR
1	1		WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR
1		1	SSPVVSKILQDMRHFPTISADYSQDKKALLGACDCTQIVKPSGV
			HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI
	1		AAFHLDRILDPRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHROVYFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
3/3/	1	313	LSISQSVHVAVKVPPLIQPFEPPPASIGQLLXIPCVVSSGDMPI
1	Į.	1	
1			RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
			ASNAAATVSRRRQLIVRVPPRFVV
5758	1	474	FRRGAGAERGEHREGERGAAGMGEPKVHRVRFFNYVPSGIRCVA
	l	1	YNNQSNRLAVSRTDGTVEIYNLSANYFQEKPFPGHESRATEALC
		l .	WARGORLFSAGLNGRIMEYDLQALNIKYAMDAFGGPIWSMAASP
	<del></del>	L	

	¥		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to Eirst	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of.	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	sequence	\=possible nucleotide insertion)
	sequence	ļ	
			SGSQLLVGCRDGSVKLFQITPDXIPV
5759	2	1240	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR
		1	MAKSSPYPTDVARVVNAPIPHVNADDPBAVIYVCSVAAEWRNTF
			NKDVGADLVCYRRRGHNEMDBPMFTQPLMYKQIHRQVPVLKKYA
			DKLIAEGTVTLQEFEEEIAKYDRICBEAYGRSKDKKILHIKHWL
			DSPNPGFFNVDGRPKSMTCPATGIPEDMLTHIGSVASSVPLEDF
		i	KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL
			NGODVERGTFSHREHVLHDQEVDRRTCVPMNHLWPDQAPYTVCN
	1		SSLSEYGVLGFELGYAMASPNALVLWEAQFGDFHNTAQCIIDQF
		ł	ISTGQAKWVRHNGIVLLLPHGMEGMGPRHSSARPERFLQMSNDD
	1	ì	
			SDAYPAFTKDF3VSQL
576C	1	1221	VRDITSDSLSLSWTVPEGQFDHFLVQFKNGDGQPKAVRVPGHED
	1	Į.	GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA
		1	PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGQFDHF
		1	LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG
		]	CRVGPVSAIGVTAAERETPTPTEPSMEAPEPPEEPLLGELTVTG
	ŧ	1	SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPQVVRVGGBESEVT
	į.	1	VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP
	1		TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT
	}	1	VOYKDRDCRPQAVRVGGQESKVTVRGLBPGRKYKMHLYGLHEGR
	i		RLGPVSAIGVT
5761	3	1275	SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCQDQN
2/61	}	12/3	VPVENPFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGPGSML
	ľ		
	1		RALGAQIBKTTNRRACRDLSGRRLRDVNHEKAMAEWVKQQAERE
	Ì		AEKEQKRLERLQRKLVBPKHCFTSPDYQQQCHBMAERLEDSVLK
		,	GMQAASSKMVSAEISENRKRQWPTKSQTDRGASAGKRRCFWLGM
		1	egletaegensesedddserapstsgmgfhapkigsngvemaak
	1 .		FPSGSQRARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK
	1	1	KHMESRMVTETERTORKKAESKEPIREEPTGAGLNKDKETEERT
	l		DGERVAEVAPBERENVAVAKLQESQPGNAVIDKETIDLLAFTSV
9		·	ARLELLGLEKLKCELMALGLKCGGTLQ
5762	2	344	GSTGQTPLHSQGGGGGGGGGRRRTPRGMPKEKYEPPDPRRMYTI
			MSSERAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN
	<b>,</b>		SLSRIPSDIAKLHNLVYLDLSSNKIR
5763	3	129	LDKDTGLIMLIARLDYELIQRFTLTIIARDGGGEBTTGRVRINV
3703	1	12.5	LDVNDNYPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ
		ł	ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL
	1	1	
			TVMAMDAGN
5764	19	441	VCARACGEMRQLIRPIDRQRYDENEDLSDVEBIVSVRGFSLEEK
	1	1	LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK
	}	1	MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE
			TPBAORDKL
5765	3	825	QKILRLMNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS
	1	1	VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS
			STGKROKVOGRPGRATGMNSALGQSVSSGGSGNPNSNSTSTSTS
	1	1	AATAGAGSCGKSKEEKPGKSOSSRGAKRDKDAGKSRKDKHDLLQ
		1	GHONGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA
	1	(	GEVSKSAPDSGIMGNSMLVKKBEREERSHRRIKKLKTEKVDPLF
	1		
	<del></del>		TVPAPPPHV
5766	1608	663	SGLFSVDPASSQAMBLSDVTLIEGVGNRVMVVAGVVVLILALVL
1	1	1	AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPB
l	}	*	PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD
1	1		IQGLPKRQAGAGSSSPKAPLRSEDSTCLPPSPGLITVRLKFLND
l		J	TEBLAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL
1	}	i	RSINITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG
	1		SLMYPYFYYLLGYYWYFRINYRQFFTAPATYSLYGYTYFPSFLY
	l	· ·	FGMYGR
F762	<del> </del>	903	NFRATPRPPTRPELRTGTEVILWYLDWRALMKRKRMKANIKLVG
5767	2	892	
İ	1	1	SGFPLPSSDLDDSLTERIDEKIGFRNDANFDWQNVADFRDAGGS
L	1	L	LTEVKVBEBERDPQSPBFBIEEEBEMLSSVIPDSRRENBLPDFP

C 0770	T 8 3! - 1 - 3	37 - 3 - 3	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	
}	amino acid		P=Proline, Q=Glutamine, R=Arginine,
ł		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	1	\=possible nucleotide insertion)
<u> </u>			HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER
1	i	ĺ	
1		ł	LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV
i	į:		NSEKPSLENELGOGEKSMLQPQDIETEKLKLERERLQLEKDRLQ
!	ł	!	FLKFESBKLQIEKERLQVEKDRLRIQKEGHLQ
5768	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSORAGPA
	1	ł	AAMVAKDYPFYLTVKRANCSLELPPASGPAKDABEPSNKRVKPL
1	i	ľ	SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSBSRPDILAPRP
1	l .	l	
		Ĺ	WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
	1		TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN
1	i .		DRCVEVIAKEGONLKELYLVSCKITDYALIAIGRYSMTIETVDV
I	0		GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY
1	!	1	
F	<del> </del>		PHITPSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
1	1		FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAGVNFAI
1		l	AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
1			WBQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS
"	100	/**	
1	<b>,</b>		FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIQQPAMLLRE
1			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
	]	j	LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
1			AFHRLLADITHDIB
5772	148	383	RENLALVSPSHPQIKARDDOPLPGVLLSLSGGLFRSNLLTODNG
1			ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWOLRIAAGE
37.73	•	123	
1	1		KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
			DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
1			LRQYNIVGLHINIDFLLNLSGHPEFEAGNVHTDFIPQHHKQLLL
			SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG
			RRLNISYTRNMTLKDGKNSK
5774	· 2	592	FVBBENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
	_	372	
1 .			VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI
			DGILIKTFIVGCKLHALFTLAQARDSVFVIVNKEKPDIFQLVSV
			KLPKSSSQRVRAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
			YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPV8KCPKKSBSLWKGWDRKAQRNGL
1			RSQVYAVNGDYYVGEWKDNVKHGKGTOVWKKKGAIYEGDWKFGK
] 1			RDGYGTLSLPDQQTGKCRRYYSGWWKGDKKSGYGIQFFGPKEYY
<b>,</b>			BGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP
			RP
5776	2	484	RLPODCVCONLSKSLGTLCPSKGLLFVPPDIDRRTVELRLGGNF
			IIHISRODPANMTGLVDLTLSRNTISHIOPFSFLDLESLRSLHL
ł I			DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL
			EDLDLSYNNLHGPAVGLRGDANVQPSTS
5777	2	0.6.0	
ا '''' ا	4	949	GODPEPGQDLFQPEREVDPSWGRGREPRLGKLRFQNDHLSVLKQ
1 I	<b> </b>		VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKARAGSTLPKNLG
] !			GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
)			YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGPRKEKR
[ ·			NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
		İ	
; I	i		DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
			YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ
			MSERRNV
5778	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAREPGS
			GGPCWLQLBEVPGPGPLGGGGPLRSPSSYSSDBLSPGBPLTSPP
j 1		i	
		•	WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS
1			LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT
ı			YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE
	,		
			TVELKIPBENOPPSKOVKPLFRHFRRIDSCLOTRVAFRGSDRIF
			TVELKIPBENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF CRVYMPDHSYVTIRSRLSASVODIIGSVTRKLAVSRRPAGPPDS
			TVELKIPBENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYRALV

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<b> </b>	sequence		\=possible nucleotide insertion)
1		i	PLPKEIQVSPGDTEIHRVEPEDVANHLTAFHWELFRCVHELEFV
5779	138	1671	DYVFHGR
3779	138	16/1	EAVQVLIKHSADVNARDKNWQTPLHVAAANKAVKCAEVIIPLLS
1		1	SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR
1			ALHWAAYMGHLDVVALLINHGABVTCKDKKGYTPLHAAASNGQI NVVKHLLNLGVBIDBINVYGNTALHIACYNGQDAVVNELIDYGA
		ļ	NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
		1	SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTPLHVAARYGH
ſ	}		RLLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG
		1	QKYSIVSLPSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI
1			KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN
1	Ì		ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK
1	<b>[</b>		EATLCLEFLLONDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE
			RTNSGFEESDSGATKSPLHLAVSEMP
5780	154	624	QFFRVITCLPFKGPDYRLYKSEPBLTTVAEVDBSNGERKSEPVS
ı	ł		EIRTSVVKGSHPPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM
1			DLRTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHCQACLREK
5781	19	941	KKGLNVIGASDQSPLQSPSNLRDNP RGSLGGHPWRPPMRAASQGCLPVSFVTGPHQBRAYGGRGPGGAF
]		}	PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE
l i		}	QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ
			VQPHFTSQDAKSAKDRAPSRHLGKHQPRSAQVGSRLDALQGPKT
			QHSIHTVTCKSPRQKEDRSPKPPQAPKHPERHGRQS\QAPPPLP
			VAPERTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR
1			CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY
			INIMD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTRAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVP9LPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISE?SAVPTDYSVSASDPSVLVSEAAVTVPEPP
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISE?SAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTFVESAVVABEHEVVPERPVTCMVSETPAMSAEPT
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISE?SAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVAREHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPRPPVSQSEISEPSAVPTDYSVSASDPSVLVSEARVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETABTFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVP9LPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPRPPVSQSEISE9SAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETFAMSAEPT VLASEPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL E9SVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISE?SAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLITVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISE?SAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTFVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSBTABTFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLE E?SVVTVPEPPVVARPDYVTIPVPVSALEPSVPVLEPAVSVLQ PSMTVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAR EHLKGDFYESEHGIBIDLNINNHLIAKEMEHNTVCAAGTSPVGE
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPRPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSBTABTFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVARPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTBVAIESTPM ILBSSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAR EHLKGDFYESEHGINIDLNINNHLIAKEMENNVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGSTLSSTGPFALEPD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVLE EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGKEPHAR EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEKKILPTSETKQRTVLDTYPGVSEADAGFTLSSTGPFALEPD ATG\TSKGI3FTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVP9LPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPRPPVSQSEISE9SAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVAREHEVVPERPVTCMVSETFAMSAEPT VLASEPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL E?SVVTVPEPPVVAEPDYVTIPVPVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVALESTPM ILESSIMSSIVMKGINISSGDONLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINHLIAKEMEHNTVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGISFTTASTISLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRO\DQ
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVP9LPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISE?SAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLITVESAVVAERHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL E?SVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTEM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAR EHLKGDFYESEHGINIDLNINNHLIAKEMENNVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGBTLSSTGPFALEPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNBPLPVKRD\DQ TLAALI\SLXESSGGEKEVPPPS*REHLPPSGFSANIEDINRAD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPPEPP PEPESSITLTPVBSAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVALESTEM ILESSIMSSHWKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMENNTVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNBELPVKRD\DQ TLAALI\SLXESSGGKEVPPPS*REHLPDSGFSANIEDINBAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFSPVQNLYSSPVV
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPRPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETABTFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVLE EPSVVTVPEPPVVARPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMTVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILBSSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAR EHLKGDFYESHGINIDLNINNHLIAKEMENMVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALRED ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLESMINLVSSDTMEPLPVKRD\DQ TLAALI\SLXESSGGKEVPPPS*REHLPDSGFSANLEDINEAD LVRPVSSPRTWNVLPSPRAGL\BGP\LLASDFGPVQNLYSSPVV \SSMP\ERASCS\SSGEKGG\TEIFVKVKDTHEKSKKNKNRDKG
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPPEPP PEPESSITLTPVBSAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVALESTEM ILESSIMSSHWKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMENNTVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNBELPVKRD\DQ TLAALI\SLXESSGGKEVPPPS*REHLPDSGFSANIEDINBAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFSPVQNLYSSPVV
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPRPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVARPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMTVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAR EHLKGDFYESHGINIDLNINNHLIAKEMENNTVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALRED ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIBGPLPAKDIHLDLPSMINLVSSDTNEPLPVKRD\DQ TLAALI\SLXESSGGKEVPPPS*REHLPDSGFSANLEDINRAD LVRPVSSPRTWNVLPSPRAGL\BGP\LLASDFGPVQNLYSSPVV \SSMP\ERASCS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSKRSKSSKHKSRKLTSESRSRRKRSSKSKS
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPPEPP PEPESSITLTPVBSAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSCQVIPTEVALESTEM ILBSSIMSSHWKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMENNVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPPALEPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHBMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLXESSGGKKEVPPPS*REHLPDSGFSANLEDINRAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSSKHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSS/RDRRRSSRSSKSRGRSVSKEKKRRSPKH RSKSRERKEKRSSSRDNRKTVRARSRTPSRRSSTTPSRRRSR SVGRRSPSISPSRSRTPSRRSTTPSRRST
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILESSIMSSHVMKGINLSGDQNLAPEIGMQBIALHSGEEPHAR EHLKGDFYESHEGINIDLNINNHLIAKEMENNVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGISFTTASTISLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNBPLPVKRD\DQ TLAALI\SLXESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLESPRAGI\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASCS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSSRHKSRLTSESRSRRRRSSKSKS HRS\QTRSRSS/RDRRRSSRSKSRFRSKSRRRSVSKKKKRRSPKH RSKSREKKRKSSSRDNRKTVRARSRTPSRRSRTFPSRRRSR SVGRRRSFSISPSRRSRTPSRRS
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMTVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILBSSIMSSHVMKGINLSSGDQNLAPEIGMGEIALHSGEEPHAE EHLKGDFYESHGINIDLNINNHLIAKEMENNVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGSTLSSTGPFALEPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLXESSGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SGEKGG\TEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSHKSRKLTSESRSRARKRSSKSKS HRS\QTTRSRSSFSKRSKSSRBKSRGRSVSKKKRKSPKH RSKSRERKRRSSSRDNRKTVRARSRTPSRRSRSTPSRRRSRF RTSRRSRTPSRRRSRSPSRRSRSRSRSRSRSRTPSRRSRTPSRRS RTSRRSRTPSRRRSRSPKRRSTPLRRSRT
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSECTQVIPTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEKKLLPTSETKQRTVLDTYPGVSEADAGGTILSSTGPFALEPD ATG\TSKGI3FTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIBGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLESSGGEKEVPPPPS*REHLPDSGFSANIEDINRAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG KKEKKRDSSLRSRSKRSKSSKHKSRKLTSESRSRRKRSSKSKS HRS\QTRSRSSKPKRSKSSRDNRKTVRARSRTPSRRSSTTPSRRRRSR SVGRRRSFSISPSRRSKTPSRRSTTPSRRSTTPSRRRRSR SVGRRRSFSISPSRRSTTPSRRSTTPSRRSTTPSRRSRT RSFRRRRRRRSRSSERGRSVVRRRSFSISPVRLRRSTTPLRRRFS RSFIRRKRSRSSERGRSPVRRRSFSISPVRLRRSTTPLRRRFS RSFIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVP9LPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVLE EPSVTVPEPPVVAEPDYVTIPVPVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVALESTPM ILESSIMSSIVMKGINLSSGDONLAPEIGMQBIALASGEEPHAR EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE EGERKILPTSETKQRTVLDTYPGVSEADAGBTLSSTGPFALEPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLXESSGGEKEVPPPS*REHLPDSGFSANLEDINRAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSSKHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSSPSRRSKTSRRSRSSRGRSVSKEKKRRSPKH RSKSREKEKRSSSRDNRKTVRARSRTPSRRSRTPSRRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRSRSVVRRSFSISPVRLRSRTPSRRRFS RSPIRRKRSRSSERGRSPKRLTSLDLDKAQLILBIAKANAAAMCAKA GVPLPPNLKPAPPPTIEBKVAKKSGGATIEKLTBKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPPKLSEPKPIFFNLNIAAAK
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPPEPP PEPESSITLTPVBSAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSECTQVIPTEVALESTEM ILESSIMSSHWKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMENNYVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNBPLPVKRD\DQ TLAALI\SLXESSGGKKEVPPPS*REHLPDSGFSANIEDINBAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFSPVQNLYSSFVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSKHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSSPNDRRTVRARSRTPSRRSRTPSRRRSR SVGRRSPSISPSRRSRTPSRRSRTPSRRSRTPSRRRSR SVGRRSPSISPSRRSRTPSRRSRTPSRRSTTPSRRRSR SVGRRSPSISPSRRRSRSVVRRSFSISPVRLRSRTPLRRRFS RSPIRRKRSSSERGKSPKRLTDLDKAQILLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEKVAKKSGGATIEKLTEKCKQIAQSKE DDDVIVNRPHYSDEREEPPFYHHPPKLSBPKPIFPININIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEKN
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVBSAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVTVPEPPVVAEPDYVTIPVPVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQGSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILBSSIMSSHVMKGINLSGDQNLAPEIGMQBIALHSGEEPHAR EHLKGDFYESEHGINIDLNINNHLIAKEMENNVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATGYTSKGISFTTASTISLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNBPLPVKRD\DQ TLAALI\SLXESSGGEKEVPPPS*REHLPDSGFSANIEDINBAD LVRPVSSPRTWNVLESPRAGI\BGP\LLASDFSPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSSRHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSSSRDNRKTVRARSRTPSRRSRTPSRRRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRRSRSVVRRSFSISPVLRRSRTPLRRRFS RSFIRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKSPVSGESQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVISTAMSERALAQKRLSENAPDLEAMSM
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVVLESSTVTVLESSTVTVL EPSVVTVPEPPVARPDYVTIPVPVSALEPSVPVLEPSVSVLQ PSMTVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPBIGMQBIALHSGEPHAE EHLKGDFYESHGINIDLNINNHLIAKEMENNVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGSTLSSTGPFALRED ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIBCPLPAKDIHLDLPSNINLVSSDTNBPLPVKRD\DQ TLAALI\SLXESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASCS\SSGEKGG\TEFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSSHKSRKITSESRSRARKRSSKSKS HRS\QTTRSRSRS/RDRRRRSSRSRSKSRGRRSVSKKKRKRSPKH RSKSRERKRKKRSSRDNRKTVRARSRTPSRRSRTPSRRRRFRSR SVGRRSFSISPSRRSRTPSRRSTTPSRRSRTPSRRS RTPSRRSRTPSRRRSRSTPSRRSTPSRRSRTPSRRS RSPIRRKRSSSERGRSVVKRKSKFPSRRS RSPIRRKRSSSERGRSVVKRKSFPSRRS RSPIRRKRSSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEBKVAKKSGGATIEBLTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSBPKPIFPNLNIAAAK GVPLPPNLKPAPPPTIEBKVAKKSGGATIEBLTEKCKGIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSBPKPIFPNLNIAAAK KODDNVFSSNLPSBPVDISTAMSERALAQKRLSENAPDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQBQLANTGAQAWI
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVP9LPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMTVSEPSVSVQBSTVTVSEPAVTVSECTQVIPTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMKHNYVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGSTLSSTGPFALREPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLÆESSGEKEVPPPPS*REHLPDSFSANIEDINRAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSHKSRKLTSESRSRAKRSSKSKS HRS\QTRSRSSF\RDRRRRSSRSSRSKSRGRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNKTVRARSRTPSRRSSETPSRRSRF RTPSRRSTPSRRSTPSRRSTPSRRSTPSRRSRTPSRRS RTPSRRSTPSRRSTPSRRSTPSRRSTPSRRS RSPIRRKRSSSERGKSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEBKVAKKSGGATIEBLTEKCKQIAQSKE DDDVIVNKPHVSDBBEEPPFYHHPFKLSBPKPIFPINIAAAK PTPPKSQVTLTKEFFVSSGSQHKKEADSVYGEWVPEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAPDLEAMSM LNRAQERIDAWAQLKSIPGCFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKNGMREGEGLGKNKEGNKEPILV
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVP9LPBEEPPTMPPLPPBE PPMTPPLPPBEPPBGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISE9SAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPBSSITLTPVBSAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASBPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSECTQVIPTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAB EHLKGDFYESBHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGGTLSSTGPPALEPD ATG\TSKGI3FTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIBGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLÆSSGGEKEVPPPS*REHLPDSGFSANIEDINRAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSSKHKSRKLTSESRSRRKRSSKSKS HRS\QTRSRSSRSKRSKSSKHKSRKLTSESRSTTPSRRRRSR SVGRRRSFSISPSRRSTTPSRRSRTPSRRSTTPSRRSRTPSRRSR SVGRRRSFSISPSRRSTTPSRRSTTPSRRSTTPSRRSRTPSRRSR SVGRRRSFSISPSRRSTTPSRRSTTPSRRSTTPSRRSRTPSRRSR GVPLPPNLKPAPPPTIEBKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSBPKPIFFNLNIAAAK PTPPKSQVTLTKEFFVSSGSQHKKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKILSENAPDLERMSM KDDDNVFSSNLPSEPVDISTAMSERALAQKILSENAPDLERMSM KDQFLRAAPVTGGRGAVLMRKMGMREGGGLGKMKEGNKEPILV DPXTDRKGLVAVGBRAQKRSGNFSAAMKDLSGKHPVSALMEICN
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPPEPP PEPESSITLTPUBSAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSECTQVIPTEVALESTEM ILBSSIMSSHWKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMENNYVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHBMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLXESSGGKKEVPPPS*REHLPDSGFSANLEDINRAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGFVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSSKHKSRKLTSESRSRAKKRSSKKS HRS\QTRSRSSSRSSSDNRKTVRARSRTPSRRSRTPSRRRSR SVGRRSPSISPSRRSTPSRRSRTPSRRSTTPSRRRSR SVGRRSPSISPSRRSTPSRRSTTPSRRSTPSRRSR SPIRRKRSSSERBNSWVRRSFSISPVRLRSRTPLRRRFS RSPIRRKRSSSERBNSWVRRSFSISPVRLRSRTPLRRRFS RSPIRRKRSSSERGKSPKLTDLDKAQLILBIAKANAAAMCAKA GYPLPPNLKPAPPPTIEBKVAKKSGGATIEBLTEKCKQIAQSKE DDDVIVNRPHVSDEBEEEPPFTHHPFKLSEPKPIFPINIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLGENAPDLEAMSM LNRAQERIDAWAQLISIPQFTCSTGVQVLTQBQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKNGMREGEGLGKNKEGNKEPILV DPKTDRKGLVAVGBRAQKRSCNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQFNCMFFLNR
5782	1693	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPPEPP PEPESSITLTPVBSAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVORSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMENNYVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGISFTTASTISLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNBEPLPVKRD\DQ TLAALI\SLXESSGGKKEVPPPS*REHLPDSGFSANIEDINBAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFSPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG KKKKRDSSLRSRSKRSKSSKHKSKLTSESRSRARKRSSKSKS HRS\QTRSRSSPRDRRRRSSRSSTPSRRSVSKEKKRSPKH RSKSRERKKKSSSRDNKTVKARSRTPSRRSFTPSRRSRT SVGRRSFSISPSRRSTPSRRSTTPSRRSRTPSRRSR SVGRRSFSISPSRRSTPSRRSTTPSRRSTTPSRRSR GPPLPPNLKPAPPPTIEKVAKKSGGATIELTEKCKQIAQSKE DDDVIVNRPHVSDBBEEEPPFHHPFKLSEPXPIPPNLNIAAK PTPPKSQVTLTKEFFVSSGSQHRKKEADSVYGEWVPVEKNGGEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAPDLEAMSM LARAQERIDAWQLKSIPCOFTGSTGVQVLTQEQLANTGAQAWI KKDQPLRAAPVTGGMGAVLMRKKGRREGEGIKNEGIKNEFILV DPKTDRKGLVAVGERAQUKRSNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFILVHDSGPDHRKHFLFRVLINGSAYQPNCMFFINR
			DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASCHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVTVPEPPVVARPDYVTIPVPVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPBIGMQBIALHSGEEPHAR EHLKGDFYESHGINIDLNINNHLIAKEMENNVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALRED ATGYTSKGISPTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGSEADIBGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLXESSGGEKEVPPPS*REHLPDSGFSANIEDINRAD LVRPVSSPRTWNVLESPRAGL\BGP\LLASDFSPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSSHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSSS/RDRRRRSSRSRSKSRGRRSVSKKKKKRSPKH RSKSRERKRKRSSRDNRKTVRARSRTPSRRSHTPSRRSR RTPSRRSTPSRRRRSRSVVRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGSPKRLTDLDKAQLLBIAKANAAMCAKA GVPLPPNLKPAPPPTIEBKVAKKSGGATIEKLTBKCKQIAQSKE DDDVIVNKPHVSDEBEEPPPYHHPPKLSEPXIPFRINIAAAK PTPPKSQVTLTKEFFVSSGSQHRKKEADSVYGEWPVEKNGEEN KDDDNVFSNLPSEPVDISTAMSERALAQKRLSENAPDLEMSM LNRAQERIDAWQLNSIPQGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGCMGAVLMRKNGWREGGGLGKWREGNKEPILV DPXTDRKGLVAVGERAQKRSGNFSAMKDLSGKHPVSALMEICN KREWQPPEFILVHDSGPDHRKHFLFRVLINGSAYQFNCMFFLNR Y DEGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM
			DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPPEPP PEPESSITLTPVBSAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVORSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMENNYVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGISFTTASTISLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNBEPLPVKRD\DQ TLAALI\SLXESSGGKKEVPPPS*REHLPDSGFSANIEDINBAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFSPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG KKKKRDSSLRSRSKRSKSSKHKSKLTSESRSRARKRSSKSKS HRS\QTRSRSSPRDRRRRSSRSSTPSRRSVSKEKKRSPKH RSKSRERKKKSSSRDNKTVKARSRTPSRRSFTPSRRSRT SVGRRSFSISPSRRSTPSRRSTTPSRRSRTPSRRSR SVGRRSFSISPSRRSTPSRRSTTPSRRSTTPSRRSR GPPLPPNLKPAPPPTIEKVAKKSGGATIELTEKCKQIAQSKE DDDVIVNRPHVSDBBEEEPPFHHPFKLSEPXPIPPNLNIAAK PTPPKSQVTLTKEFFVSSGSQHRKKEADSVYGEWVPVEKNGGEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAPDLEAMSM LARAQERIDAWQLKSIPCOFTGSTGVQVLTQEQLANTGAQAWI KKDQPLRAAPVTGGMGAVLMRKKGRREGEGIKNEGIKNEFILV DPKTDRKGLVAVGERAQUKRSNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFILVHDSGPDHRKHFLFRVLINGSAYQPNCMFFINR
			DRSMMSMAADSYTDSYTDTYTEAYMVP9LPPEEPPTMPPLPPEE PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISE?SAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVVVLESSTVTVLESSTVTVL E?SVVTVPEPPVARPDYVTIPVPVSALEPSVPVLEPAVSVLQ PSMTVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTPM ILBSSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEEPHAE EHLKGDFYESHGINIDLNINNHLIAKEMENMVCAAGTSPVGE IGBEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGISFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIBCPLPAKDIHLDLPSMINLVSSDTMPPLPVKRD\DQ TLAALI\SLXESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\BGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\TEIFVKVKDTHEKSKKNKNRDKG BKEKKRDSSLRSRSKRSKSSHKSRKLTSESRSRARKSSKSKS HRS\QTTRSRSRS/RDRKRTVRARSRTPSRRSRTPSRRSR RYGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR RYGRRSFSISPSRRSRTPSRRSTTPSRRSRTPSRRSR RYPSRRSRTPSRRRSRSVVRKRSFSISPVLKRGSKTPLRRRFS RSPIRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEBKVAKKSGGATIEKLTBKCKQIAQSKE DDDVIVNKPHVSDEBEEPPFYHHPPKLSEPKPIFPNLNIAAAK GYPLPPNLKPAPPPTIEBKVAKKSGGATIEKLTBKCKQIAQSKE DDDVIVNKPHVSDEBEEPPFYHHPPKLSEPKPIFPNLNIAAAK KRDQFLRAAPVTGCMGAVLMRKMGNREGGGLGKNKEGNKEPILV DPKTDRKGLVAVGERAQKRSGNFSAMKDLSGKHPVSALMEICN KRRWQPPEFILVHDSGPDHRKHFLFRVLINGSAYQFNCMFFLNR Y DEGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ

0770	1 Day 31 - 1 - 3	North about and	Daving and assessed to the second
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
9	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
<u> </u>	Događania		LHGDIKSSNVVIKGDFRTIKICDVGVSLPLDENMTVTDPEACYI
1	1		
1	ł		GTEPWKPKBAVEBNGVITDKADIFAFGLTLWEMMTLSIPHINLS
į.	1		NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEBLDESYQKVIE
			LFSVCTNEDPKDRPSAAHIVEALETDV
5784	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
	}		GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
1	]		RMLTATQYLAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
j			QDNYNLGSFTFQATLLMDGRIIFGYKBIPVLVTQISSTNHPVKV
			GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
	ł.		TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
			VDSGCPBESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
l	]		
I			E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
1			HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
			WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5785	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
1			GILSNTHRQAARVNLSPDFPFYGHFLRBITVATGGFIYTGEVVH
]			RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
1			QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV
1			GLSDAFVVVHRIQOIPNVRRRTIYEYHRVKLQMSKITNISAVEM
	į		TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
1	ì		VDSGCPEESKEKMCKNTEPVET\FLEPPQP*ERQPPSSGS*LPP
1			B/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAABKKGGTL
į į			HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
1			
			WPAMKFRRGSCHPAYAEVEPVGEKEGFIVSEQC
5786	2532	1674	SYKLPAAERRASSCSQPPTPTRRRWPAPGRTSRGHRPQM*SGTP
			APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC+SLN+M
[			S*H*KRNLSQRSSSMSRRPLSCARPHR**ROGLTVAARLPTWAK
-			SPPLACSPCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP
1			SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST
Į i			GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA
			TGGSTATAPPKRFPRNWNPMMAB
5787	2	1460	MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL
<b>l</b>		•	T\RYCEIP\GPD\LEBSP\TCP\LCKEPFRP\GSFRPNWQLANV
1			VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMQLCVVCR
		·	EAGERATHTMRFLEDAA\APYREQIHKCLKCLIKBREBIOBIOS
i I			RENKRMQVLLTQVSTKRQQVTSBFAHLRKFLEEQQSTLLAQLES
		ľ	QDGDILRQRDEPDLLVAGEICRFSALIERLEEKNERPARELLTD
			IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF
			LEKLCFELDYEPAHISLDPOTSHPKLLLSEDHORAOFSYKWONS
1		-	1
	}		PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS
]			EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP
			ROVRVSLDYBVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG
			RGSSFSLSS
5788	2	6B60	EHSVSGRSSÄYGDATABGHPAGPGSVSSSTGAISTTTGHQEGDG
			segegegetegdvhtsnrlhmvrlmllerligtlpqlrnvggvr
]			AIPYMQVIIMLTTDLDGEDEKDKGALDNLLSQLIABLGMDKKDV
i	İ		SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS
1			ATAAALLSSGAVDYCLHVLKSLLEYWKSQONDBEPVATSQLLKP
<b>j</b>			HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI
i i			KKITDINSRIPPPVFDHSWFYFLSEYLMIQOTPFVRRQVRKLLL
ļ		,	FICESKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA
			l · · · · · · · · · · · · · · · · · · ·
j			SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY
]			FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS
1			SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKEGETSGSQEDQ
}			LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH
<b>i</b> i			IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK
			TPOTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVRF
			DGYYLESDPCLVCNNPKVPFCYIKLSSIKVDTRYTTTOOVVKLI
	×		GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA
j i			RWHKAKKVQLTPGQTEVKTDLPLPIVASNLMIBFADPYENYQAS
			TETLOCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDFF
			TOTHNOT MONTH AND AND AND AND AND AND AND AND AND AND

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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	N=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
<u> </u>			LCNACGECKYAREDEMLYAKECCAVDEIKNEEDRKKAVSNINTL
<b>I</b>			LDKADRVYHOLMGHRPOLENLLCKVNKAAPEKPODDSGTAGGIS
	i		STSASVNRYILQLAQRYCGDCKNSFDRLSKLIQKVFASRKELLE
			The state of the s
1			YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG
1			CASAVTEHCITLLRALATNPALRHILVSQGLIRBLFDYNLRRGA
ı			AAMREEVRQIMCLLTRDNPEATQQMNDLIIGKVSTALKGHWANP
ŀ			DLASSLQYEMLLITDSISKEDSCWELRLRCALSLFLMAVNIKTP
1	l		VVVENITLMCLRILQKLIKPPAPTSKKNKDVPVBALTTVKPYCN
1	1		BIHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSKLRH
	1	•	LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFTPAT
	ŀ		QAARQAACTIVEALATIPSRKQQVLDLLTSYLDELSIAGECAAB
ł	ł		YLALYQKLITSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA
Į.	1		TLSTDLQQGYALKSLTGLLSSFVEVESIKRHPKSRLVGTVLNGY
			LCLRKLVVQRTKLIDETQDMLLEMLEDMTTGTESETKAFMAVCI
			BTAKRYNLDDYRTPVFIFERLCSIIYPBBNBVTBFFVTLBKDPQ
			QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICQDCDLVALLED
1	l		DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEPMRIVYRMRG
ŀ	l i		LLGDATERFIESLDSTTDEEEDREEVYKMAGVMAQCGGLECMLN
	·		RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNRQQLVKLEMNTLN
1			VMLGTINLALVAEQESKDSGGAAVAEQVLSIMEI\IQAEPNVEP
	<u> </u>		LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLCGLLRIIP
			YLSFGEVERMQILVERFKPYCNFDKYDEDHSGDDKVFL\DCFCK
ł			IAAGIK\NNSNGHQL\KDL\TLQKGITQNALD\YMKKHIP/SAA
1			RIWDADI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI
1			PNLHKLEQVS\SDEGIGTLA\ENL\LESLREHPDVNKKIDA\AR
}			RETRAEKKRMAMAMROKALGTLG\MTTNEKGQVVD/TRTALLEA
-33-			DWBELLKEP\GLTCCICREGYKFQPTKVLGIYTFTKRVVLGGVW
			ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREBWESAA
1			LONANTKCNGLLPVWGPHVPESAFATCLARHNTYLQECTGQREP
1			TYOLNIHDIKLLFLRFAMEOSFSADTGGGGRESNIHLIPYIIHT
			GLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFTV
1	-		•
1	*		LALHILPPEQWRATRVBILRRLLVTSQARAVAPGGATRLTDRAV
			KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLAEYIR
	<b>!</b>		HNDNPIYEAADKALKTFQREFMPVETFSEFLDVAGLLSEITDPB
			SFLKDLLNSVP
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ
1			TBEKEKKEKPKSDKTREIAEEBETVPPKAKQVKKKAEPSEVDMN
1			SPKSKKAKK\KERPSQNDISPKTKSLRKKKEPIEKKVVSSKTKK
1 1			VTKNEEPSEBEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP
1	ļ		EPDCNPSRAASBESNSEIBQEIPVEQKEG\APSNFPISBETIKL
1			LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL
1	į į		IEKLHG\KLQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL
i			SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT
1	ŀ		KLNHVVLDBVDQMLDMGFADQVBEILSVAYKKDSBDNPQTLLFS
			ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH
1		•	WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD
[ ]			AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD
]			LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEBYQLVQ
]			VEQKAGIKFKRIGVPSATRIIKASSKDAIRLLDSVPPTAISHFK
1			QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM
			ILQCSTEMPNISYAWKBLKEQLGEBIDSKVKGMVPLKGKLGVCF
			DVPTASVTEIOEKWHDSRRWOLSVATEQPELEGPREGYGGFRGQ
]			REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK
[			GOKRSFSKAFGQ
5790	3786	1585	ARRORDPLQALRRRNQELKQQVDSLLSESQLKKALEPNKRQHIY
] 5.50	3,00	7707	ORCIOLKOAIDENKNALOKLSKADESAPVANYNORKEEEHTLLD
			1
			KLTQQLQGLAVTISRENITKVGAPTEEEEESESEDSEDSGGEEB
1			DAEEEERKEENESHKWSTGERY IAVGDFTAQQVGDLTPKKGEI
	İ		LLVIEKKPDGWWIAKDAKGNEGLVPRTYLBPYSEEREGQESSEE
			GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN
1		•	HVSFCYLIVLMRNRMETVEDTNGSETGFRAWNVQSRGRIFLVSK

PCT/US00/34263

-	T		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	1
1			W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			PVLQQINTVDVLTTMGAIPAGFRPSTLSQLLEEGNQFRANYFLO
j.		1	PELMPSQLAFROLMWDATEGTIRSRPSRISLILTLWSCKMIPLP
1			GMSIQVLSRHVRLCLFDGNKVLSNIHTVRATWOPKKPKTWTFSP
1		I .	QVTRILPCLLDGDCFIRSNSASPDIGILFELGISYIRNSTGERG
1		1	· · · · · · · · · · · · · · · · · · ·
j .		į.	KLSCGWVPLKLFDASGVPIPAKTYELFLNGGTPYRKGIRVDPSI
l .	ľ	1	SRRAHGSVFYQIMTMRRQPQLLVKLRSLNRRSRNVLSLLPETLI
	ì	<u> </u>	GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLISHPMLATFPML
l .	i		LEQPDVMDALRSSWAGQES\TLKRSEKR\PKZFLKVPRFILLVYH
	ŗ		\GCVLPLL/HTPTRLPPFRWAEBETETARWKVITDFLKONOENQ
I	l .	Į.	GALQALLSPDGVHBPFDLSEQTYDFLGEMRKNAV
5791		1636	
2\ar	3	1030	LRVAEPAGTSR/IGAGLIQPLHRAPARDHGLIRGGAAPALSVSH
I	1	ļ	GN/GKQL/AMSSQGSDDEQIKRENIRSLTMSGHVGFESLPDQLV
1	I	İ	NRSIQQGPCFNILCVGBTGIGKSTLIDTLFNTNFBDYBSSHFCP
ŀ	1		NVKLKAQTYELQESNVQLKLTIVNTVGFGDQINKEESYQ⊇IVDY
1	1		IDAQFEAYLQEELKIKRSLFTYHDSRIHVCLYFISPTGHSLKTL
1		ł	DLLTMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLMSELVSNG
1	l	1	VQIYQFPTDDDTIAKVNAAMNGQLPFAVVGSNDEVKVGNKMVKA
}	1		ROYPHGVVQVENENHCDFVKLREMLICTNMEDLREQTHTRHYBL
1		1	YRRCKLEEMGFTDVGPENKPVSVQETYBAKRHEFHGERQRKEEB
ſ	ŀ		
1	i		MKQMFVQRVKEXEAILKEAERBLQAKFEHLKRLHQEBRMKLEEK
i I		i	RRLLEBETTAFSKKKATSETFHSQSFLATGSNLRKDKDRKNSQF
		ľ	FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVICFITSIFGEQPQ
			LLIFMEKYFQVQGQYISQSK
5792	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
			LARRPKLOL\RHSFTTTRSHLGAENNIDLVLNVEDFDVBSKFER
		l .	TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT
	!	i	YMVPKPEEINILTGESDTQQIEADKKPTSALDEPVSHWRPRLAL
	]	ţ.	1
i ·		ĺ	NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN
	1		RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ
1	i		FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
i i	i i	i	ISFNKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP
i l		i i	AGVGAAIBLWKVKKALKMTIFWRGLMPEFQPGTYSESBRKTBEY
1 !			DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
			YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
			IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
			1
			EKATRAPHID
5793	2263	653	AAAAPSPAWWCGVFVVXVVHTCWVMYGIVYTRPCSGDASCIQPY
[ ]			LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER
]			TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT
]			YMVPKPREINLLTGESDTQQIRADKKPTSALDEPVSHWRPRLAL
, ,			NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN
	,		RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ
ļ l			FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
j !		0	YOU THE THE TAX AND THE TAX AN
, !			ACREA A TRE GREEKEN THANKS THE CONTROL MOREODOCTOR OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF T
ا ۱	'		AGVGAAIRLWKVKKALKMTIFWRGLMPEFQFGTYSESERKTBEY
			DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
			YAPGPLPMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
			IITMPTSHRLACPRODVVFLVYLYQRWLYPVDKRRVNEFGESYE
			EKATRAPHTD
5794	1	5016	MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV
	· 1	2020	KGOKGERGLPGLOGVIGFPGMOGPEGPOGPPGOKGDTGEPGLPG
1			
			TKGTRGPPGASGYPGNPGLPG1PGQDGPPGPPG1PGCNGTKGER
			GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG
			FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM
			GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG
	ļ .	İ	EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG
			YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT
1			
l l			PGPRGEPGPKGPPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD
! <b>!</b>			RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP
[ [			GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG
	i		PPGEIGPPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK

CEO	Predicted	1 801371113 113	
SEQ	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
"0:	location	corresponding	
ı	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P-Proline, Q=Glutamine, R-Arginine,
ł	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	sequence	sequence	Codon, /=possible nucleotide deletion,
	осциение	<u> </u>	\=possible nucleotide insertion)
		1	GBPGBFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG
ł	į	l	PKGSPGSVGLKGERGPPGGVGFPGSRGDTGPPGPPGYGPAGPIG
1	İ	}	DKGQAGPPGGPGSPGLPGPKGBPGKIVPLPGPPGAEGLPGSPGF
İ		ì	PGPQGDRGPPGTPGR\PGL\PGEKGAVG\QPGIGFPGPPGPKGV
1		!	DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL
1		1	PGLPGIPGTPGKKGSIGVPGVPGKHGAIGPPGLQGIRGEPGPPG
l			LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGBKGFPG
1	İ	İ	FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGPPG
1			SKGEMGVMGTPGQPGSPGPWGAPGLPGERGD\HGFPGSSGPRGD
1	<b>!</b>	ĺ	PGLKGDKGDVGLPGKPGSMDKVYMGSMKGQKGDQGEKGQIGPIG
1	1		EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP
	1		GPKGSVGGMGLPGTPGBKGVPGIPGPQGSPGLPGDKGAKGEKGQ
!			AGPPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS
1			PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDGIPGVKGEAGLPG
1			TPGPTGPAGQKGEPGSDGIPGSAGRKGEPGLPGRGFPGPPGAKG
			DKGSKGEVGPPGLAGSPGIPGSKGEQGFMGPPGPQGQPGLPGSP
1			GHATEGPKGDRGPQGQPGLPGLPGPMGPPGLPGIDGVKGDKGNP
İ			GWPGAPGVPGPKGDPGFQGMPGIGGSPGITGSKGDMGPPGVPGF
i	1		QGPKGLPGLQGIKGDQGDQGVPGAKGLPGPPGPPGPYDIIKGEP
ı	<b>!</b>		GLPGPEGPPGLKGLQGLPGPKGQQGVTGLVGIPGPPGIPGFDGA
ŀ	ì		PGQKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFL
I	[	- 0	VTRHSQTIDDPQCPSGTKILYHGYSLLYVQGNERAHGQDLGTAG
1			SCLRKFSTMPFLFCNINNVCNFASRNDYSYWLSTPBPMPMSMAP
1		- 4	ITGENIRPFISRCAVCRAPAMVMAVHSQTIQIPPCPSGWSSLWI
ł			GYSFVNHTSAGAEGSGQALASPGSCLBBFRSAPFIECHGRGTCN
			YYANAYSPWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR
5795	1192		RT
3793	1192	61	STRSPTVBYISAHPHILFMLLKGYRAPQIALRCGIMLRECIRHE
1	i i		PLAKIILFSNOPRDFFKYVELSTFDIASDAFATFKDLLTRHKVL
1			VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN
			PAIMTKY ISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH
ì	ł .		KTQPIVBILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI
5796	2	1078	RDLKKTAP+RALRDSKR
3736	1 4	1078	GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
			PGEIGLLDPGMDVYGGENTELGIKVWLCGGSMEVLPCSRVAHIE
1	]		RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
	1		GIDIGDVSERRALRKSLKCKNPQWYLDHVYPEMRRYNNTVAYGE
[ !			LRNNKAKDVCLDQGPLENHTATLYPCHGWGPQLARYTKEGFLHL
1			GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ
			NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R
1	1		EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG
5797		891	OHRDPG
""		OJT	PRVRQKTLVDVTLENSN1KDQ1RNLQQTYRASMDKLREKQRQLE
			VAQVENQLLKMKVESSQRANABVMREMTKKLYSQYEEKLQEEQR
]	. ]		RHSARKRALLBETNSFLKAIERANKKMQAARISLERKDQRIGEL
	[		DRLIERMEKERHOLOLOLLEHETEMSGELTDSDKERYQQLEEAS
			ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ
			LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP
5798	644	110	SQTGRTREIVMPSRNYTPYTRVLBLTMKKTLT
3,30	074	115	KIIGSRWKSNSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR
		4.	TCIVDGKKLRIG3YKQLMRSRRQEMRQFFTVGQQPQIPITTGTG
			VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT
5700			DGGSLAGNEMINGEDEMEMYDDYBDDPKSDYSSENBAPEAVSAN
5799	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
	ł		TLSSVASTDVLATVLEBMPPFPERBSSILAKLKRKKGPGAGSAL
	<b>.</b>		DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
1.		-	PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPRDIGPPIP
			EADBLLNKFVCKNNGVLFKNQLLQIGVKSEFRQNLGRMYLFYGN
[ ]	j		KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
1 1	ŀ		NIBCLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
. !	i i		AAQDFFQRWKQLSLPQQBAQKIFKANHPMDAEVTKAKLLGFGSA
	L		The state of the s

		T 5 33 3 3 3	Amino acid segment containing signal peotide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L-Leucinc, M-Methionine, N-Asparagine,
!	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ī	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•••	\=possible nucleotide insertion)
	Bequence		LLDNVDPNPENPVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
	,	1	
			RTSKEPVSRHLCRLLAQQF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
	1		TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
	l		DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
	i	ļ	PASAGAGNLLVDVFDGPAAQPSLGPTPREAFLSPGPEDIGPPIP
i		ł	EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
Ì	İ	[	KTSVOFONFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
	1	}	NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
	}		AAQDFFORWKQLSLPQQEAQKIFKANHPMDARVTKAKLLGFGSA
	<u>i</u>		LLDNVDPNPENFVGAGIIQTKALQVGCLLRLRPNAQAQMYRLTL
<b> </b> *	1		
			RTSKEPVSRHLCELLAQQF
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII
	1	1	QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQP
ŀ			CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPRE
1			QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
1	1		DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS
į .	ļ	1	NGSNSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA
	1	l	GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT
	j	1	KVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH
ł	1	}	NMAPPSDWSPSWVMWLRLPRCLYNCKDIVLRRNTAGSLGFCIVG
l	ļ	1	GYERYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
	1	1	
			MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMBRIMDLPTLLRHAFREMFSVGGLFHMFRIRIILCLM
}	•	į.	GAFFYLISPLDFVPRALFGILGFLDDFFVIFLLIYISIMYRBV
	A		ITQRLTR
5803	2234	1299	RAQFGTTARIYAYREEQDFGIBIVKVKAIGRQRFKVLBLRTQSD
l ,			GIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC
			SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE
1	1		WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
			LRCELDIMNKCTSLCCKQCQETBITTKNEIFSLSLCGPMAAYVN
l	· ·		PHGYVHETLTVYKACNLNLIGRPSTEHSWPPGYAWTVAQCKICA
1	ł .		SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
1			rcr .
F 204	ļ <u>.</u>	1707	EMEKOROEBORKRTERERKRRIEQDMLEKRKTORELAKRAEQIE
5804	2	1/0/	
			DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE
		1	REBKERIKYBEDKRIRYEBQRPSLKEAKCLSLVMDDEIESBAKK
		1	ESLSPGKLKLTFEELERQRQENRKKQAEEBARKRLEEBKRAPEE
l		ŀ	ARROMVNEDBENODTAKI PKGYR PGKLKLS FEEMER QRREDEKR
}		i	KABEEARRRIEBEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP
l	1	I	GKLEINFEELLKQKMEEEKRRTBEERKHKLENBKQBFEQLRQEM
1	1	1	GKKBERNBIFGLSREYEKLIKLKRSGSIQAKNLKSKFEKIGQLS
Í			EKEIOKKIBEERARRRAIDLEIKEREAENFHEEDDVDVRPARKS
1		İ	EAPFTHKVNMKARFEQMAKAREBEEQRRIBEQKLLRMQFEQREI
1	1		DAALQKKREBEEEEGSIMNGSTAEDEEQTRSGAPWFKKPLKNT
l		Ī	
l		1	SVVDSEPVRFTVKVTGEPKPBITWWFEGEILQDGEDYQYIERGB
	<b></b>		TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDL1ALLDLAEHASS
1	T.		APKESQQQSBDREYBVKERLYPKSKRRYDTYNLAGYQGEIEVGL
ļ		1	YTIQILQLIPFPDNKNELSKRYMVNFVSGSSDIPGDPNNBYKLA
1		ł	LKNYIPYLTKLKFSLKKSFDFFDBYFVLLKPRNNIKQNEBAKTR
			RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSBPLQVERCRRNLV
1	I	1	ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	AVFTPHNHGRTANLYSLHSNLGITTVFLFACQRFLGFAVPLLPW
1	1	1	ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
j	ł	l	RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	RESKKTERREMAVDIQPACLGLYCGKTLLEKNGSTRIYGRCGVC
Į		1	PRGQRTNAQKYCQPCTESPELYDWLYLGFMAMLPLVLHWFFIEW
1			YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV
}			
	<u> </u>		LMLSDWYTMLYNPSPDYVTTVHCTHBAVYPLYTIVFIYYAFCLV

SEQ	Predicted	Predicted end	Amino haid gogment controlled a signal needed
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide		
NO:		location	Glutamic Acid, P=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			IMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLOAVGG
			GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRLIVL
}	Ì	}	FSHWLLHAYGIISISRVDKLEQDLPILALVPTPALFYLFTAKFT
			EPSRILSEGANGH
5808	2	433	SLPDSGVVEYLSNGGVADNHKDFGELRYNEC:MNFSCNGKNGSS
3600		433	
1			EGRITHGFQLKSAYENNLMPYTNYTFDPKGVIDYIFYSKTHMNV
1			LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP
	<u> </u>		LVNGVHLPNRR
5809	464	2422	ILVPGPQGILHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG
		]	RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP
1	Ī	1	EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW
i			ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE
ł	1		SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWQ
1		1	INSRRINPKISYVISIKGORLDPMESVREKTVNLTTDSRTPEVC
1	1		LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI
1			SIFNBTCLKLNRRSRKVGSEHMYOFTVLGORWYLANFSHATSFN
1	į.	ľ	FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPA
1			VKOTISNISGFNETCLRWRSIKTADMEEMYLFHIWGORWYOKEF
1	1		
ł	1		AQENTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSBLPVVISL
1 .			TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQVLV
1	İ		LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM
İ	Į.		RIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV
			WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV
5810	3	1641	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIKAFVS
l .			BIESFFNTIEENCSKNEKRLBEQNREMMKKVLAQYDRKAQSFEE
[	j		VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVRBAEBLDBAVFLT
ł			SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDOMLK
			QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME
			BPQDDQEVNELVEEYRLTVKESYCIFEDLBPDRCYQVWVMAVNF
l	1		TGCSLPSRRAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPRA
1			TETYTLEYCROHSPEGEGLRSPSGI KGLOLKVNLOPNDNYFFYV
1	1		RAINAFGTSEQSEAALISTRGTRFLLLRETAHPALHISSSGTVI
i			SFGERRRLTEIPSVLGEELPSCGQHYNETTVTDCPAYRLGICSS
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	}		SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR
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5811	1918	851	AAALADPLPEDKWSABKRRPLKSSLGYEYTFSLLNPDPKSHDVY
1			WDIEGAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDS
1	)		ASSSYYLDMHSLPHVINPVESRIGSSAASLYPVLNPILLYVPELA
	]		HSPLYIQDKDGAPVATNAFILSPRWGGIMVYNVDSKTYNASVLPV
i i			RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT
1 .			weldrilmarsvenlatattiltslaqligkisnivikddvase
ļ			VYKAVAAVQKSAERLASGHLASAFVASQEAVTSSELAFFDPSLL
i :			HLLYPPDDQKFATYIPLFLPMAVPILLSLVKIFLETRKSWRKPE
]			KTD
5812	5204	2744	GGRORCORGRSCGAREHEVEPGTARPPPAASAMDASLEKIADPT
J		U. 32	LAEMGKNLKEAVKMLEDSQRRTEBENGKKLISGDIPGPLQGSGQ
ļ i			DMVSILQLVQNLMHGDEDEBPQSPRIQNIGEQGHMALLGHSIGA
j !			YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHEERE
			GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ
			YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG
į	ļ		RLPLLLVANAGTAAVGHTÖKIGRLKELCEQYGIWLHVEGVNLAT
			LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA
[			LTLVAGLTSNKPTDKLRALPLNLSLQYLGLDGFVERIKHACOLS
		: I	QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV
			PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA
			EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR
			ERFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDESSLKSYPQ
			GENIHAGLLKKLNELESDLTFKIGPRYKSMKSCLYVGMASDNVH
			AABLVETIAATAREIEDNSRLLENMTEVVRKGIQBAQVELQKAS
			BERLLBEGVLRQIPVVGSVLNNFSPVQALQKCRTFNLTAGSLES

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Deginning	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
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SINSYGERRAICZELQWINSIGAGLIAYEDESPIK PLANDERSITY (NORCODENLE, CONTONIOLOS) SIGSTES INFKLUCOPLEDYNAWARIAS HITTATIACODRUVTA ATELLORISPHNIVAPGAESAVASPYOLIAARALQUAPDAVITA ATELLORISPHNIVAPGAESAVASPYOLIAARALQUAPDAVITA PRIVMFYPRQETEDY I GOSIMIYYDMEMGKIPVQLEWYDSFYHI, GQVALRISLELMMITDYSQUNESYMRYDDLIATLEKSGADYNKYY URERNOGQUEPSSLORILAKRISGVUADBGAPHNIYY GSIYDTARNINVSYPRULEPIKA, ETNINGS-QOTAKALADUANG LGRAIYKLAGENSTUVADBGYDYRILLGY, LIKAMISWEG LIQGDIRSYLG*RGIPQH/YLAV\SSYTHITY/VLQYALAMIN TGTVVULTIRGQODESVUSSINDAUBYSWOQDHASHISTTORLE RCVESTARLARALSPA'RISGWSSTEYSTWYSRKROIRARIYL LGRAIXKLAGINAPGILIPSILVYTCINAKADVLFIAPREPGA VSY  ALKCEPRRULALLOGPQDEMBEGAAVAVCWYPPLMSERESI. LASKELELITLIVOFQODEMBEGAAVAVCWYPPLMSERESI. ALKCEPRRULALLOGPQODEMBEGAAVAVCWYPPLMSERESI. ALKCEPRRULALLOGPQODEMBEGAAVAVCWYPPLMSERESI. CETAQVYMKTHNIN'I YPVDGSKSENFPRVLEGRETPKRVIRA\I AAPIIDAAIQCYNGTIJA\TOOT\AGSKITTMMSSEDHLAVI, GGERAAQTGAAVAVLKEGGNINGSPHICHTITTHTSEDHLAGICONG KPLITRISOWRWYVADLITBEVYTSEMALMITKGEKSHINDLA GGERAAQTGAAVAVLKEGGNINGSPHICHTITHTSEDHLAGICONG KPLITRISOWRWYVENDIALGERPKTRILCTTTPWYSPETITALQPAST NYNDSKUTRILONGLGGPRYTRILCTTTTYPSFETITATAQPAST NYNDSKUTRILONGLGGPRYTRILCTTTTYPSFETITATAQPAST NYNDSKUTRILONGLGGPRYTRILCTTTTYPSFETITATAQPAST NYNDSKUTRILONGLGGPRYTRILCTTTTTYPSFETITATAQPAST NYNDSKUTRILONGLGGPRYTRILCTTTTTYPSFETITATAQPAST NYNDSKUTRILONGLGGPRYTRILCTTTTTYPSFETITATAQPAST NYNDSKUTRILONGLGGPRYTRILCTTTTTYPSFETITATAQPAST NYNDSYNDSHINIALKERINITHMUTRYNISISHIL LERIDESVCSSBOPPSNITALLSKENITHMUTRYNISISHIL LERIDESVCSSBOPPSNITALLSKENITHMUTRYNISISHIL LERIDESVCSSBOPPSNITALLSKENITHMUTRYNISISHIL KRARREVYNELGKINKHKININAOQPHI PTHITTTKTHKISISHIL LERIDESVCSSBOPPSNITALLSKENITHMUTRYNISISHILONGLEBKAN NDORGHAYWEGARAGANAVARBOULDARMISSSVELLARKEN ORKOJLIHETSHINIALKERININGLONGLEBHATATAQESDOLGNIGE NDORGHANINALDYNINANANANANANANANANANANANANANANANANANAN	1	Į	j	
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GETAQVYMKTHINVIYPUGSKSVNFDRVLHGNETPKNYYEA\1 AAP I IDSAIGSYNGTIFA\19G2*\ASGKIYTIMGSEDELGVIPQ GOPHGHEPQKI* *EVPLDRFILLEVSYMETYMTSTEDLLGTORM KPLITREDVINNVVADLTBEVYTSEMALKUITKGEKSRHYGE TKHNQRSSGSHTIFRAILGSRERGENCEGSVKVSHLINJULA GSERAAQMAAGVEKEGCNINRSPILGQVIKKLSDGQVGGFI NYRDSKLITILQNSLGGNPKTRIICTITPVSPDBTLTAILQYAST AXYMKNTPYVWEVSTDEALLKYRKSIMDLKKQLESVSLSTRAQ AMSKOQLAQLLERKOLLQKVQNEKIENLTRHLYTSSSLTLQQSL KAKKRRVTWCLGKINKMKNSNYADQFIPTNITTTTHKLSIHL LERIDESVCSSDVFSNTLDTLSSHBWPATKLINGSNIESEIN GLRADYDDIJVLJUPQLETREEMELKLKKNOLDBFRALBRYK KOPROLIHBISNLKNIVRREWPUGDENNLSSEVBLEKEKSI QIKKLQEYIDSQKLENIKHDLSYSLESIEDPKOMKOTLFDAETV ALDAKRSSAFLRSENIELKKKMKELATTYKURBDIQLYGGGE AKKMOVDLERELGSARNSITKLISILIDGKVPKOLLCILEEGK 'TTOLQKELNKEVBENRALRREVILLSELKSLGSEVERLERER IQD KSEKLHIITTSEKDKLPSEVVHKESRVQGLEREIGKTKODLATTQ SNYKSTOQEPONFKTLHMDFEQKYKMVLEERKERROEIVNLSKE AQKFDSSLGALKTELSYKTQBLQREKTREVGERINGENGLEGGE NROSELGVVEREKYLTITEKLQQTLEREVTLTQREODLADLQLGESL QIERDQLKSDIHDTVNNNIDTQEQLRNALESLKQHQETINTLKS KISESVSRNHHMERNTGETKOBFOQNMYGINKQDLEAKNTYCTL TADVKDNETIEQGERIFLIGDELKQQBLVAORKHIATKGEGGEISR TCDRLASVERKLEKERSQULQREQQLLNVQERMEENQKENGEI KRNIEMTIENQBEIRLLGDELKQQBLVAORKHIATKGEGGEISR TCDRLASVERKLEKERSQULQREQQLLAVORKHIATKGEGGEISR TCDRLASVERKLEKERSQULQREQQLAVORKHIATKGEGGEISR TCDRLASVSKTADLINTQDLEKSHTKLIQRE IPVLHERGBLIP NYKKVSRTQBTMMELBULTEQSTTROSTTLARIEMERLEINEREP BILKNELKHKELITLEHMETERLELAQKINENYERSVESITKERRUL KELGKSPETRENDHLRGYIRRI BRATGLOKKERIBETLAKTQE SOSKOEGIAKSLTKRENDALKTIKBALEVKRODKERIBETLAKTQE SOSKOEGIAKSLTKRENDALKTIKBALEVKRODKERIBETLAKTQE SOSKOEGIAKSLTKRENDALKTIKBALEVKRODKERIBETLAKTQE SOSKOEGIAKSLTKRENDALKTIKBALEVKRODKERIBETLAKTQE LLKRLQBSHDEMKSVAKERKDDLQRLQBEVAGSEDQLKENIKEIV ARHLETBERLKVAHCCLKEGERTINELRURJKEFFEIGTIQKQ LLKRLGBSHDEMKSVAKERKDDLQRLQBESCDLKENIKEIV ARHLETBERLKVAHCCLKEGERTINELRURJKEFFEIGTIQKQ LLKRLGBSHDEMKSVAKERKDOLQRLQBEVAGSEDLKENIKEIV ARHLETBERLKVAHCCLKEGERTINELRURJKEFFEIGTIQKQ LLGRINDKLORGLIKERTENTERLENDERGENKRYQUEA LQEBOQLKENTKERUDENTERGENTERGENTERGENTERGE LEBRENGRVAHCCHKERGENTERGENTERGENTERGENTERGENTERGENTERGENTERGENTERGENTERGEN	5814	8500	432	
AAPI IDSAIQCYMCTIPA, YGCT\ASGKTYTMMGSEDHLGVI PO GQFHGHSQKY * EVPLDREFILEWSYNEITNETITICLGTORM KDLI IREDVNRWYWADLTBEWYYTSEMALKHITKGEKSHYGE TKMNQRSGSHTI FRMILESREKGEPSNCESSYKVSHIANJULA GSERAAQTGAAGVRIKEGCNINRSLIPIIGQVIKKLSDGQVGGFI NYRDSKLIRILQNSLGGMPYRRIICTITPYSPETITALQPAST AXYMKNTPYVWEVSTDRALLKRYKREIUMLKKQLEKVSLETRAQ AMSKODLAQLLEKKULLQKVOMBRIENLTRMLTYSSLTIQOSL KAKRKREVTWCLGKINKMKNSNYADQPNIPTNITTKTHKLSINL LERIDBSVCSSSDVFSNTLDTLSSEIBHNPATKLLNOENIESELN SLRADYDNIVLIDYBCJFTREKERBLKILKERNDLDBFFALERIN KOQRMQLHIBISNLKNLVKRREVYNQDLENELSSKVELLEKED QIKKLQBYIDSQKLENIKMDLSYSLSIEDPKOMKQTLFIDATV ALDAKRESAFLESENLELKEKMKELATTYKQMKNDTOLLCYNLELEGK ITDLQKEINKRVERNEALRREVILLSELKSLPSEVERLEKED AKKNOVDLEKRLQSAPNBTTKLTSLDGKVPKDLLCYNLELEGK ITDLQKEINKRVERNEALRREVILLSELKSLPSEVERLEKEIQ KSERLHIITSEKDKLFSEVVHKESRVQGLLEBIGKTKDDLATTQ SNYKSTDQEPQNFKTLHMDFGCKYKMVLEBRERNOEIVNLEKE AKKPSDGJEJGALKTRISYKTORLOEKSTREVQERLINERDLEKOLE NROSPLOTVEREKTLITEKLQQTLEBVKTLTVEXDDLKQLESCL QIERQJLISDIHDIVNNNIDTQSCLKRALESIKQHGETITNTLKS KISESVSNIHMERSTGSTKDEFOQMVGTDKKODLARNTYDL TADVKONEIIBQQREIFSLIGEKKROQLENVGENDLAKNTYDL KRNIEMTIENQBELRLIGDBLKCQGULNVQERWSPQKKINBIE NLKNELRIKELTLEHMSTERLELAQKINDRSVIAEKEQLKTDI KRNIEMTIENQBELRLIGDBLKCQGULNVQERWSPQKKINBIE NLKNELRIKELTLEHMSTERLELAGKINDRSVYKSRUL KELQKSFFTERDHLRGYIRBIBATGLOTKERKIKLAHIHKLRENGE TIDELRRSVSKKTAQI INTQDLEKSHTKLQEETPVLHERDERLIP NYKKVSFTORTMIRBILLITEQSTKOSTILAREBERNIKERP QESGEIKSLTKERDNLKTIKRBLEKHRLOEKSHQKKINBIE LEKRLQSSFTTMENDLKTIKRBLEKHRLOESCHLKENIKRITKERP QESGEIKSLTKERDNLKTIKRBLEKHRLOESCHLKENIKRIU LEKRLOSSBEMMSVAREKODLCREVKHOLKERHERTLAKTQE SGSKGEGSLMMKEKNNETTRIVSEMROPKRUSALLRIEBENG LEKRLDSBEMMSVAREKODLCREVKHOLKERHERTLAKTQE LEKRLOSSBEMMSVAREKODLCREVKHOLKERHERTLAKTQE LEKRLOSSBEMMSVAREKODLCREVKHOLKERETRETISTICKQ LEARNDKLQNKIGEIYEKEBGMNIKGISSVQEKWELKGFKEER KAKDSALGSIESCHLMEITNELQSSGEIQTMKEKREWREVQER KAKDSALGSIESCHLMEHTNELGSSGEIQTMIKERKERENKRUGE LEARNDKLORSTYKKRU	3022	0500	754	
CQPHGHPSQKI * EVVLDRPPLLRVSYMEITNETTIDLLCGTQKM KPLIIREDVNRNVYVADLTEEVVYTSEMALKMITKGEKSRHYGE TKMQRSGRSHI IPMILESREKGEPSNCGSSVKVSHLNIJVDLA GSGRAAQMAAGVRLKEGCNINRSLPILGQVIKKLSDGQVGGFI NYRDSKLIRILQNSLGGNPKTRILCTITPVSFDETLTALQPAST AXYMKNTPYVWEVSTDEALLKRYKKEIMDLKKQLBEVSLETRAQ AMEKDQLAQLLERKDLLQKVQNEKIENLTRMLVTSSSLTLQQSL KAKRKRVTWCLGKINKMKNSNYADQPNIPNITTKTHKLSINL LERIDESVCSSSDVFSNTLDTLSSIBMNPATKLLNOENIESSLN SLRADYDNILVLDYBGLRYBKEEMELHLKRENDLDBFFALBRKTK KDQFMQLIHBISNLKNLVKHREVVNQDLENBLSSKVBLLERKEN ALDAKRESAFLRSENLEILKREMKELATTYKQMENDTQLVQSQLB AKKNOVDLEKRLQSAPNBITKLIIDGKVPBDLLCNLELBGK TITULGKELNKRVBERNLERBEVILLSBLKSLPSEVERLRREIQD KSERLHIITTSEKDKLFSEVVHKSSRVQGLLBEIGKTKDDLATTQ SYNKSTDQFPQNFTLIMDFEGXYKMVLERNERNOEIVNLSKE AQKFDSSLGALKTBLSVKTQELQEKTREVQERLNENGOLKGLE NROSPLQFVDEREKTLITEKLQQTLERVEKTTQEKDDLKGQLE NROSPLQFVDEREKTLITEKLQQTLERVGKYMOLERNERNOEIVNLSKE AQKFDSSLGALKTBLSVKTQELQEKTREVQERLNENGOLKGEL NROSPLQFVDEREKTLITEKLQQTLERVGKYMOHESVIRAKGLSK KISEBVSRNLHMERNTGETKDEFQQKMYGIDKKQDLEAKNTQTL TADVKONSIIBQQRKIPSLAQGKLRSVAKALBESLKQHKTDL KRIPMTIENGGERLALLGGBLKKGRUFSVAREKEGLSR TCDRLAEVERLLERBETKERLAQKLNPESVERSITERRVL KLGKSFFTERDHLRGYIRRIERATGLQYKERVERSENSTRERGL KLGKSFFTERDHLRGYIRRIERATGLQYKERVERSEVKSITERRVL KLGKSFFTERDHLRGYIRRIERATGLQYKERVERSEVKSITERRVL KLGKSFFTERDHLRGYIRRIERATGLAYKERVERSEVKSITERRUL KLGKSFFTERDHLRGYIRRIERATGLAYKERVERSEVKSITERRUL KLGKSFFTERDHLRGYIRRIERATGLAYKERVERSETLARHIHKEPLA KLGKSFFTERDHLRGYIRRIERATGLAYKERVERSETLARHIHKEPLA KLGKSFFTERDHLRGYIRRIERATGLAYKERVERSETLARHIHKEPLA KLGKSFFTERDHLRGYIRRIERATGLAYKERVERSETLARHIGKEP GSGRE KSLTKREDNLKSTIKRSLEVHOOLKSHIRRIV AKHLETEBERKVANCKLOCKEGEBTINERURALREFEISTIQKQ LSKRIGSHEMSVAKEKODLQRUGVALEKPETLARTOR LSKRLQSSHDEMKSVAKEKODLQRUGVALEKPETLERLGCH LSKRLQSSHDEMKSVAKEKODLQRUGVALEKPETLERLGKG KAKDSALGSITSKWHELNERGERTHERTLARTURGERELARNERGERADDLAKTRIKRIV AKHLETEBERKVANCKLOCKEGEBTINERURANERGERSELKGPKREER KAKDSALGSITSKWHENTIKRIVALGESQEEIQMIKERKEPKREVGKRE KAKDSALGSITSKWHENTIKRIVALGERGERTHERTLRKRUPGEN LORENDLKENTREIVANKERSQEKGVANTERTORMETORMCE LORENDLKENTREIVANKERSQEKGVANTERTORMETORMCE	1			
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TRIMORESERHT I FIRM LESREKGEPSINCEGSVKVSHLINLVDLA GSERAAQTAAAGVRLKEGCINRISLICQVLKUSDGVGGFI NYBDSKLTHI LQNSLGGPKTRI I CTITPVSPBETLTALQPAST AXYMKHTPVNEVSTDEALLKRYRKSIMDLKKQLBEVSLETRAQ AMEKDQLAQLLERKULLQKVQNEKIEMLTRMLVTSSLITLQQSL KARRRRVTWCLGKINKMKNSNYADQFNI PINITTRTHKISIML LRRIDESVCSESDVFSNYLDTLJSHIMNDATKLLNQENIESELN SLRADYDNLVLDYRQLRTEKEEMELKLKEKNDLDEFFALERKTK KOQEMQLIHEISNLKNLVMREVYNQDLENBLSSKVELLREKD QIKKLQBYIDSQRLENIKMDLSYSLESIEDPKOMKOYLFDAETV ALDAKRSAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKRMOVDLERKELQSAFNEITKLTSLIDGKVPDDLLCHLEBK 1TOLQKELMKRVBENBEALRERVILLSELKSLESEVERLEREIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLERIGKTKDDLATTQ SNYKSTDQEFQNFKTLHHDDFGQKYKMVLEENERMOGIVNLSKE AQKFDSSLGALKTBLSYKTQBLQEKTREVQERLNEMGDLKGLDE NRDSPLQTVEREKTLITEKLQQTLEVKTLTQEKDDLKQLGESL OIERDQLKSDIHDTVMMIDTQTQQLRNALBSLKGNGETTNTLKS KISESVSRNLHMERBTGFTKDEFQOKMVGIDKKODLEAKNTQTL TADVKONEIIEQGRKIFSLIQEKGLEQMLESVIKAGLEKCHCTDL KENIBMTIENQEELKILGDBLKKQQEIVAQRENHAIKKGEGLSR TCDRLAEVERKLKRSQQLQRKQQLLNVQREMSEMQKKINBIE NLKNELKNKELTLEHMBTERLELAQKLKENTAEVSE ITKERKVL KELQSFFTRENPLLEGYTELTGTTLACHTEKLAHIHLKEHGE TIDBLRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEGELLP NYKKVSETQETMNSLELLLEGSTITLOSTTLARIEMERRIKHERG GESGEKIKSLYKRENDLKTIKRALBEVKHOLKKHIREITAKTGE SQSKQEGSLNMKEKDNETTKIVSABEVKHOLKEHIREITAKTGE SQSKQEGSLNMKEKDNETTKIVSBEQFKPKDSALLRIEIEMLG LSKRLGSSHDEMKSVAREKDDLQRLQSVLQSESDQLKENIKEIV ARHLETBEBLKVAHCKLKGERTINELTURJEKSFTBISTICKQ LEAINDKLQNKIQEIYEKEBQLNIKQISVQEKVNBLKQFKHER KAKOSALGSIESKMLEHINGLYGSGETQIMIKERBERNKKVGEA LEAINDKLQNKIQEIYEKEBGLNIKQISVQEKVNBLKQFKHER KAKOSALGSIESKMLEHITNRLQESGEETQIMIKERBERNKKVQEA LQIEJQLKENIKRIVALBENETENINRLYDILMERREBREKKVQEA		·		
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NYRDSKLTRILQNSLGENPXTRILCTITPVSFDERTLTALQPST AKYMKNTPYNEVSTDEALLKRYRKEIMDLKKQLEEVSLETEAQ AMEKDQLAQLLEEKDLLQKVQNERIEMITRMLVTSSITTLQQSL KAKRRRVTWCLGKINKMKNSNYADQPNIPTNITTKTHKLSINL LRRIDESVCSESDVFSNTLDTLSEIBMPAYKLLNQENIESBLN SLRADYDNLVLDYEQLRITREMEMELKLKERNDLDSFRALBRITK KDQRMQLIHEISNLKNLVKHREVYNQDLENKLSSKVELLREKED QIKKLQBYIDSQKLENIKKHDLSYSLGSIEDPKOMKQTLFDABTV ALDARRESAFLRSENLELKEKMKELATTYKOMRDIOLOTYGOLDE AKKKMOVDLEKRLQSAFNBITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELMKRVEKNBALRREVILLSBLKSLPSEVERLRKBIOD KSEKLHIITSEKDKLFSEVVHKESTVGGLLERIGKTKDDLATTQ SNYKSTDQPPQNFKTLHMDFEQKYKMVLEENERNNQEIVNLSKE AQKFDSSLGALKTELSYKTQELOEKTREVQERLMEMEQLKRQLE NRDSPLQTVERERKTLTEKLQTLEBVEKTLOEKDDLAKDQLES QIERDQLKSDIHDTVNNNIDTQEQLRNALESLKQHQETINTIKS KISESVSRILHMERSTGETTDEFQONVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLJQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELKLLGDELKKQQKIVAQEKNHAIKKEGELSR TCDRLAEVEKKLKEKSOOLQERQQQLLNVQEKNHAIKKEGELSR KENIEMTIENQEELKLLGDELKKQQKIVAQEKNHAIKKEGELSP INLKNELTHERMETERLELAQKLNENYBEVKSITKERKVL KELQKSFFTERDHLRGVIREIBAGKLNENYBEVKSITKERKVL KELQKSFFTERDHLRGVIREIBAGKLNENYBEVKSITKERKVL KELQKSFFTERDHLRGVIREIBAGKLNENYBEVKSITKERKVL OESGEEIKSLTKRENDILKTIKRALEVKHOOLKEHIRETLAKIGE GOSGEIKSLTKRENDILKTIKRALEVKHOOLKEHIRETLAKIGE SQSKOEGSLNMKEKDNETTKIVSEMEOPKPKDSALLRIEIEMLG LSKILGESHDEMKSVAKEKODLQPLOSVLOSEEDLKENIKEIV ARHLETEBELKVAHCCILKEGEFTINELRVNLSKEFTEISTICKQ CESGEIKSLTKRENDILKTIKRALEVKHOOLKEHIRETILATIGE GOSGEIKSLTKRENDILKTIKRALEVKHOOLKEHIRETISTICKG LEAINDKLQNKIQEIYEKBEQLNIKQISEVQEKVNBIKQFKEER KAKGSALGSISSKMELTTRIQESGEIQIMIKEKBENKKVQEA LQIEDQLKENTKEIVANKESQEEIQIMIKEKBENKKVQEA LQIEDQLKENTKEIVANKHESQEKSVOFLKMTAVNETOREMCE IEHLKEOPETOKINEENIETEKNIRLTAGLUKHENLEDENSVYKERD				
AXYMKTPYVNEVSTDEALLKRYRKEIMDLKKQLEVSLETRAQ AMEKDQLAQLLEKKULLQKVQNEKIERLTRALVTSSSITLQQSL KAKRRRVTWCLGKINKMKSNYADQWI PINITYKTKIELSINI. LREIDESVCSESDVFSNTLDTLEBIBWNPATKLLNQENIBSELN SLRADYDNLVLDYEQLRITEKEEMELKLKEKNDLDBFEALBRYTK KOQEMQLIHBISNLKNLVKHREVYNQDLENKISSKVELLREKED QIKKLQBYILDSQKLENIKMDLSYSLESIEDPKOMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATYKQMENDIOLYGSQLE AKKMQVDLEKRLQSAFNBITKLTSLIDGKVPKDLLCNLELESK ITDLQKELMKRVBENBALKREVILLSBLKSLPSEVERLRKBIQD KSEKLHIITSEKDKLPSEVVHKESRVQGLLERIGKTKDDLATTQ SNYKSTDQEPONFKTLHMDEGGKYRWVLEENERNQEIVNLSKE AQKFDSSLAALKTBLSYKTQBLQBKTREVORRLMENGLEGKIL NRDSPLQTVEREKTLITEKLQQTLEBEKTRUQEKQLEGLINGLESL QIERDQLKSDIHDTVMMIDTQBECLRALESLKQHGETINTLKS KISEVSRNLHAMERNIGETKDEFQQKWGILKKQDLEAKNTQTL TADVKUNBIIBQGRKIFSLVGEKNELQQMLESVIAEKEQLKTDL KRNIBNTIENQESLRILGDBLKKQQBLVAOCKHNBIKGEGISR TCDRLAEVEKKLKBKSQQLQLLNVQEBMSEMQKKINEIE NIKKNELKNKELTLEHHETERLBLAQKLENYGEWGKTERWDE KELQKSPETERDHLRGYIRBIBATGLYKEELKIAHIHLKEHQE TIDBLERSVSBKTAQIINTQDLEKKITKLGEBILVLHEEQBILD NYKKYSFTQETMNELBLIJETQSTKDSTTLARIEMERILARIQE SGSKGGGSLINMEKDNETTKIVSEMEGFKKDGESEDQLKENIKEIV ARHLSTEBELKVAHCCIKKSQESTINELRVNLSKRETEISTIQKG LESRICLGSHDEMKSVAKENGDLQRLQEVLQSESDQLKENIKEIV ARHLSTEBELKVAHCCIKKSQESTINELRVNLSKRETEISTIQKG LEAINDKLQNKIQEIYEKEBQLNIKQISEVQEKVNBIKQFKEER KAKDSALGS ISSKMLELTTRLQESGELQIMIKKKBEMKKVQEA LGJEJOLKENITKEIVANKESQEKEKYOPLKMITANTSQERMCE	1			
AMEKDQLAQLLERKULLQKVQMBKIENLTTMIUTSSSITLQQZL KAKRKRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LRRIDSSVCSESDVFSYTLDTISHEBWPATKLLMQENIESELN SLRADYDNLVLDYEQLKTEKEEMELKLKEKNDLDBFEALBRKTK KOQRMQLIHEISNLKNLVKHRBVYNQDLENBLSSKVELLREKED QIKKLQBYIDSQKLENIKMULSYSLESIEDPKQMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKOMKNDIQTYGGLE AKKMQVDLEKRLQSAPNBITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELMKRVERNRALRRBVILLSBLKSLPSEVERLRKBIQD KSEKLHIITSEKDKLFSEVVYKESRVQGLLBRIGKTKDDLATTQ SNYKSTDQPPQNFKTLIMDFBQKYKMVLEENRRNQSIVNLSKB AQKFDSSLGALKYRLSVKTQBLQBKTREVQERLMEMEQLKBQLE NRDSPLQTVEREKTLITEKLQTLEEVKTLTQEKDDLKQDESL AKRIEMTIENQBELRLLGQTLEEVKTLTQEKDDLKQLQESL KSIEBVSRNLHMERTGETKDEFQQKMGIDKKQDLEAKNTQTL TADVKNNEIIEQQRKIFSLIQGKNELQQMLESVIAEKGLKTDL KKNIEMTIENQBELRLLGDBLKKQQRIVAQEKNHAIKKBEGLSR TCDRLABVERKLKRBSQOLQBRQQQLLMVQERSEMQKKINBIE NLKNELKNKELTLEHMETERLBLQKLNENYBEVKSITKERKVL KELQKSFBTERDHLRGVTRIBARTGLYKEBLKIAHIHLKEHQB TIDBLRSSYSKTAQIINTQDLEKSHTKLQEBIPVLHBEQBLLP NYKKYSTQBTMMELBLLITEQSTTKDSTTLARIBMERLRLNEKP QESQEGISKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEGSLNMKKKDNETTKIVSENGPYERVDSALLRIBIEMLG SGSKGEGSLNMKKKDNETTKIVSENGPYERVDSALLRIBIEMLG LSKRLQSBIDEMKSVAREKDDLQRLQBVLQSEBQLKENIKBIV AKHLSTBEBLKVAHCCLKEGEBTIRELRVNLEKEPTBISTIQKQ LBANDKLQNKJQEIYBKEBQLNIKQISENGRKNBLKGPKBER KAKDSALQSIESKMLBLITNELQESGERIQHIKMEKBERKVQEA LGAINDKLQNKJGEIYBKEBGLIN IKQISBVQRKNBLKQFKBER KAKDSALGSIESKMLBLITNELQESGERIQHKMIKKNERMCVGEA	1 .			
KAKRRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LRRIDESVCSESDVFSNYLDTLEBIBWNDATKLINQENIBSELIN SLRADVDNIVLDYBQLERIBSIBWNDATKLINQENIBSELIN KDQEMQLIHBISNLKNLVKHREVYNQDLENKLSSKVELLRKKED QIKKLQBYDSQKLENIKMDLSYSLBSIBDPKOMKOTLFDABTV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKRMOVDLEKKLQSAFNBITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKRVBENRALRRBVILLSBLKSLPSEVERLRKBIQD KSBELHIITSEKDKLFSEVVHKESRVQGLLBEIGKTKDDLATTQ SMYKSTQQFONFKTLINDFEQKYKNVLHENDERNQSIVNLSKB AQKFDSSLGALKTELSYKTQBLQEKTREVQBRLNEMEQLKBQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDIKKQLQES QIERDQLKSDIHDTVNMNIDTQEQLKNALBSLKQHQETINTLKS KISESVSRNLHMERNTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQBKKRQQKIVACKHNAIKKEGELSR TCDRLAEVERKLKBKSQOLQBKQQQLLNVQERMSEMQKKINBIE KKNIENTIENQEBLRLLGOBLKKQQBIVACRNHAIKKEGELSR TCDRLAEVERKLKBKSQOLQBKQQQLLNVQERMSEMQKKINBIE NLKNELKNKELTLEHMETERLBLAQKLNENYBEVKSITKERKVL KELQKSFETERDHLRGYTRBIBATGLQTKEBLKIAHIHLKBERQB TIDBLRRSVSSKTAQIINTQDLEKSHTKLQBEIFVLHEBQBLLP NYKKVSTQBTMMELBLLITEQSTTKDSTTLARIBMERLRLNEKP QESQEGIKMKKRDNETTKIVZBREQFKPKDSALLRIEIEMLG SQSKQDGSLMMKKRDNETTKIVZBREQFKPKDSALLRIEIEMLG SQSKQDGSLMMKKRDNETTKIVZBREQFKPKDSALLRIEIEMLG AKHLETEBELKVAHCCLKEQEBTINELRVNLSKEPTEISTIQKQ LEAINDKLQNKIQEIYEKEBQLNI KQISBVQRKVNBLKQFKEBR KAKDSALQSIESKMLBLITNELLGSGERIQIMKKEKBERTEISTIQKQ LEAINDKLQNKIQEIYEKEBQLNI KQISBVQRKVNBLKQFKEBR KAKDSALQSIESKMLBLITNELLGSGERIQIMKKEKBERERER				AKYMKNTPYVNEVSTDEALLKRYRKBINDLKKQLBEVSLETRAQ
LRRIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN SLRADYDNLVLDYEQLATTEKEEMELKLKEKNDLDEFFALERKTK KOQRMQLIHEISNLKNLVKHREVYNQDLENKISSKVELLREKED QIKKLQEYIDSQKLENIKHDLSYSLESIEDPKOMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIQLYQSQLE AKKNOVDLEKEKLQSAFNEITKLTSLIDGKVEKDLLCNLELEGK ITDLQKELNKEVEKNENALRREVILLSELKSLSSLSSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SMYKSTDQEPONFKTLHMDFGQKYKMVLEENERMNOGIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLINEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLGESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEEVSRNLHMERNTGETKDEFOOKMYGIDKKOLLEAKNTQTL TADVKDNEIIEQQRKIFSLIQBEKNELQQMLESVIAEKEQLKTDL KKNIEMTIENQBELKLLGDBLKKQQETVAGKENHAIKKEGELSR TCDRLAEVERKLKEKSQQLQERQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLMENYEVKSITKERKVL KELQKSFETERDHLRGYIRBIBATGLQTKEELKIAHIHLKEHQE TTDELRERSVSEKTLQIINTQDLEKSHTKLQEESPVLHEEGGELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRIEKEP GEGGEIKSLTKRRDNLKTIKBALEVKHDQLKEHIRETLARIQE SQSKQEQSLNMKEKDNETTKIVSEMEGFKPKDSALLRIELEMEKP GEGKEIKSLTKRRDNLKTIKBALEVKHDQLKEHIRETLARIQE SQSKQEQSLNMKEKDNETTKIVSEMEGFKPKDSALLRIELEMEN AKHLETEBELKVAHCCLKEQEBTINELRVNLSEKETRISTIQKQ LEAINDKLONKIGEIYEKEBQLNIKQISEDQLKENIKEIV AKHLETEBELKVAHCCLKEQEBTINELRVNLSEKETRISTIQKQ LEAINDKLONKIGEIYEKEBQLNIKQISEQEUQIMIKEKEMKRVQER KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQER KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVGER IEHLKEQFETQKLNLENIETENIRLTQILLENLEEMSVYKERD		•		
SLRADYDNLVLDYEQLRTBKEEMELKLKERNDLDBFEALERKTK KNORMOLIHBISNLKNLVKHREVYNDDLENKISSKVELLREKED QIKKLQBYIDSQKLENIKMDLSYSLESIEDPKOMKOTLFDAETV ALDAKRESAFLRSENLELKERMKELATTYKOMENDIOLYQSQLE AKKKMOVDLBKELQSAFNBITKLTSLIDGKVPKDLLCNLELEGK ITDLQKRINKKVEKNEALREVILLSELKSLPSEVERLREGIOD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SMYKSTDQEPONFKTLHMDFEQKYKMVLEENERMEQEIVHLSKE AQKFDSSLGALKTBLSYKTQELQBKTREVQERLNEMEQLREQLE NRDSPLQTVSREKTLITEKLQQTLEEVKTLTQEXDDLKQLQESL QIERDQLKSDIHDTYNNUNIDTQEQLRNALESLKCHQETINTLKS KISEEVSRNLHMEBNTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQREIFSLLGEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQBELRILGDBLKKQQEIVAQEKNHAIKKEGELSR TCDRLABVERKLKRESQOLQBKQQLLLNVQEBMSEWQKKINEIE NLKNELKNKELTLEHMBTERLBLQKLNENYEEVKSITKERKVL KELQKSFBTERDHLRGYIRRIBATGLOTKEELKLAHIHLKEHQB TIDBLRRSVSSKTAQIINTQDLEKSHTKLQEEIPVLHEBOBLLP NYKKVSETQBTMNELELLTEQSTTKOSTTLARIEMERLRINEKP QESGEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKGEQSLMMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG SQSKGEQSLMMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQBULGSESDQLKENIKBIV AKHLETBEBLKVAHCCLKEQBETINELRVNLSEKETBISTIQKQ LEAINDKLQMKIQEIYEKBEQLNIKQISEVQEKVMBLKQFKEFR KAKDSALQSIESKMLETTRIQESQEEIQIMIKEKBEMKRVQEA LQIEZDQLKENTKRIVAKKESQQKEVGFKMTAVNETQEKMCB IEHLKEQFFETQKKNLENIETENIRLTQILHENLEEMRSVTKERD	1			KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL
KDQRMQI.HBISNLKNIVKHREVYNQDLENBISSKVBLIREKED QIKKLQBYIDSQKLBNIKMDLSYSIBSIEDPKOMKQTIFDABTV ALDAKRESAFIRSENISLKEKMKELATTYKOMENDIQI.YQSQLB ARKMOVDLERBLQSAFNBITKLTSI.DGKVPKDILCNLELEGK ITDLQKELNKKVEKNEALRBEVILLSBLKSLPSEVERLRKBIQD KSEKLHIITSEKDKLFSEVVHKESKVQGLLBEIGKTKDDLATTQ SNYKSTDQEPQNFKTLHMDFEQKYKMVLEBNERMNQEIVNLSKE AQKFDSSIGALKTBLSYKTQBLQEKTREVQEKLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL OIERDQLKSDIHDTVNMNIDTQEQLRNALBSIKGHQETITMTLKS KISEEVSRNLHMEBNTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRRIFSLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVERKILKBESQOLQBKQQQLLNVQBEMSEMQKKINBIE NLKNELKNKBLTLEHMETERLBLAQKINENYBEVKSITKERKVL KELQKSPETERDHLBGYIRBIBATGLQTKEBLKIAHIHLKEHQB TIDBLRRSVSEKTAQIINTQDLEKSHTKLQEEIFVLHEEGBLLP NVKKVSBTQETMNBLELLTEQSTTKDSTTLARIEMBERLAKHE QESGEEIKSLTKERRNIKATIKBALEVKHOOLKEHIRETLAKIQE SQSKQEQSLIMKEKDNETTKIVSEMEQPKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV AKHLETBEBLKVAHCCLKEQEBTINELRVNLSEKETBISTIQKQ LEAINDKLQNKIQEIYEKBBQLNIKQISEVQEKVMBLKQPKEER KAKDSALQSIESKMLEKBRQKEKSYQFLKMTAVNBIQEKMCB IEHLKEQFETQKLNLENIETENIRLTGLIHMIKEKBEMKKVQEA				LRBIDESVCSESDVFSNTLDTLSEIBWNPATKLLNQENIBSBLN
QIKKLQBYIDSQKLENIKMDLSYSLBSIEDPKOMKQTLFDAETV ALDAKRSAFLASENLEILKEKMKELATTYKOMENDIQLYQSQLE AKKKMQVDLEKELQSAFNBITKLTSLIDGKVPKDLLCNLELEGK TITOLQKBLNKEVBENBALREVILLSELKSLPSEVERLREIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEBIGKTKDDLATTQ SNYKSTDQEPQNFKTLHMDFEQKYKMVLEBNERMNQEIVNLSKE AQKFDSSLGALKTBLSYKTQBLQBKTREVQBERLMEMEQLKBQLE NRDSPLQTVEREKTLITEKLQQTLEBVKTLTQEKDDLKQLLGESL OIERDQLKSDLHDTVANNIDTQEQLRNALBSLKQHQETINTLKS KISEBVSRNLHMEBNTGETKDEFQQKMVGIDKKODLEAKNTQTL TADVKNNEIIEQQRKIFSLIQBKLKQQKTVAQEKNHAIKKBGELSR TCDRLABVERKLKBKSQQLQBLLNVQEKNHAIKKBGELSR TCDRLABVERKLKBKSQQLQBLLNVQEKNHAIKKBGELSR TCDRLABVERKLKBKSQQLQBLLNVQEKNHAIKKBGELSR NLKNELLKNKELTLEHMETERLELAQKLMENYBEVKSITKERRVL KELQKSFBTBRDHLRGYIRBIBATGLQTKEELKIAHIFLKEHQE TIDBLRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHBEDBLLP NVKKVSRTQBTMNBLELLITEQSTTKDSTTLARIBMERLRINEKF QESGEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKGEQSLMMKEKNDETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQBSHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV AKHLETBEBLKVAHCCLKEQBBTINELRVNLSKETEISTIQKQ LBAINDKLQNKIGEIYEKBEQINIKQLSEVOREKVNBLKGPKEFR KAKDSALQSIESKMLBLINTRLQBSQEBIQIMIKBKBEMFKRVQBA LGJESDQLKENTKEIVAKMKBSQBKBVGFLKMTAVNBTQEKMCE IGHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD				SLRADYDNLVLDYEQLRTBKEEMELKLKBKNDLDBFEALERKTK
ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIQLYQSQLE ARKKMOVDLBKBLQSAFNBITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVBERBALKBEVILLSELKSLPSEVERELRKEIQD KSBELHIITSKOKLFSEVVHKESRVQGLLREIGKTKDDLATTQ SMYKSTDQEPQMFKTLHMDFEQKYKMVLEENBRMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQBKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL OIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEBVSRNLHMEENTGETKDEFQQMMCSLKKQDLEAKNTQTL TADVKONEIIEQQRKIFSLIGEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELKLLGDBLKKQQBIVAQEKNHAIKKEGELSR TCDRLAEVEBKLKBKSQQLQBKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMFTERLELAQKLMENYBEVKSITKERRVL KELQKSFBTBRDHLRGYIRBIBATGLQTKESLKALHIHLKEHQE TIDBLRRSVSEKTAQIINTQDLEKSHTKLQBEIFVLHEEQELLP NVKKVSBTQETMMELELLTEQSTTKDSTTLARIEMERLBLNEKF QESQEEIKSLTKRRDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQBSHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKEIV AKHLETBEBLKVAHCCLKEQBBTINELRVBLSEKETBISTIQKQ LEAINDKLQNKIQEIYEKEBQLNIKQISBVQEKVNBLKQFKEFR KAKDSALQSIESKMLBLTNRLQESQEEIQIMIKEKBEMKRVQEA LQIESDQLKENTKRIVAKMKBSQEKEYQFLKMTAVNBTQEKMCB IGHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	1 1			KDQRMQLIHBISNLKNLVKHREVYNQDLENKLSSKVELLREKED
ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIQLYQSQLE ARKKMOVDLBKBLQSAFNBITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVBERBALKBEVILLSELKSLPSEVERELRKEIQD KSBELHIITSKOKLFSEVVHKESRVQGLLREIGKTKDDLATTQ SMYKSTDQEFQMFKTLHMDFEQKYKMVLEENBRMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQBKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL OIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEBVSRNLHMEENTGETKDEFQQMVGIDKKQDLEAKNTQTL TADVKONEIIEQQRKIFSLIGEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELKLLGDBLKKQQBIVAQEKHNAIKKEGELSR TCDRLAEVEBKLKBKSQQLQBKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMFTERLELAQKLMENYBEVKSITKERRVL KELQKSFBTBRDHLRGYIRBIBATGLQTKESLKALHIHLKEHQB TIDBLRRSVSEKTAQIINTQDLEKSHTKLQBEIFVLHEEQELLP NVKKVSBTQBTMMBLELLTEQSTTKDSTTLARIEMERLBLNEKF QESQEEIKSLTKRRDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQBSHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKEIV AKHLETBEBLKVAHCCLKEQBBTINELRVBLSEKETBISTIQKQ LEAINDKLQNKIQEIYEKEBQLNIKQISBVQEKVNBLKQFKEFR KAKDSALQSIESKMLBLTNRLQESQEEIQIMIKEKBEMKRVQEA LQIESDQLKENTKRIVAKMKBSQEKEYQFLKMTAVNBTQEKMCB IGHLKBQFETQKLNLENIETENIRLTQILHENLEBMRSVTKERD				
AKKKMOVDLEKRLOSAFNEITKLTSLIDGKVPKDLLCNLELEGK  ITDLOKREINKEVERENALIRREVILLISELKSLESEVERLEKEIOD  KSEELHIITSEKDKLESEVENKESRVOGLLEEIGKTKDDLATTO  SMYKSTDQEPONFKTLHMDFEQKYKMVLEENERMINGEIVNLSKE  AQKFDSSLGALKTELSYKTOELQEKETREVOGRINEMEOLKEQLE  NRDSPLOTVEREKTLITEKLQOTLEEVKTLTQEKDDLKOLQESL  OIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS  KISEEVSRNLHMEENTGETKDEFQOKMVGIDKKODLEAKNTOTL  TADVKDNEIIEQORKIPSLIQEKNELQOMLESVIAEKEQLKTDL  KENIEMTIENQEELRLLGDELKKQOBIVAORKHMAIKKEGELSR  TCDRLAEVERKLKEKSOQLQERQQQLLNVQEEMSEMQKKINBIE  NLKNELKNKELTLEHMETERLELAQKINENYEEVKSITKERKVL  KELQKSPBTERDHLRGYIREIBATGLOTKEBLKAHIHLKEHQB  TIDBLERSVSEKTAQIINTQDLEKSHTKLQBEIPVLHEBOELLP  NVKKVSBTQBTMNBLELLTEQSTTKDSTTLARIEMERLEKEP  QESQEEIKSLTKERDNLKTIKRALBVKHDOLKEHIRETLAKIQE  SQSKQEQSLNMKEKDNETTKIVSEMEQPKPKDSALLRIEIEMLG  LSKRLOESHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV  AKHLETBEBLKVAHCCLKEQBETINELRVNLSEKETEISTIQKQ  LEAINDKLQNKIQEIYEKEBQLNIKQISBVQEKVBLKQFKEFR  KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKBEMKRVQBA  LQIESDQLKENTKRIVAKMKBSQEKEYQFLKMTAVNBTQEKMCB  IGHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD				
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KSERLHIITSEKOKLFSEVVHKESRVOGLLERIGKTKODLATTO SMYKSTOQEFOMFKTLHMDFEQKYKMVLERIKRMNQETVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERINEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKODLKQLQESL OIERDQLKSDIHDTVMMNIDTQEQLRNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKONEIIEQQRKIFSLJOEKNELQQMLESVIAEKEQLKTDL KENIBHTIENQEELKLLGDELKKQQRIVAQEKNHAIKBGELSR TCDRLABVEEKLKBKSQQLQBKQQQLLNVQEEMSEMQKKINBIE NLKNELKNKELTLEHMETERLELAQKLMENYEEVSSTTKERKVL KELQKSFBTERDHLRGYIRBIBATGLQTKEELKIAHIHLKEHQE TIDBLERSVSEKTAQIINTQDLEKSHTKLQBEIPVLHEBQELLP NVKKVSETQETMMELELLTEQSTTKDSTTLARIEMERIRINEKP QESQEEIKSLTKERDNLKTIKBALBVKHDQLKEHIRETLAKIQE SQSKGEGLSIMMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQBEVPCDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQBEVPCDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQBEVPCBKNELKEPTLAKIQE AKHLETBEBLKVAHCCLKEQBETINELRVBLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEBQLNIKQISBVQEKVBURGKERER KAKDSALQSIESKMLBLTNRLQESQEEIQIMIKEKBEMKRVQBA LQIESDQLKENTKRIVAKMKBSQEKEYQFLKMTAVNBTQEKMCB IGHLKEQFETQKLNLENIETENIRLTQILHENLEDMRSVTKERD				
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NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISESUSRNLHMERNTGETKDEFQQKWVGIDKKQDLEAKNTQTL TADVKDNEI IEQQRKIFSLIGEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGBELKKQQEIVAQEKHHAIKKEGELSR TCDRLAEVERKLKBKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKINENYEEVKSITKERRVL KELQKSPBTERDHLRGYIREIBATGLQTKEBLKTAHIHLKEHQB TIDBLRRSVSEKTAQIINTQDLEKSHTKLQBEIPVLHEBQELLP NVKKVSETQETMNBLELLTEQSTTKDSTTLARIEMERLRIEKFP QESQEEIKSLTKERDNLKTIKRALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQPKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV AKHLETEBBLKVAHCCLKEQBETINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEBQLNIKQISBVQEKVBLKQFKEFR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKBEMKRVQBA LQIESDQLKENTKRIVAMKESQBKEYQFLKMTAVNBTQEKMCB IEHLKBQFETQKLNLENIETENIRLTQILHENLEBMRSVTKERD				
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SQSKQEQSLNMKEKDNETTKIVSEMEQPKPKDSALLRIEIEMIG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEBBLKVAHCCLKEQEBTINELRVNISEKETEISTIQKQ LEAINDKLQNKIQEIYEKBEQLNIKQISEVQEKVVBLKQFKEFR KAKDSALQSIESKMLBLTNRLQESQEBIQIMIKEKBEMKRVQBA LQIEZDQLKENTKBIVAKMKBSQKKEYQFLKMTAVNBTQEKMCB IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD				nvkkvsetqetmnelellteqsttkdsttlariemerlrlnekf
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DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH		ì	]	TENPKEGERIGKENPENTRIKUTKTLÄTPHENPERWESALKEED
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	S=serine, lainreonine, vavaline,
1			W-Tryptophan, Y-Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
			QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR
		1	IAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEK
1		1	IQBLKANEHQLITLKKOVNBTQKKVSEMEQLKKQIKDQSLTLSK
į.		1	LEIENLNLAQKLHENLZEMKSVMKERDNLRRVEBTLKLERDQLK
1		ŀ	ESLQETKARDLBIQQELKTARMLSKEHKETVDKLREKISEKTIQ
ł	l	į	ISDIQKDLDKSKDBLQKKIQBLQKKELQLLRVKEDVNMSHKKIN
l			EMEQLKKOFEPNYLCKCEMDNFOLTKKLHESLEEIRIVAKERDK
ļ			
ļ			LRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQ
ł	ļ		HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
1	ì		RIMKKLKYVLSYVTKIKEEQHBCINKFEMDFIDEVBKQKELLIK
	1		IQHLQQDCDVPSRBLRDLKLNQNMDLHIBBILKDFSESBFPSIK
I	1		TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV
1	1		NNFFNNRI LAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF
1	1		KNYQTLKTSLASGAQVNPTTQDNKNPHVTSRATQLTTEKIRBLE
1	1		NSLHBAKESAMHKESKI I KMQKBLEVINDI I AKLQAKVHBSNKC
1	ļ		LEKTKETIQVLQDKVALGAKPYKEBIEDLKMKLGKIDLEKMKNA
	i		KEPEKEISATKATVEYOKEVIRLLRENLRRSQQAQDTSVISEHT
1	1		DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN
ţ	j		ROLIKOKNELLSNNOHLSNEVKTWKERTLKREAHKOVTCENSPK
i			SPKVTGTASKKKQITPSOCKERNLODPVPKESPKSCFFDSRSKS
i			LPSPHPVRYFDNSSLGLCPBVQNAGAESVDSQP\GPWARLFQGK
ŀ	<b>i</b> .		DVP\ECKTO
5815	23	1460	SELVMWTVONRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
2012	ده	1400	
l			VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
i	1		TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
ł			SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
ľ			QNCTLRIESYGYTTDDIEFYWNGGRGAVTGVNKIELFQFSIVDY
ļ			RMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
ĺ			SWYSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
1	Į į		AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA
j	1	3	NEKNKLEMNKVQVDAHGNILLSTLBIRNETSGSEVLTSVSDPKA
1 .	ł		TMYSYDSASIQYRKPLSSRB\A+GRAP>RHGVPSKGRIRRRAS\
	•		QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
5816	861	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
			TVYHERORLELCAVHALNNVLOOOLFSOEAADBICKRLAPDSRL
	i j		NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
			VIGLILNLPSPVSLGLLSLPLRRRHLRWPCARL/VTVSYYNLDS
			K\LRAPEGPGGLRTE\*GPFLAAALAQGLCEVLLVVTKEVEEKG
			SWLRTD
5817	0F1	330	
2011	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
			VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVQK
	[		KKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG
]			RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLSP
			GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA
			HPQALMGRGFPSGMAAAGRHLCFL
5818	3	3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
			DRRLGKKPIFSSSQQRKQVSDSGDIKIKSWRGNNKKECWSYLST
			NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI
			TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA
			TAAAAATGQKNLLNGKGVRNQEGQISGARPKVLTGNLNVQAKAK
		,	Pikkatgkdspclsiagpssrstdssmefsistecldepkengs
			TEEEKPSGHKLSPCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
	'		
			NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS
			NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV
			AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK
	İ		KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHBTSTVQKSMFH
	,		DVRDNNNKDSVSEQKPHKPLINLASEISDABALQSSCRP\DPQK
			PLNDQBKEKLALBCQN18KLDKSLKHELBSKQ1CLDKSETKFPN
			HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL
			NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVXDVS
	1		LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	
	to first		L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P-Proline, Q-Glutamine, R-Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
- [			ATADSDVSSKCFSGQLSEKNSPKNMETSBSPBSHBTPETPFVGH
1	1		WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSQDDD
ì			GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK
		Ì	MKKQSSNDLFQVNSTSDDBIPRKRPEIWSRSAIVHSRERENIPR
	1	Ì	GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ
1			GIINLAFEDATENECREFSANKKFKRSVLLSVDECRELGSDEGE
{			VHTPFQASVDSFSPSDVPDGISHEHHGRTCYSRFSRBSEDNILE
1	]		CKONKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL
1			SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL
i			DLHQRBPNSD1PKNSSTKSLDSFRSQVLPQEGPVKBSHSTTTEK
1			ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIRAFEO
1			KVESIHVTDMDF+DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV
	į		PEDLSLAQYLINGTLLLARDSSKPQGITHIDTLNRWSELTSPLD
1	]		SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLI GALHLVMTLVVAAARAEKEAFVQSESI I BVLRFDDGGL
			LQTETTLGLSSYQQKSISLYRGNCR?IRFBPPMLDFHEQPVGMP
1	Į		KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFONRKILPGGNT
1			SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY
			RLRPFLGARVTVNSSFSPI INIHNPHSEPLQVVEMYSSGGDLHL
1			RLPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
1			TNASDSTEFIILPVEVBVTTAPGIYSSTEMLDFGTLRTQDLPKV
i			LNI.HLLNSGTKDVPITSVRPTPQ\NDAITVHPKPITLKAS\ESK
1			YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLBIPYQAEV
i			LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL
i l			LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
ł		-	NILLITYASKFHLPVRVYTGFLDYFVLPPKIBERFIDFGVLSAT
i	(7)		EASNILFAIINSNPIBLAIKSWHIIGDG\LSIBLVAVDRGNRTT
1			IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH
			DGAIQITTDYBILTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI
1			VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG
			KKSKIANIYFDPGLQCGDHCYVGLPPLSKSEPKVQPGVAMQEDM
1			WDADWDLHQSLPKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI
1 1			TABLSWPSILSSPRHLKFPLTNTNCSS\REEITLENP/SQDVPV
	1		YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN
1			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
			RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR
i 1			PKITEALLKDCTDSLKLRBPNFTLKRTFKVENTGQLQIHIETIE
1 1	1		ISGYSCEGYGFKVVNCQBFTLSANASRDIIILFTPDFTASRVIR
			BLKFITTSGSBFVPILNASLPYHMLATCARALPRPNWKLALYII
1 1	]		ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPPD
	i		VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
1 1	İ		GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA
	1		SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS
	· I		PLEQHPOPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
1	ł	•	SSEDSDITSLIRAMDKDFDHHDSPALHVFTEQPPSPLPKSKGKG
	l	I	KPLCRKVKPPKKQBEKEKKGKGKPQEDBLKDSLADDDSSSTTTB
] ]	ì	İ	TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI
! i	ł		KKBIPTDVKPSSLBLPYTPPLESKQRRNLPSKIPLPTAMTSGSK .
ļ I	!	l	SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP
	ł	Ì	PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
1 1	1	l	PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA
1 1	i		SLPGKNGNPTFAAVTAGYDK9PGGNGFAKVSSNKTGPSSSLGIS
[	j		HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
	ļ		VFSKLGLSRSCNQASQRSWNKFNSGPSYLWESPATDPSPSWPAS
	*		SGSPTETATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN
]			TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
			RSSDPWSNSHFPHRN
5820	310	1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ
			SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEEKMN
		İ	ENNKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\
<u> </u>			SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS

SRQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
İ	sequence	Bequence	\=possible nucleotide insertion)
		<del></del>	DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS
			ESEYIBEVRAKKKSSEEREKATEKTKKKKKHKKKSKKKKKAA
	i	1	SSSPDSP+H+EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF
			GIIPGLFSSHSDATV
5821	179	915	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
1	i		PT/IKDCSIAATGKRPSARFPHQRRKKRREMDDGLAEGGPQRSN
İ			TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS
1			SPLPPLPEDEEG\SEVTNSKSR+CVQACPPTHTPGGQPKNACR\
			SRIPSPLAALRMQGTP*RWSPFBPEPSPSTLIYRNMQRWKRIRO RWKEASHRNQLRYSBSMKILREMYERO
5822	464	4379	QTLKEMPIVMARDLEETASSSEDEEVISQEDHPCIMWTGGCRRI
1			PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
			HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHPPRSYB
}			LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLLPABYABFCNSYS
			KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP
			LLIDDFXPDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
			NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY LKQEGRDTTALMAHVEDLIIKTIISAKLAIATACKTFVPHRSSC
			FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD
			MFTVVGFVCQDPAQRASTRPIYPTFESSRRNPFQKPQRCRPLSA
		141	SDAEMKNLVGSAREKGPCKLGGSVLGLSMEEIKVLRRVKBENDR
			RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG
			APELKI+SINSKAKLHAALYERKILSLEVRKRRRRSSRLRAMRP
			KYPVITQPAEMNVKTETESEREREVALDNEDERQEASQEESAGF
	0		LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG
1			QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL
			LERTRILAHQLGDFIIVYNKETEQMABKKSKKKVEREKEDGVNM
	·		ENFORFIRQASEAELEEVLTFYTOKNKSASVFLGTHSKISKNNN
			NYSDSGAKGDHPRTIMEEVKIKPPKQQQTTBIHSDKLSRFTTSA
			EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS
]			LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP RCRSGSHTIGPPSSFQSAAHIYSQKLSRPSSAKAGSCYLNKHHS
1			GIAKTQKEGEDASLYSKRYNQSMVTABLQRLABKQAARQYSPSS
			HINLITQQVININLATGIINRSSASAPPTLRPIISPSGPTWSTO
			SDPOAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH
	İ		KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQA1FGSQT
			LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL
		i	VPKPPPNHEQVLRRATSQKASKGSSABGQLNGLQSSLNPAAFVP
5823	42	2293	ITSSTDPAHTKIMNHKHTEKQPVHHSWVHD LLTALSMBGGGGRDEPSACRAGDVMMDDPKKRDILLLADEKFDF
			DLSLSSSSANRDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
			TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
			DSPLLGPPVGRPRILLASSPALPSSGAQARLTRAPGPPHSAHALP
0.			RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAARKPKK
			BIPASPSRTKIPABKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
			RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGAS5A CTPQPVAKAKSSEFASIPAN+LPGLCPNISKS\GRMGPAMLRPA
			L\PAGPVG\ASSMQAKRVDVSBLAARQLTAPP\SASPTQPQTPE
	j		GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
! !	1		QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
1 1	l		RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
j 1	)		PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
] ]	1		GSPPSRVPQALNFSPEESDSTFSKSTATEVARBEAKPGGDAAPS
] ]	ļ		RALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPRAHVAVGSB
Į 1	[		SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPRADK ENVDSPLLKF
5824	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKPDP
			DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEOPPLP
LI			T8KSPPAWSPLAGEKPVEVYKRAHLLALHIESSSRNQAAQAAKP

Do beginning   location   location   location   location   corresponding   location   location   corresponding   lof irst   amino acid   amino acid   amino acid   amino acid   sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation   Cortesponding				(A-Alapina C-Compains B Asserbis Asid R
Cocresponding   to first   amino acid   amino acid   ceidue of   amino acid   ceidue of   amino acid   ceidue of   amino acid   ceidue of   amino acid   ceidue of   amino acid   ceidue of   amino acid   ceidue of   amino acid   ceidue of   amino acid   ceidue of   cei				Glutamic Acid R-Dhonylala-ing C Clumina
Leucine, Methonine, Neaparagine,   Percidue of   residue of   residue of   amino acid   sequence   Securine, Tethreonine, Vevaline,   Securine, Tethreonine, Vevaline,   Securine,   Tethreonine, Vevaline,   Securine,   Tethreonine, Vevaline,   Securine,   Tethreonine, Vevaline,   Securine,   Tethreonine, Vevaline,   Securine,   Tethreonine, Vevaline,   Securine,   Tethreonine, Vevaline,   Securine,   Tethreonine, Vevaline,   Securine,   Tethreonine,   Vevaline,   Securine,   Tethreonine,   Vevaline,   Securine,   Tethreonine,   Vevaline,   Securine,   Tethreonine,   Securine	, , , ,			Halistidine I-Teoleveine V-Lucino
to first union acid residue of anion acid sequence  sequ	1			L=Leucine M=Methionine N-America
samino acid residue of amino acid sequence sequence  sequence  sequence  sequence  sequence  sequence  sequence  seq	· f		1	P=Proline, O=Glutamine, N=Arginine
mino acid sequence    Sequence		J		SeSerine TeThreonine Welleline
sequence    Codon, /=possible nucleotide deletion,    -possible nucleotide insertion    EDFRSGVERFIGESKF\KINIFEKKERKESFTSLKEFTYLK   EDFRSGVERFIGESKF\KINIFEKKERKESFTSLKEFTYLK   EDFRSGVERFIGESKF\KINIFEKKERKESFTSLKEFTYLK   EDFRSGVERFIGESKF\KINIFEKKERKESFTSLKEFTYLK   EDFRSGVERFIGESKF\KINIFEKKERKESFTSLKEFTYLK   EDFRSGVERFIGESKF\KINIFEKKERKESFTSLKEFTYLK   EDFRSGVERFIGESKF\KINIFEKKERKESFTSLKEFTYLK   EDFRSGVERFIGESKF\KINIFEKKERKESFTSLKEFTYLK   EDFRSTETTLARAGOANGREGUTERAGOANCERAGOAN	1			W=Tryptophan Y=Tyrosina Y=Unknown t=Ston
Sequence   Impressive multiple mulcotide insertion	1		e e e e e e e e e e e e e e e e e e e	Codon /=nossible nucleotide deletion
EDPRESGVERPIGESER KEINLEPEKERMENSPTSLAGETYTIS.  BSPLIAPPROPERLAIASSPALPSSCAGARLTRAGEPERSHALAP  ERSCITHAASQAATQREGTELLLERAASVERGETGAAKETRE  ERPSSPTKTTERKERERENDLADREAGAVAVPAASGIGGOK  ERLEVP\NKLGISKTLLLERAASVERGETGAAKETRE  ERPSSPTKTTERKERERENDLADREAGAVAVPAASGIGGOK  ERLEVP\NKLGISKTLLLERAASVERGETGAAKETRE  ERPSSPTKTTERKERERENDLADREAGAVAVPAASGIGGOK  ERLEVP\NKLGISKTLLLERAAGVATISKS CORDALIBOR  L\PAGFUG\ASSGAGAKVUTUSELAARQUTAEP\SASPTQPQTBE  GGG\GUINSGCOMESSSQALESSAGATESSAGATVHISTER  ERSSPAGSILGAMEVSALPTPASERCGGIPMTPETTMERAVES  PLACVUTAURISSEGREKENAMTERTERSKERKTERER LYDVSEPR  ERSSPAGSILGAMEVSALPTPASERCGGIPMTPETTMERAVES  PLACVUTAURISSEGREKENAMTERTERSKERKTERER LYDVSEPR  ERSSPAGSILGAMEVSALPTPASERCGGIPMTPETTMERAVES  ERSSPAGSILGAMEVSALPTPASERCGGIPMTPETTMERAVES  ERSSPAGSILGAMEVSALPTPASERTICHIDETIPETHAVAVGES  ERSSPAGSILGAMEVSALPTSASGELLELIDETIPETHAVAVGES  ERSSPAGSILGAMEVSALPTSASGELLELIDETIPETHAVAVGES  ERSSPAGSILGAMEVSALPTSASGELLIDITETHAVAVGES  ERSSPAGSILGAMEVSALPTSASGELDITETHERESTANTAVASEBAGGETYVESG  SEPESSVEQALAFSEBESDETTSASTATEVAREREREREGGARAS  ERLEVTRAGENERATIVASSTATEVAREREREREREGGARAS  ERLEVTRAGENERATIVASSTATEVAREREREREREGGARAS  ERLEVTRAGENERATIVASSTATEVAREREREREREGGARAS  ERLEVTRAGENERATIVASSTATEVAREREREREREREGGARAS  ERLEVTRAGENERATIVASSTATEVARERERERERERERERERERERERERERERERERERER	Í	l .	J Degas	\=possible mucleotide incortion\
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BCPCQAASEVGRBEFLDRLIRSEDGEIVSTPRLQYYDKVLELLD VIGDPELVIQLATSATTPASDDW\KSQATL\RTCIPKHHL\DLG \\ \text{UNSQAYGSL} * PQIPDSSRQLDCLRQLUVULCERGQLQDLVEFS \\ \text{YVNLHNEVVGIIESRARAVDLMTHNYYELLYAPHIYRHNYRKAG} \\ \text{TVMPEYGMRLGRBVRTLRGLERQCNCYLAALNCLRLIRPEYAMI} \\ \text{VQFVSGAVYDRPGASPKRHHOGECTAAPTMRQIEILELEDLEKE} \\ \text{CSLARIRLTLAQHD?SAVAVAGSSSAEEMVTLLVQAGLEFDTAIS} \\ \text{LCQTPKLPLTPVYEGLAPKCIKLQPGGEAAQARAWAWIAANQLS} \\ \text{SVITTKESSATDRAMRLLSTYLERYKVQNNLYHHCVINKLLSHG} \\ \text{VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC} \\ \text{VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC} \\ \text{VSQLLRDHSAAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR} \\ \text{AAAQRSRQKHTDKADALHQQHESLEKDMLALRKEIQSLQAELAW} \\ \text{WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPQGQHG} \\ \text{CREQLELPQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP} \\ \text{AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLGALQPSLTAQTA} \\ \text{WGRLVVDPSPPLLAFPLLSSAQVHP} \\ \text{VGLVVDPSPHPLLAFPLLSSAQVHP} \\ \text{VGGUVVDPSPHPLLAFPLLSSAQVHP} \\ \text{VGGGENSALKSYTLREPPPTLPSGLAVYPAVLQDGKFASVFVYK} \\ \text{RRHEDKVNKAAKVP**HLKTLRHPCLLRFLSCTVBADGIHLVTE} \\ \text{RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL}	1 .		•	
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WQGLVVDPSPHPLLAFPLLSSAQVHP  5827 194 2287 GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK RENEDKVNKAAKVP++HLKTLRHPCLLRFLSCTVRADGIHLVTE RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL	j	1		
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RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL	~~~′	154	4401	
		i		
		l		SSVFVSRDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS		ŀ		
SPOQTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL	] [	ļ		
TLKSREEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP	L			THESERBETER FREE LEDRYSCLSEELIASRLVPLLLNQLVPARP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			VAV\KSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLF
			EVHEEHVRMVLLSHIKAYVGALSLREQLKKV\IL\PQVLLG\LR
			D\TSDSIVAITLHSLAVLVSLLGPEVVVGGERTKIFKRTAP\SF
1		Í	TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKK
l	ì	}	SBEWPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV
ì			BESSWDDCRPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT
l l			RESMPWKSSLPQKISLVQRGDDADQIBPPKVSSQBRPLKVPSBL
ļ			GLGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRT
İ	i e		RMVPKKDDVSPVMQFSSKFAAABITEGRAEGWEEEGELNWEDNN
			W
5828	2	257	AREGGSLGAVAACGELSYSCDPCPARPHTSW_TRFVKMEFQAVV
į .			MAVGGGSRMTDLTSSIPKPLLPVGNKFLIWY?LNLLERVGFEEV
1	J	I	IVVTTRDVQKALCABFKMKMKPDIVCIPDDADMGTADSLRYIYP
1		1	KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMLMRKGODSI
1	}	]	EPVPGQKGKKKAVEQRDFIGVDSTGKRLLFMANEADLDEELVIK
1			GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS
1		ŀ	RL\IPYLV/RGKQFSSASSQQGTRKEKEGGSKGKRGLKSFRISY
1		l	SFY*KEANYTGTGAPY\D\ACWI
5829	260	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS
			GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN
]	i	i	YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGGELP
			ASGGADTOVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY
ı	,		PRTPHPHERKVETVEDFFLHLLRLIOSLR*SICRSLLPLLWISF
1	1		LLILPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQQPRKRK
i	!	· .	QKT+VTSPVKVK/VSIPLAVTDALBHIMEQLNVLTQTVSILEOR
1	1	. 4	LTLTEDKLKDCLENQQKLFSAVQQKS
5830	4496	3139	GGKMAAPERROLTQEQTEKLLQFQDLTGIESMDOCRHTLEOHNW
****	1		NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR
ļ		0	POPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRPDPRSKV
l			TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELRFL
			LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPE
			GYRVSQALRENTYPFLAMINLKDRRE*PV\VGRLEGLI\QPDDL
	1		INQLTFIMDANQTYLVSERLERBERNQTQVLRQQQDEAYLASLR
1	}		ADQEKERKKREERERKRRKKEEVQQQKLABEERRQNLQEEKERK
			LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHPSOSLTVIHDF
			LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLOE\A
	Į i		GLSHTEVLEVQDLTDE
5831	71	2897	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSBRQVKD
****	'*	,	TDDIESPKRSIEDSGYIDCWDSERSDSLSPPRHGRDDSFDSLDS
		*	FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS
1			ARRISHGEPKSAVPFNOYLPNKSNOTAYVPAPLRKKKARREEYR
1	1		
			I KEMELVLEDVCITIKKVIVUALIDDE, DAGZUUVDELEMBURDE :
			KSWSTATSPAGLGKKALQDYGPRT\PVS\DDABSTSMFDMRCEE RAAVOPHSRAROFOLOLINNOLPRRDDKWODDLAPMKSRKPSVS
			KAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS
			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKKMEKLLAGEDGTSERRKSIKTYRBIVQEKERRE
			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKKMEKLLAGEDGTSERRKSIKTYRBIVQBKERRE RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILB
			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKKMEKLLAGEDGTSERRKSIKTYRBIVQBKERRE RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILB RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS
			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKEBERKKMEKLLAGEDGTSERRKSIKTYRBIVQBKERRE RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTPK
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEBRKMEKILLAGEDGTSERRKSIKTYRBIVQBKERRE RELHEAYKNARSQEBAGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSPLNDDNPMKYLRQQSLPPPKFTATVBTTIARAS VLDTSMSACSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEBKERECPTVAPAHSLTKSQMPPGVARVH
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKRMEKLLAGEDGTSERRKSIKTYRBIVQBKERRB RELHEAYKNARSQBEARGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSACSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEKERECPTVAPAHSLIKSQMFSGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTEKTEPNSQBDKND
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKKMEKLLAGEDGTSERRKSIKTYRBIVQBKERRB RELHEAYKWARSQEBARGILQQYIERFTISEAVLERLEMPKILB RSHSTEPNLSSFLNDPNPMKYLKQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTPK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEEPSSPQLKND
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKKMEKLLAGEDGTSERRKSIKTYRBIVQEKERRE RELHEAYKWARSQEBARGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFESVARVH GSPLELKQDNGSIEINIKKPNSVPQELAATTRKTEPNSQEDKND GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVBFPSSPQLKND VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPFLD
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKKMEKLLAGEDGTSERRKSIKTYRBIVQBKERRB REHEAYKWARSQEBARGILQQYIERFTISEAVLERLEMPKILB RSHSTRPNLSSFLNDPNPMKYLRQQSLPPPRFTATVETIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMPBGVARVH GSPLELKQDMGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVBFFSSPQLKND VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPFLD KMPBANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEBERRR
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEBRKRMEKLLAGEDGTSERRKSIKTYRBIVQBKERRE RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSACSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLITKSQMPPGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVBFPSSPQLKND VSEKKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTPFFLD KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKWAWDPERERRR QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEKEERRY
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKMEKLLAGEDGTSERRKSIKTYRBIVQBKERRE RELHEAYKNARSQEEABGILQQXIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLITKSQMPEGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVBFPSSPQLKND VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLITPFLD VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLITPFFLD KMPEANQLHLPNLNSQVDSPSSEKSPVTTFPKFWAWDPEBERRR QKWQQEGSRLLQBRYQ\KEQDK\LKEE\WEKAQKEVBKEERRY YBBEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL
-			EAAVQPHERARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKRMEKLLAGEDGTSERRKSIKTYRBIVQBKERRB RELHEAYKWARSQBEARGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEBKERECPTVAPAHSLITKSQMFFGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTEKTEPNSQBDKND GGRSRKGNIELASSEPQHPTTTVTRGSPTVAFVBEPSSPQLKND VSEKKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPFLD KMPBANQLHLPNLNSQVDSPSSEKSPVTTPFKFMAWDPEBERRR QEKWQQEQBRLLQERYQ\KEQDK\LKEE\MEKAQKEVEREERRY YEBEP*II\RDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDBKQDRRWKKSPQGDDSDLLLKTRESDRLBEKGSLTEGAL
-			EAAVQPHERARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKKMEKLLAGEDGTSERRKSIKTYRBIVQBKERRB RELHEAYKWARSQBEARGILQQYIERFTISEAVLERLEMPKILB RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVBTTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VOGKVSVNGETVHREEBEERECETVAPAHSLITKSQMPFGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGNIELASSEPQHPTTTVTRCSPTVAFVEFPSSPQLKND VSEBKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLIFPFLD KMPBANQLHLPNLNSQVDSPSSEKSPVTTPFKFMAWDEBEBERRY YBBBP*II\RDPVPFTVSSSADQLSTSSSMTEGSGTMKIDL GNCQDBKQDRRWKKSFQGDDSDLLLKTRESDRLBEKGSLTEGAL AHSCNPVSKGVPEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKKMEKLLAGEDGTSERRKSIKTYRBIVQBKERRB RELHEAYKWARSQBEARGILQQYIERFTISEAVLERLEMPKILB RSHSTEPNLSSFLNDPNPMKYLKQOSLPPPKFTATVBTTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTPK VDGKVSVNGETVHRBEEKERECETVAPAHSLITKSQMFEGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGNIELASSEPQHFTTTVTRGSPTVAFVBFPSSPQLKND VSEKDQKKPENEMSGKVBLVLSQKVVKPKSPEPEATLTFPFLD KMPEANQLHLLPNLNSQVDSPSSEKSPVTTFPKFMAMDPEBERRR QBKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKBVBEEERRY YBBEP*II\EDPVVPFTVSSSSADQLSTSSMTEGSGTMNKIDL GNCQDEKQDRRWKSPQGDDSDLILKTRESDRLBEKGSLTEGAL AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEBRKRMEKLLAGEDGTSERRKSIKTYRBIVQBKERRE RELHEAYKNARSQEKARGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSPLNDPNPMKYLRQQSLPPPKFTATVBTTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEBEKERECPTVAPAHSLTKSQMPPGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGHIKLASSEPQHFTTTVTTRCSPTVAFVBFPSSPQLKND VSEKKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTPFFLD KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKMAWDPEBKRRR QBKWQQEQBRLLQERYQ\KEQDK\LKEE\WEKAQKEVEKEERRY YBBBP*II\EDPVVPFTVSSSSADQLSTSSSMTEGGFTMNKIDL GNCQDBKQDRRWKKSPQGDDSDLLLKTRESDRLBEKGSLTEGAL AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKICSSCGL PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR
-			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKRMEKLLAGEDGTSERRKSIKTYRBIVQBKERRE RELHEAYKNARSQEBAGGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLITKSQMPPGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVBFPSSPQLKND VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTPFLD KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPERERRR QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEKEERRY YBEBP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDEKQDRRWKKSPQGDDSDLLLKTRESDRLBEKGSLTEGAL AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PLGKGAAMIIETLMLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL
5832	2454	829	EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKRMEKLLAGEDGTSERRKSIKTYRBIVQBKERRB RELHEAYKNARSQEBARGILQQYIERFTISEAVLERLEMPKILB RSHSTBPNLSSFLNDPNPMKYLRQQSLPPPKFTATVBTTIARAS VLDTSMSACSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLITKSQMPEGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGNIELASSBPQHFTTTVTRCSPTVAFVBFPSSPQLKND VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLITPFFLD KMPBANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPBEKRRR QBKWQEQBRLLQBRYQ\KEQDK\LKEB\WEKAQKEVBEEERRY YBEBP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDBKQDRRWKKSFQGDDSDLLLKTRESDRLEBKGSLTEGAL AHSGNPVEKGVHEDWQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PILGKGAAMIIETLNIYFHLQCFRCG\ICKGQLGDAVSGTDVRIR NGLINCNDCYMRSRSAGQPTTL PGRFFRHGSCAFQKQCIMLHICQYFLQGBCKFGTSCKRSHDFSN
5032	2454	829	EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKBEERKRMEKLLAGEDGTSERRKSIKTYRBIVQBKERRE RELHEAYKNARSQEBAGGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLITKSQMPPGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBDKND GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVBFPSSPQLKND VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTPFLD KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPERERRR QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEKEERRY YBEBP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDEKQDRRWKKSPQGDDSDLLLKTRESDRLBEKGSLTEGAL AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PLGKGAAMIIETLMLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Bequence	\=possible nucleotide insertion
	Bequence		VPOGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
1			RVHFHLPYRWQFLDRGKWEDLDNMELIREAYCNPKIRRILCSES
		1	ASTPHSHCINFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
	Í	ŀ	YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
i	ł		PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN+KGLPQTQIR\AP
1	ĺ		QDVTTMQTCNTKFFGPKSIPDYWDSSALPDPGPQKITLSSSSEB
	i		YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG
ļ			GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF
l			ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
<u> </u>	İ		GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV
			TPSILLALGSLFSSRQ
5833	170	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
			ROGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
1	!		GRDWNVKWBENTLHAVAKNYTILQTIPPFERPFKDHQVCLENNM
Į.			GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKPPRF
1	ł	ŀ	RNRKLKATRORMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN
			EMYGTPSVFLTREGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
		<u> </u>	DISFNGGQIVVTTSIGQDLKSYHNQTISFREDPHYNDTAGYFII
			GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
1			YYRRCABVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR
į			PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG
i			GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV FYETGLNVPRDOLOGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
į į			YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVBTIRLKDDBIL
1	2.		KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP
1		(4)	EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
			KKAASKGLEQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EB\MGN
l		2	PDASYNLGVLHLDGIFPGVPGRNQTLAGEYPHKAAQGGHMEGTI.
1			WCSLYYTTGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
1			AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
		~	GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLELS
			VOMYAQAALDGDSQGPFNLALLIEEGTIIPHHILDFLEIDSTLH
} `	8.	7	SNNISILORLYERCWSHSNEBSFSPCSLAWLYLHLRLLWGAILH
			SALTYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
1			STASPAVTPAADASDODOPTVTNNPEPRG
5834	17	4020	RFRRGGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG
			SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV
	!		TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR
	Ì		NAFVTGIARYIEQATVHSSMNEMLKEGQEYAVMLYTWRSCSRAI
			POVKCNBOPNRVBIYEKTVBVLEPEVTKLMNFMYFQRNAIBRFC
			GEVRRLCHARRRKDFVSRAYLITLGKFINMFAVLDELKNMKCSV
			KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ
			QQLEVISGYEBLLADIVNLCVDYYENRMYLTPSEKHMLLKVMGF
			GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI
			KLARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
] .			RFISELARYSNSEVVTGSGRQEAQKTDABYRKLFDLALQGLQLL
]			SONSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
			ERKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ
		i e	VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
	ļ		RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK
		·	KTLRSSLEGPTILDIEKPHRESFFYTHLINFSETLQQCCDLSQL
1			WFREFFLELTMGRRIOFPIEMSMPWILTDHILETKEASMMEYVL
			YSLDLYNDSAHYALTRENKOFLYDRIEABVNLCFDOFVYKLADO
			YSLDLYNDSAHYALTRFNKQFLYDBIEABVNLCYDQFVYKLADQ IFAYYKVMAGSILLLDKRLRSECKNOGATIHLPPSNRYETLLKOR
			IPAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR
			IFAYYKVMAGSILLDKRLRSECKNQGATIHLPPSNRYETILKQR HVQILGRSIDINRLITQRVSAAMYKSIBLAIGRFRSBDLTSIVE
			IFAYYKVMAGSILLDKRLRSECKNQGATIHLPPSNRYETLLKQR HVQILGRSIDLNRLITQRVSAAMYKSLELAIGRFRSEDLTSIVE LDGLLEINRMTHKLLSRYLTLDGFDAMFRKANHNVSAPYGRITL
			IFAYYKVMAGSILLDKRLRSECKNOGATIHLPPSNRYBTILKOR HVQILGRSIDLNRLITORVSAAMYKSLBLAIGRFBSBDLTSIVB LDGLLEINRMTHKLLSRYLTLDGFDAMFRBANHNVSAPYGRITL HVPWBLNYDFLPNYCYNGSTNRFVRTVLPPSOEFORDKOPNAOP
			IPAYYKVMAGSILLDKRLRSECKNOGATIHLPPSNRYBTILKOR HVQILGRSIDINRLITORVSAAMYKSLELAIGRFBSBDLTSIVE LDGLLEINRMTHKLLSRYLTLDGFDAMFRKANHNVSAPYGRITL HVPWBLNYDPLPNYCYNGSTNRFVRTVLPPSOEFORDKOPNAOP QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV
			IFAYYKVMAGSILLDKRLRSECKNQGATIHLPPSNRYETILKQR HVQLLGRSIDLNRLITQRVSAAMYKSLBLAIGRFRSEDLTSIVE LOGILEINRNTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL HVPWBLNYDFLPNYCYNGSTNRFVRTVLPFSQEFQRDKQPNAQP QYLHGSKALMLAYSSIYGSYRNFVGPHFQVICRLLGYQGIAVV MKKLLKVVKSLLQGTILQYVKTLMBVMPKICRLPRHEYGSPGIL
		*	IPAYYKVMAGSILLDKRLRSECKNOGATIHLPPSNRYBTILKOR HVQILGRSIDINRLITORVSAAMYKSLELAIGRFBSBDLTSIVE LDGLLEINRMTHKLLSRYLTLDGFDAMFRKANHNVSAPYGRITL HVPWBLNYDPLPNYCYNGSTNRFVRTVLPPSOEFORDKOPNAOP QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV

PCT/US00/34263

SRQ			
	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=:)
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		buquene	\=possible nucleotide insertion)
	sequence	L	
			LIBRLGTPQQIAIAREGDLLTKERLCCGLSMFEVILTRIRSFLD
		i	DPIWRGPLPSNGVMHVDECVEFHRLWSAMQFVYCIPVGTHEFTV
		}	EOCFGDGLHWAGCMIIVLLGOORRFAVLDFCYHLLKVOKHDGKD
		1	
		i	EIIKNVPLKKMVERIRKPQILNDBIITILDKYLKSGDGEGTPVE
		į.	HVRCFQPPIHQSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPBVVVSRCMLQNNNNL
ددود	4203	1304	
			DACCAVLSQBSTRYLYGBGDLNFSDDSGISGLRNHMTSLNLDLQ
		i .	SONTYHHGREGSRMNGSRTLTHSISDGQLQGGQSNSKLFQQEPQ
		1	TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSQQT
		}	PRFNPIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPQGNSIYI
		1	RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC
		1	PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS
i		i	SOSSAHSOYNIONISTGPRKNOIEIKLEPPORNNSSKLRSSGPR
	l	•	
i		!	TSSTSSSVNSQTLNRNQPTVYIAASPPNTDRIMSRSQPKVYISA
	l	I	NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH
	l	1	HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP
		i	GVVSPTFELTNLLNHPDHYVETENIHHLTDPTLAHVDRISETRK
	1	F	
		1	LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A
		I	QEFETSWGNIWRLRLYRRF*NYAGNVAHTCSPSYSVD*ALLVHQ
	l	i	KARMERLORELBIOKKKLDKLKSEVNEMENNLTRRRLKRSNSIS
		i	
		1	QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI
	ĺ		HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTEDDEGAQWNCTA
		i	CTFLNHPALIRCEQCEMPRHF
5836	361	2303	FAITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK
3030	302	1 2303	SDVNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGBIFSGIK
		1	
		,	VZAEBNDTQILFNYLSSCKNESEILSLFSBVQGPWSFIYYQASS
	191		HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE
-		1	VPAS\DFSBLILSLISFPDALFYNCILGNIFLGRILLKKMLIA*
			1110 1010000000000000000000000000000000
	l	<u> </u>	TYPOOPYOUT YOU COMPRISE THE WILL BY STACKET UNDER TAUT
			VXFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHNRLIAVI
			FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR
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	•	o.	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE
	-	9	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPLDB PIDLLNVAFIAEKKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA
			FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEKKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSMB
		,	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSMB BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQBG
		·	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEKKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSMB
			FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSMB BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQBG
			FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPI.DE PIDLLMVAFIAEBKTMPTTFMREGNKQKNKCKIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIMNFVEINVSME BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQBG VKSYQSNAKVVLTGIGADEQLAGYSRHEVRFQSHGLBGLINKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW
			FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEBKTMPTTENREGNKQKNKCKIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQBG VKSYQSNAKVVLTGIGADEQLAGYSRHEVRFQSHGLBGLNKEIM MELGRISSRNLGRDDRVIGDHGKKARFPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
	<u>.</u>		FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGMLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLBGLNKEIM MELGRISSRNLCRDDRVIGDHGKKARFPFIDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKETKL
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEBKTMPTTENREGNKQKNKCKIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQBG VKSYQSNAKVVLTGIGADEQLAGYSRHEVRFQSHGLBGLNKEIM MELGRISSRNLGRDDRVIGDHGKKARFPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPLDB PIDLLNVAFIAEBKTMPTTFMREGNKQKNKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWMFVEINVSMB ELQKLRRTRICHLIRPLDTVLLDDSIGCAVFASRGIGMLVAQBG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLBGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGBKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMBKINEKASDKCGRLQIMSLENLSIBKETKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIFFLDB PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME ELQKIRRTRICHLIRFLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLITASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKBTKL NGNAVAQAPVTNCCYJATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVEERLWLTLEWPSNQPTQLVSSCFGGELLQWDLT
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPI.DE PIDLINVAFIAEBKTMPTTFMREGNKQKNKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME BLQKIRRTRICHLIRPLDTVILDDSIGGAVWFASRGIGNLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW BKANLTLPRGIGBKILLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKKTKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPYQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPI.DE PIDLLMVAFIAEBKTMPTTFMREGNKQKNKCKIPSEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIMNFVEINVSME BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHEVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGBKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKETKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSNRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPI.DE PIDLLMVAFIAEBKTMPTTFMREGNKQKNKCKIPSEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIMNFVEINVSME BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHEVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGBKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKETKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSNRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCKIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIMNFVEINVSM BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLBGLINKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKLNEKASDKCGRLQIMSLENLSIBKRTKL NGNAVAQAPVTNCCYLATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVCDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCMHPTKEGCLAFGT
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIFILDB PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIMMFVEINVSME BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKLNEKASDKCGRLQIMSLENLSIBKRTKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNESRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVMNTLSIKNNYDVKNFMQCVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIFFLDB PIDLLNVAFIAEBKTMPTTFRNEGNKQKNKCEIPSEFSKDVAA AAADSPNKHVSVPPRITGRAGLKELQAVSPSRIMNFVEINVSME ELQKIRRTRICHLIRFLDTVLDDSIGCAVWFASRGIGMLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLRLAAVELGLITASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKBTKL NGNAVAQAPVTNCCYJATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVCDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGFPVPPMSLGGE GDRPSLALYSCGGGIVLQHNPWKLSGEAFDINKLIRDTNSIKY
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADHIPILDE PIDLLNVAFIAEBKTMPTTFNREGNRÇKKKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSMB ELQKIRRTRICHLIRPLDTVILDDSIGGAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLARLAAVELGLITASALLPRRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKETKL MGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVCDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCTGGEGIVLQHNPWKLSGEAFDINKLIRDTNSTKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDE PIDLINVAFIAEBKTMPTTFNREGNRÇKNKCEIPSBEFSKDVAA AAADSPNKHVSVPPRITGRAGLKELQAVSPSRIWNFVEINVSMB ELQKIRRTRICHLIRPLDTVILDDSIGGAVWFASRGIGMLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLALAAVELGLIASALLPRRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKETKL MGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVCDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCTGGEGIVLQHNPWKLSGEAFDINKLIRDTNSTKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPI.DB PIDLINVAFIAEBKTMPTTFMREGNKQKNKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSMB BLQKIRRTRICHLIRPLDTVILDDSIGGAVWFASRGIGNLVAQBG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW RKANLTLPRGIGRKILLRLAAVELGLITASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKETKL MGNAVAQAPVINCCYLATGSKDQTIRIWSGSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPYQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCIGEGGIVLQHNPWKLSGEAFDINKLIRDTNSTKY KLPVHTRISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPI.DB PIDLINVAFIAEBKTMPTTFNREGNRQKNKCKIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSMB BLQKLBRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQBG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW RKANLTLPRGIGGKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKKTKL NGNAVAQAPVINCCYLATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIBIFQ\IPPLKLICTIQQH HKLVMTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDB PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRASLKELQAVSPSRIVMFVEINVSME ELQKURRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKKARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKLNEKASDKCGRLQIMSLENLSIBKRTKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGPAYSLAFSSVDIGSLAIGVCDG MIRVMNTLSIKNNYDVKNFWQGVKSKVTALCMHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGEGGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVMAMEPHIH*MEGL VFCPPIDGYSPGCWD\AFPGKEAPVAIPRG\HQGRLLCVAWSPL
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPI.DB PIDLINVAFIAEBKTMPTTFNREGNRQKNKCKIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSMB BLQKLBRTRICHLIRPLDTVLDDSIGCAVWFASRGIGNLVAQBG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW RKANLTLPRGIGGKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKKTKL NGNAVAQAPVINCCYLATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIBIFQ\IPPLKLICTIQQH HKLVMTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDB PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSEFSKDVAA AAADSPNKHVSVVPDRITGRAGLKELQAVSPSRIMMFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQBG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLBGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKETKL NGNAVAQAPVTNCCYLATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSMRRKYTLFSASSEGQNISRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGFPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIBIFQ\IPMLKLICTTQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPTQGHTAQDYPVMAWBPHIH*WEGL VFCPFIDGISPGGMD\AFFGKEAPVAIFRG\HQGRLLCVAMSPL DPDCTYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ
5837	4792	903	FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDB PIDLINVAFIAEBKTMPTTFNREGNKQKNKCEIPSEFSKDVAA AAADSPNKHVSVPPRITGRAGLKELQAVSPSRIWNFVEINVSME ELQKIRRTRICHLIRPLDTVLLDDSIGGAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW RKANLTLPRGIGBKLLLRLAAVELGLITASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKBTKL NGNAVAQAPVTNCCYLATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSVDLGSLAIGVCDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCGEGEIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTRISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLWNTISWHHR\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWBPHIH*WBGL VFCPPIDGYSPGCWD\AFPGKBAPVAIFRG\HQGRLLCVAWSPL DPDCTYSG\ADDPCVHKWLTSMQDHSRPPQGKKSIELEKKZLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEBSMKENSGPVENGVSDQ
5837		903	PPMCHLQERYFKSYLLMYT*KEVIQQPIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDE PIDLINVAFIAEKKTMPTTFNREGNKQKKKKEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME BLQKIRRTRICHLIRPLDTVILDDSIGGAVWFASRGIGMLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLFIW KKANLTLPRGIGEKLLLALAAVELGLIASALLPRRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKEKTKL MGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGWMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRWMNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSTKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVMAWEPHIH*WEGL VFCPPIDGYSPGCWDAFPGKRAPVAIPRG\HQGRLLCVAWSPL DPDCTYSG\ADDFCYHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKARPKKKKKPTIRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV
5837	4792	903	PPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDB PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIVMFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKKARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKLNEKASDKCGRLQIMSLENLSIBKRTKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGGLLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGPAYSLAFSSVDIGSLAIGVGDG MIRVMNTLSIKNNYDVKNFWQGVKSKVTALCMHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCTGEGGIVLQHNPWKLSGEAFDINKLIRDTNSTKY KLPVHTEISWKADGKIMALGNEGSEBIFQIPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWBPHIH*WEGL VFCPPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCTYSG\ADDFCYHKWLTSMQDHSRPPQGKKSIELEKKZLSQ PKAKPKKKKPTLRTPVKLESIGBREESKMENSGPVENGVSDQ EGREQAREPELPCGLAPAVSREPVICTPVSSGFBESKVTINNKV ILLKKEPPFKEKFETLIKKRKARSLLPLSTSLDHRSKEELHQDCL
5837	4792	903	PPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDB PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIVMFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKKARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKLNEKASDKCGRLQIMSLENLSIBKRTKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGGLLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGPAYSLAFSSVDIGSLAIGVGDG MIRVMNTLSIKNNYDVKNFWQGVKSKVTALCMHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCTGEGGIVLQHNPWKLSGEAFDINKLIRDTNSTKY KLPVHTEISWKADGKIMALGNEGSEBIFQIPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWBPHIH*WEGL VFCPPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCTYSG\ADDFCYHKWLTSMQDHSRPPQGKKSIELEKKZLSQ PKAKPKKKKPTLRTPVKLESIGBREESKMENSGPVENGVSDQ EGREQAREPELPCGLAPAVSREPVICTPVSSGFBESKVTINNKV ILLKKEPPFKEKFETLIKKRKARSLLPLSTSLDHRSKEELHQDCL
5837	4792	903	PPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDB PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSEFSKDVAA AAADSPNKHVSVPDRITGRASLKELQAVSPSRIVMFVEINVSME ELQKIRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLCRDDRVIGDHGKKARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKLNEKASDKCGRLQIMSLENLSIBKRTKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSECQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGPAYSLAFSSVDIGSLAIGVCDG MIRVMNTLSIKNNYDVKNFWQGVKSKVTALCMHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQIPPLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVMAMSPHIH*WEGL VFCPPIDGYSPGCWD\AFPGKEAPVAIPRG\HQGRLLCVAWSPL DPDCTYSG\ADDFCYHKWLTSMQDHSRPPQGKKSIELEKKZLSQ PKAKPKKKKPTLRTPVKLESIDGNEEBSMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSRBPVICTPVSSGFERSKVTINNKV ILLKKEPPPKERPSTLIKKRKARSLLPLSTSLDHESKEELHQDCL VLATAKHSRBLNEDVSADVEERFHIGLFTDRATLYRMIDIEGKG
5837	4792	903	PPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDB PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSBEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIMMFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKLNEKASDKCGRLQIMSLENLSIBKRTKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGBLLQWDLT QSWRRKYTLFSASSEGQNESRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCMHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGEGGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIBIFQ\IPNLKLICTTQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAMSPHIH*MBGL VFCFPIDGYSPGCMD\AFFCKEAPVAIFRG\HGGRLLCVAWSPL DPDCTYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKARPKKKKKPTLRTPVKLASIDGNEEBSMKENSGPVENGVSDQ EGERQARPBELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKFPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRBLNEDVSADVERFFHLGLFTDRATLYRMIDISGKG HLENGHPELPHQLMLWKGDLKGVLQTAAERGBLTDNLVAMAPAA
5837	4792	903	PPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDB PIDLLNVAFIAEBKTMPTTFNREGNKQKNKCEIPSEFSKDVAA AAADSPNKHVSVPDRITGRASLKELQAVSPSRIVMFVEINVSME ELQKIRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLCRDDRVIGDHGKKARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKLNEKASDKCGRLQIMSLENLSIBKRTKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSECQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGPAYSLAFSSVDIGSLAIGVCDG MIRVMNTLSIKNNYDVKNFWQGVKSKVTALCMHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQIPPLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVMAMSPHIH*WEGL VFCPPIDGYSPGCWD\AFPGKEAPVAIPRG\HQGRLLCVAWSPL DPDCTYSG\ADDFCYHKWLTSMQDHSRPPQGKKSIELEKKZLSQ PKAKPKKKKPTLRTPVKLESIDGNEEBSMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSRBPVICTPVSSGFERSKVTINNKV ILLKKEPPPKERPSTLIKKRKARSLLPLSTSLDHESKEELHQDCL VLATAKHSRBLNEDVSADVEERFHIGLFTDRATLYRMIDIEGKG
5837	4792	903	PPMCHLQERYFKSYLLMYT*KEVIQQPIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGEIDSMVIATLADRHIPILDB PIDLLNVAPIAEBKTMPTTFNREGNKQKNKCEIPSEFSKDVAA AAADSPNKHVSVYPDRITGRAGLKELQAVSPSRIMNFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGMLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRPQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLRLAAVELGLITASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKBTKL NGNAVAQAPVTNCCYLATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RIVKWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGFPVPPMSLGGE GDRPSLALYSCTGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTBISWKADGKIMALGNEDGSIBIFQ\IPMLKLICTIQQH HKLUNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAPBSPSDPLQSPYRTPPQGHTAQDYPVMAWEPHIH*WEGL VFCPPIDGYSPGCMD\AFPGKEAPVAIFRG\HQGRLLCVAMSPL DPDCTYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKZLSQ PKARPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGERQARPBLPCGLAPAVSREPVICTPVSSGFRKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRBLNEDVSADVEEFHLGLFTDRATLYRMIDIEGKG HLENGHPELPHOLMILWKGDLKGVLQTAAERGBLTDNLVAMAPAA GYHVWLWAVBAPAKQLCFQDQYVKAASHLLSIHKVYKAVELLKS
5837	4792	903	PPMCHLQERYFKSYLLMYT*KEVIQQPIDVLSVAVKKRVLCIPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPI.DB PIDLINVAFIAEBKTMPTTFINEGRIDSMVIATLADRHIPI.DB PIDLINVAFIAEBKTMPTTFINEGRIQKNKCEIPSEFSKDVAA AAADSPNKHVSVPPRITGRAGLKELQAVSPSRIMNFVEINVSME ELQKIRRTRICHLIRPLDTVILDDSIGGAVWFASRGIGMLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLINKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW RKANLTLPRGIGEKLLLRLAAVELGLITASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKBTKL NGNAVAQAPVTNCCYLATGSKDOTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDLGSLAIGVCDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCMHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGEGEIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTRISWKADGKIMALGNEDGSIBIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVWAWBPHIH*WBGL VFCPPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL DPDCTYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKSLSQ PKAKPKKKKRPTLRTPVKLBSIDGNEBBSMKENSGPVENGVSDQ EGEBQARBPELPCGLAPAVSRBPVICTPVSSGFEKSKVTINNKV ILLKKEPPKBKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRBLNEDVSADVEERFHIGLFTDRATLYRMIDIESKG GYHYMLMAVBAFFAKQLCFQDQYVKAASHLLSIHKVYRAVESLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
5837	4792	903	PPMCHLQERYFKSYLLMYT*KEVIQQPIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPILDE PIDLINVAPIAEBKTMPTTFMREGNKQKKKCEIPSBEFSKDVAA AAADSPNKHVSVYPDRITGRAGLKELQAVSPSRIWNFVEINVSMB ELQKIRRTRICHLIRPLDTVILDDSIGGAVWFASRGIGMLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW RKANLTLPRGIGRKILLARLAAVELGLIASALLPRRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKEKTKL MGNAVAQAPVINCCYLATGSKDQTTRIWSGSRGRGWMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRWNNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGB GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSTKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPGGHTAQDYPVMAWEPHIH*WEGL VFCFPIDGYSPGCWD\AFFGKBAPVAIPRG\HQGRLLCVAWSPL DPDCTYSG\ADDFCYHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKARFKKKKKPTLRTPVKLBSIDGNEBESMKENSGPVENGVSDQ EGEBQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVERFHIGFTDRATLYRMIDISGKG HLENGHPELPHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLMAVEAFAKQLCFQDQYVKAASHLLSIHKVYBAVEELKS NHFYREAIAIAKARLRPEDPVIKDLYLSWGTVLERDGGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
5837	4792	903	PPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPILDB PIDLLNVAFIAEBKTMPTTFINEGNKQKNKCEIPSEFFSKVVAA AAADSPNKHVSVPDRITGRASLKELQAVSPSRIVMFVEINVSME ELQKURRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKKARPFFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKLMEKASDKCGRLQIMSLENLSIBKRTKL NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGPAYSLAFSSVDIGSLAIGVCDG MIRVMNTLSIKNNYDVKNFWQGVKSKVTALCMHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVMAMSPHIH*MEGL VFCPPIDGYSPGCWD\AFPGKEAPVAIPRG\HQGRLLCVAWSPL DPDCTYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKZLSQ PKARPKKKKKPTLRTPVKLESIDGNEEBSMKENSGPVENGVSDQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPSTLIKKRKARSLLPLSTSLDHESKEELHQDCL VLATAKHSRELNEDVSADVEERFHIGLFTDRATLYRMIDIEGKG HLENGHPELPHQLMLWKGDLKGVLQTAAERGELTINLVAMAPAA GYHWHMAVBAFAKQLCFQDQYVKAASHLLSIHKVYEAVELKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAARVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGGRLVFCLLEKLSRHLE
5837	4792	903	PPMCHLQERYFKSYLLMYT*KEVIQQPIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPI,DB PIDLLNVAPIAEBKTMPTTFNREGNKQKNKCEIPSEFSKDVAA AAADSPNKHVSVVPDRITGRAGLKELQAVSPSRIMMFVEINVSME ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLBGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKETKL NGNAVAQAPVTNCCYLATGSKDQTTRIWSCSRGRGVMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNISRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGFPVPPMSLGGE GDRPSLALYSCGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTRISWKADGKIMALGNEDGSIBIFQ\IPMLKLICTTQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPBSPSDPLQSPYRTPPQGHTAQDYPVMAWBPHIH*WEGL VFCPPIDGYSPGCMD\AFFGKEAPVAIFRG\HQGRLLCVAMSPL DPDCTYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKAKPKKKKRPTLRTPVKLESIDGNEEBSMKENSGPVENGVSDQ EGERQAREPELPCGLAPAVSREPVICTFVSSGFERSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDISGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGBLTDNLVAMAPAA GYHVWLMAVBAPAKQLCFQDQYVKAASHLLSIHKVYRAVEELKS NHFYREAIAIAKARLRPSDPVLKDLYTLSWTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLOGGRLVFCLLBKLLSKILB KKOLSEGKSSSYHTWNTGTFEGPFVERVTAVWKSIFSLDTFEQY
5837	4792	903	PPMCHLQERYFKSYLLMYT*KEVIQQPIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPILDE PIDLINVAPIAEBKTMPTTFMREGNKQKKKCEIPSBEFSKDVAA AAADSPNKHVSVYPDRITGRAGLKELQAVSPSRIWNFVEINVSMB ELQKIRRTRICHLIRPLDTVILDDSIGGAVWFASRGIGMLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARPPFLDENVVSFLNSLPIW RKANLTLPRGIGRKILLARLAAVELGLIASALLPRRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIBKEKTKL MGNAVAQAPVINCCYLATGSKDQTTRIWSGSRGRGWMILKLPFL KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRWNNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPFVPPMSLGGB GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSTKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPGGHTAQDYPVMAWEPHIH*WEGL VFCFPIDGYSPGCWD\AFFGKBAPVAIPRG\HQGRLLCVAWSPL DPDCTYSG\ADDFCYHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ PKARFKKKKKPTLRTPVKLBSIDGNEBESMKENSGPVENGVSDQ EGEBQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVERFHIGFTDRATLYRMIDISGKG HLENGHPELPHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLMAVEAFAKQLCFQDQYVKAASHLLSIHKVYBAVEELKS NHFYREAIAIAKARLRPEDPVIKDLYLSWGTVLERDGGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA

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maino acid residue of antino acid sequence codon, /-possible nucleotide deletion, /-possible n				P=Proline, O=Glutamine, R=Arginine,
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SPYKQPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP PPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSTSHRAQEFGV KSAFPPSVRALLDSSEMCDRLSSSPGLFGAFSVRGNEPGSDRSP SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHDVPHRS LFSPQNTLAAPTGHPPTSGVEKVLASTISTISTIEFKNMLKNAS RKPSDDKHFCQAPSKGTPSDGVSLSNLTQPSLTATDQQQBEHY RIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQT VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDMGPSSASELA SLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFTFEHH LPPSPLEHGTPFQREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLSNPFTKRALAHAADPPPPGEHSGIPFPPPPPPPPPPPRERISS SGGGVPFSTPPPPPPPPPPPPPPPPPPPPPPPPPPPPRERISS	1	1	1	
PPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSYSHRAQEFGV KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP SPSKNDSFFTPDSNIHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS LPSPQNTLAAPTGHPPTSGVEKVLASTISTTSTIEPKNMLKNAS RKPSDDKHPGQAPSKGTPSDGVSLSNLTQPSLTATDQQQBEHY RIETRVSSSCLDLPDSTERKGAPIETLGYHSASNRRMSGEPIQT VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDMGPSSASELA SLGGGGSGGLTGFKTAPYKERAPQFQBSVGSFRSNSFNSTFEHH LPPSPLEHGTPFQRBPVGPSSAPPVPPKDHGGIPSRDAPTHLPS VDLSNPFTKRALAHAAPPPPCHHSGIPFPPPPPPPPGEHSS SGGSGVPFSTPPPPPPPPPVDHSGVVPPPAPPLAEHGVAGAVAVPP	I	1	I	
KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS LFSPQNTLAAPTGHPPTSGVEKVLASTISTISTIEFKNMLKNAS RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQBEHY RIETRVSSCLDLPDSTEEKGAPIETLGYHASANRRMSGEPIQT VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA SLGGGGGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH LPPSPLEHGTPFQREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLSNPFTKRAALAHAAPPPPPGEHSGIPFDTPPPPPPPGEHSS SGGSGVPFSTPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP	1	1	i	
SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS LFSPQNTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNAS RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQBEHY RIETRVSSSCLDLPDSTREKGAPIETLGYHSASNRRMSGEPIQT VESIRVPGKGNNGHGREASRVGWFDLSTSGSSFDNGPSSASELA SLGGGGGGLTGFKTAPYKERAPQFQESVGSYRSNSFNSTFEHH LPPSPLEHGTPFQRBPVGPSSAPPWPPKDHGGIFSRDAPTHLPS VDLSNPFTKRAALAHAAPPPPPCEHSGIPFDTPPPPPPPGKHSS SGGSGVPFSTPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP	1	1	1	
LPSPONTLAAPTGHPPTSGVEKVLASTISTTSTIEPKNMLKNAS RKPSDDKHPGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQBEHY RIETRVSSSCLDLPDSTBEKGAPIETLGYHSASNERMSGEPIQT VESIRVPGKCNNGGHGREASRVGWFDLSTSGSSFDNGPSSASELA SLGGGGGGITGFKTAPYKERAPQFQESVGSYRSNSFNSTFEHH LPPSPLEHGTPPQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLSNPFTKRALAHAADPPPPGCHSGIPFPTPPPPPPPGKHSS SGGSGVPFSTPPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP	1	1	1	KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP
LPSPONTLAAPTGHPPTSGVEKVLASTISTTSTIEPKNMLKNAS RKPSDDKHPGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQBEHY RIETRVSSSCLDLPDSTBEKGAPIETLGYHSASNERMSGEPIQT VESIRVPGKCNNGGHGREASRVGWFDLSTSGSSFDNGPSSASELA SLGGGGGGITGFKTAPYKERAPQFQESVGSYRSNSFNSTFEHH LPPSPLEHGTPPQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLSNPFTKRALAHAADPPPPGCHSGIPFPTPPPPPPPGKHSS SGGSGVPFSTPPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP	1	1		SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS
RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQBEHY RIBTRVSSSCLDLPDSTBBKGAPIBTLGYHSASNRRMSGBPIQT VESIRVPGKGNRGHGREASRVGAFDLSTGGSSFDMGPSSASELA SLGGGSGGLTGFKTAPYKERAPOFQBSVGSYRSNSFNSTFEHH LPPSPLEHGTPFQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLSNPFTKRALAHAADPPPCHSGIPFPTPPPPPPPGKHSS SGGGVPFSTPPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP	1	1	1	
RIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQT VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDMGPSSASELA SLGGGGGGLTGFKTAPYKERAPOFQESVGSFRSNSFYEHH LPPSPLEHGTPFQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLSNPFTKRALAHAADPPPPGEHSGIPFPPPPPPPPPGEHSS SGGGVPFSTPPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP	1		1	
VESTRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA SLGGGGSGGLTGFKTAPYKERAPQFQESVGSYRSNSFNSTFEHH LPPSPLEHGTPFQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLSNPFTKRAALAHAAPPPPPGEHSGIPFPTPPPPPPGEHSS SGGSCVPFSTPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP	1			
SLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH LPPSPLEHGTPFQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLSNPFTKRAALAHAAPPPPPGEHSGIPFPTPPPPPPGEHSS SGGSCVPFSTPPPPPPVDHSGVVPPPAPPLAEHGVAGAVAVFP	1		I	
LPPSPLEHGTPFQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS  VDLSNPFTKRAALAHAAPPPPGEHSGIPFPTPPPPPPGEHSS  SGGSCVPFSTPPPPPPVDHSGVVPPPAPPLAEHGVAGAVAVFP	1		1	
VDLSNPFTKRAALAHAAPPPPPGEHSGIPFPTPPPPPPPGEHSS SGGSCVPFSTPPPPPPVDHSGVVPPPAPPLAEHGVAGAVAVFP			1	
VDLSNPFTKRAALAHAAPPPPPGEHSGIPFPTPPPPPPPGEHSS SGGSVPFSTPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP	1			LPPSPLEHGTPFQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS
SGGSCVPFSTPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP	1		1	
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
E .			
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R-Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
l		aequence	
	sequence	<u></u>	\=possible nucleotide insertion)
l		1	TLPSHSLEHLGPPHGGGGGGSNSSSGPPLGPSHRDTISRSGII
İ	1		LRSPRPDFRPREPFLSRDPFHSLKRPRPPFARGPPFFAPKRPFF
Į	1	i .	PPRY
5841	1908	762	GLRLFLVLTVWPMMKPSWLSRTEPSKRLLCRTLWCQSGWSSRSY
1	ł	ŧ.	TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW
1	i	i	RHCWMTARSCSGEKGGHWAFRQVGVYLLPGRVGCVSSRVSPSFP
Į.	-		GDGLDSGLARRGSAVSALASGLVREPMLGPPFHPTPRFKAVSAK
	1		SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND
1	ļ		
	1	l .	QSTSDYLVVYLRLLTSGYLQRBSKFFRHFIEGGRTVKEFCQ\QB
1	1	1	\VEPMCKESDHIHIIALAQGLQRVHPGWBYMGPRPRAATTNPHI
ľ		1	FP+GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA
	L		LGHCYRGPSVVVKWSYPTPFPLSHDPPPMFY
5842	307	1918	QBPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
l	]	1	WSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHGQAABKGP
l	I.	[	HRSRDTAEPSFPKIPLDGTLAPPESQGNGSTLQPNVVYITLRSK
	ľ	ì	RSKPANIRGTVKPKRRKKHAVASAAPGQEALVGPSLQPQBA\EG
1	1	1	KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLQPSS
	l .	i	RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA
1			RLLVLEGGAPGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRILGL
·	1	i	NRTLPSVSRKABFIODGRPCPIILWDASLSSASNDTHSSVKLTW
ļ	ł	1	GTYQQLLKQKCNQNGRVPKPESGCTEIHHHBWSKMALFDFLLQI
		Ī	YNRLDTYCCGFRPRKEDACVQNGLRPKCDDQGSAALAHI IQRKH
			DPRHLVFIDNKGPFDRSEDNLNFKLLEGIKEPPASAVYVLKSOH
	ł		LROKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN
		j	AHGVKVLPMNR
5843	500	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGM
3043	300	7423	1
1			RSSRMSQPPQCLRRAQSSCCHFMVKLLDDGTFMIPGEKVAHTSL
l		1	DALVTFHQQKPIEPRRBLLTQPCRQKDPANVDYBDLFLYSNAVA
			BEAACPVSAPBEASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL
	Į.	i	LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCBLVVT
	ļ	Į.	LGCPRIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
ĺ	-	1	LTAPGTKRQKGPHQEGREVGQLH*GDPRGQELAPNGSRSPILPG
<b></b>			VQARAPGLGRA
5844	202	2471	FDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI
		<b>j</b>	KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHL
ĺ		1 ' '	QYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEQG
	I	1	PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM
	1	I	PGKPGAMCMPGAKGRIGQKGRIGPHGIP*PQGPPGPHGLPGIGK
i	l	}	PGCPGLPGOPGPKGDRGPKGLPGPOGLRGPKGDKGPGMPGAPGV
1	(	ſ	KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP
<u> </u>			GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGRQGL
	Ì	Ì	PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA
1	l	ŀ	PGIGGPPGEPGIPGPMGPPGAIGFPGPKGRGGIVGPQGPPG
İ	1	1	PKGKPGLQGFPGKPGFLGBVGPPGMRGFPGPLGPKGEHGQKGVP
		i	The state of the s
ł	*		GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI
}		[	PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGL
ł			PGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG
l	,		AKKGKNGGPAYEMPAFTAKLTAPFPPVGAPVKFNKLLYNGRQNY
l	j		NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD
l	1		EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS
	1		SFSGYLLYPM
5845	215	2061	HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER
			GPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP
			KPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
			PFPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNBFFGEGKT
1			ROAARHNAAMKALQALONEPIPERSPONGESGKOMDDDRDANKS
l			-
			BISLVPEIALKRNMPVSFEVIKESGPPHMKSPVTRVSVGEFSAE
			GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HPFKKRPKT
			IVKAGPEYGQGMNPISRLAQIQQAKKEKEPDYVLLSERGMPRRR
		Ţ	EPVMQVKVGNEVATGTGPNKKIAKKNAAEAMLLQLGYKASTNLQ
	1	I	DOLEKTGENKGWSGPKPGFPEPTNNTPKGILHLSPDVYQEMBAS

	7 - 31 1 3	71.4.3 223	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.			
į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	ведиелсе	Codon, /=possible nucleotide deletion,
}	sequence	l <del></del>	\=possible nucleotide insertion)
<u> </u>	Sequence		
1			RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM
		ŀ	NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGPQVHYC
j .	}	l	DRQSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC
	l		YGPARKWKAIKMRAMCAHAALLSLIHYLLAPSARLEKSKLFALG
ì	[	ľ	N.
	135		
5846	1126	456	FSKLIMKTPIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF
l	ł	İ	KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS
ł	1	1	TDQESABBIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEBCKR
1	i	1	RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
l	ł		KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
ŀ	į	<b>,</b>	· ·
	ļ.,	<u> </u>	IQGVI
5847	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE
I	1	i	WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE
1	}	1	PWIMEPSIPVGTCADWETRLENSVSAPEPDISEERLSPEVIVEK
I	1	Į.	HKRDDSWSSNLLESWEYEGSLERQQANQQTLPKKIKVTEKTIPS
1		1	
l .	<b>!</b>	l	WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK
1	]	j	KEKSCKCNECGKAPSYCSALIRHQRTHTGEKPYKCN*/CVEKAP
	ŧ.	j	SRSENLINHQRIHTGDKPYKCDQCGKGFIEGPSLTQHQRIHTGE
ĺ	1		KPYKCDECGKAFSQRTHLVQHQRIHTGEKPYTCNBCGKAFSQRG
l .	ì	{	HEMEHOKIHTGEKPEKCDECDKTFTRSTHLTQHQKIHTGEKTYK
i	•	(	CNECGKAPNGPSTFIRHHMIHTGEKPYECNECGKAPSOHSNLTO
i	ì		
ì	Į.	}	HOKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYKCNEC
į .	j	i	GKAPSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNQHQKT
1	1	i	HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYQCHECGKTF
i	1		SYGSSLIQHRKIHTGERPYKCNECGRAFNQNIHLTQHKRIHTGA
		i	KPYECAECGKAPRHCSSLAQHQKTHTEEKPYQCNKCBKTFSQSS
		į.	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTOHORIHTGEKPYK
ŀ	!	ì	CNECGK/TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N
		1	Checor /1536311116061138016161616161616161616161616161616161616
		1	MIONEHINGT
L			KHORLHPGI
5848	22	2961	AAPRRILINGGOGORTPREPLPALLINGGPPAEAAPERKMPAVSK
5848	22	2961	
5848	22	2961	AAPRRILINGGOGORTPREPLPALLINGGPPAEAAPERKMPAVSK
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEABIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLPIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG
5848	22	2961	AAPRRILIRGGDGDRTPRFPLPALIRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEABIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLIGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSBLIRLINNAIKNDLASRNPTFMGLALHCIASV
5848	22	2961	AAPRRILIRGGDGDRTPRFPLPALIRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMARAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL
5848	22	2961	AAPRRILRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIRRINKRLANIRSKPKGDKAL DGYSKKKYVCKILIFIFILGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSBLIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMARAFAGEIPKVLVAGDTMDSVKQSAALCILRIYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVHLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMARAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMCDWTSRVVHLLNDQHLGVVTAATSLITTLAQKFEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVMLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKDLASRNPTFMGLAHCIASV GSREMAEAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHILINDGHLGVVTAATSLITTLAQKVPEBPKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVHLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMARAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMCDWTSRVVHLLNDQHLGVVTAATSLITTLAQKFEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVMLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKDLASRNPTFMGLAHCIASV GSREMAEAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHILINDGHLGVVTAATSLITTLAQKVPEBPKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEABIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSBLIRLINNAIKMDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRITECLETTINKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQPLQHRETNLRYLALESMCTLA SSBFSHEAVKTHIBTVINALKTBRDVSVRQRAVDLLYAMCDRSN
5848	22	2961	AAPRRILRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIRINKRLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLIGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCILRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTT**FCPGFLGLSVKLLRLLQCY PPPPPAVRGRLTECLETILNKAGPPPKSKVQHSNAKNAVLFEA ISLITHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBFSHEAVKTHIETVINALKTERDVSVRQRAVDLLXAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVHLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSRMARAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKWPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLYECLETIINKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQPPLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLBTADYSIRERIVLKVAILARKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVMLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMCDWTSRVVHILINDQHLGVVTAATSLITTLAQKFPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEEMLLVRACMQLGQFLQHRETNLRYLALESMCTLA SBEFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD TILMLIRIAGDYVSEEWWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVMLLSSNRTTEKQIG YLFISVLVNSNSBLIRLINNAIKDLASRNPTFMGLAHCIASV GSREMAEAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHILINDGHLGVVTAATSLITTLAQKNPEBPKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLITHHDSEPNLLVRACNQLGQFLQHRETNLRYLALSSMCTLA SSBFSHEAVKTHIETVINALKTERDVSVRGRAVDLLYAMCDRSM APQIVAEMLSYLBTADYSIREBIVLKVAILABKYAVDYTW\YVD TILNLIRLAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLLAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPTIQDVLRSDSQLRNADVBL
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVMLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMCDWTSRVVHILINDQHLGVVTAATSLITTLAQKFPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEEMLLVRACMQLGQFLQHRETNLRYLALESMCTLA SBEFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD TILMLIRIAGDYVSEEWWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVMLLSSNRTTEKQIG YLFISVLVNSNSKLIRLINNAIKNDLASRNPTFMGLAHCIASV GSREMAEAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBPKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBESHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPTIQDVLRSDSQLRNADVBL QQRAVBYLRLSTVASTDILATVLEKMPPPPERESSILAKLKKKK
5848	22	2961	AAPRRILRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIRINKELANIRSKEKGDKAL DGYSKKKYVCKILFIFILGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCILRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTT*FCPGFIGLSVKLIRLLQCY PPPDPAVRGRLTECLETILNKAGPPPKSKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBESHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD TILMLIRIAGDYVSEEVWYRVIQLVINRDDVQGYAATTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFIL CSVPTRALLLSTYIKFVNLFPBVKPTIQDVLRSDSQLRNADVBL QRAVBYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPFDAPASTSAVSTPSPSADLLG
5848	22	2961	AAPRRILRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKFKGDKAL DGYSKKKYVCKLLFIFILGHDIDFGHMEAVHLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCILRLYRTSPDL VPMGDWTSRVVHLLINDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFIGLSVKLLRLLQCY PPPPDFAVRGRLYECLETTLINKAGEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLVAMCDRSN APQIVAEMLSYLBTADYSIREBIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVCGYILGEFGNLLAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPTIQDVLRSDSQLRNADVBL QQRAVBYLRLSTVASTDILATVLERMPPPPRESSILAKIKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSFSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNPA
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSRMARAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLYECLETTINKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQPPLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLBTADYSIRERIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLSTYIKFVNLFPBVKPTIQDVLRSDSQLRNADVBL QQRAVEYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGFBPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRMFIFYGNETSTQFL
5848	22	2961	AAPRRILRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKFKGDKAL DGYSKKKYVCKLLFIFILGHDIDFGHMEAVHLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCILRLYRTSPDL VPMGDWTSRVVHLLINDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFIGLSVKLLRLLQCY PPPPDFAVRGRLYECLETTLINKAGEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLVAMCDRSN APQIVAEMLSYLBTADYSIREBIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVCGYILGEFGNLLAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPTIQDVLRSDSQLRNADVBL QQRAVBYLRLSTVASTDILATVLERMPPPPRESSILAKIKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSFSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNPA
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSRMARAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLYECLETTINKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQPPLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLBTADYSIRERIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLSTYIKFVNLFPBVKPTIQDVLRSDSQLRNADVBL QQRAVEYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGFBPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRMFIFYGNETSTQFL
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVMLLSSNRYTEKQIG YLFISVLVNSNSBLIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMCDWTSRVVHILINDCHLGVVTAATSLITTLAQKPEBEPKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRITECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLITHHDSEENLLVRACMQLGQFLQHRETMLRYLALESMCTLA SBEFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLBTADYSIREBIVLKVAILABKYAVDYTW\YVD TIMLIRIAGDYVSEEWWRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVCGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVBL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQICKSBFRQNLGRMFIFYGRKTSTOFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQPRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIRINKRLANIRSKEKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTT*PCPGFFLGLSVKLLRILQCY PPPDPAVRGRLTECLETILNKAQEPPKSKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBESHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD TILMLIRIAGDYVSEEVWYRVIQIVINRDDVGGYAAKTVFEALQ APACHENLVKVCGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPBVRPFIQDVLRSDSQLRNADVBL QQRAVEYLRLSTVASTDILATVLERMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLIG LGAAPPAPAGPPPSSGGSGLLVDVYSDSASVVAPLAPGSEDNPA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRWFFIFYGNTTSTOPI NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIBCVSD FTERPVINIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP
5848	22	2961	AAPRRILRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAUNLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKNDLASRNPTFMGLALHCIASV GRRMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTT*FCPGFLGLSVKLLRLLQCY PPPPDPAVGGRLTECLETTLINKAQEPPKSKKVQHSNAKRAVLFEA ISLIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBESHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEWWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVCGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPFIQDVLRSDSQLRNADVBL QQRAVBYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRMFIFYGRBTSTOFL NFTPTLICSDDLQPNLNIQTKFVDDTVEGGAQVQQVVNIECVSD FTERPVINIQFRYGGTFQNVSVOLPLILNKFPQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSXEAV
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRTTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSRMAEAFAGEIPKVLVAGDTMDSVKQSAALCILRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFIGLSVKLLRLLQCY PPPDPAVRGRLYECLETTINKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQPLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQLVAEMLSYLBTADYSIREIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVCGYILGEFGNLIAGDPRSSPLIQPHLLHSKFHL QQRAVBYLRLSTYIKFVNLFPBVKFTIQDVLRSDSQLRNADVBL QQRAVBYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGEFBPAPASTSAVSTPSFSADLLG LGAAPPAPAGPPPSSGGSCLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNETSTOFL NFTETILCSDDLQPNLNIQTKPVDDTVEGGAQVQQVVNIECVSD FTEAPVLNIQPRYGGTFQNVSVQLPITLNKFPQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIGFGSALLEEVDP NPAMFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQP
5849	22 3545	2961	AAPRRILRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAUNLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKNDLASRNPTFMGLALHCIASV GRRMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTT*FCPGFLGLSVKLLRLLQCY PPPPDPAVGGRLTECLETTLINKAQEPPKSKKVQHSNAKRAVLFEA ISLIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBESHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEWWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVCGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPFIQDVLRSDSQLRNADVBL QQRAVBYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRMFIFYGRBTSTOFL NFTPTLICSDDLQPNLNIQTKFVDDTVEGGAQVQQVVNIECVSD FTERPVINIQFRYGGTFQNVSVOLPLILNKFPQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSXEAV
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRTTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSRMAEAFAGEIPKVLVAGDTMDSVKQSAALCILRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFIGLSVKLLRLLQCY PPPDPAVRGRLYECLETTINKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQPLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQLVAEMLSYLBTADYSIREIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVCGYILGEFGNLIAGDPRSSPLIQPHLLHSKFHL QQRAVBYLRLSTYIKFVNLFPBVKFTIQDVLRSDSQLRNADVBL QQRAVBYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGEFBPAPASTSAVSTPSFSADLLG LGAAPPAPAGPPPSSGGSCLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNETSTOFL NFTETILCSDDLQPNLNIQTKPVDDTVEGGAQVQQVVNIECVSD FTEAPVLNIQPRYGGTFQNVSVQLPITLNKFPQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIGFGSALLEEVDP NPAMFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQP
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRTTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMCDWTSRVVHILINDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVGRLTECLETTINKAQEPPKSKKVQHSNAKNAVLFEA SSEFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQLVAEMLSYLBTADYSIRERIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQPHLLHSKFHL CSVPTRALLLSTYIKFVNLFPEVRFIQDVLRSDSQLENADVBL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKK GPSTVTDLEDTKRDRSVDVNGGFBPAPASTSAVSTPSPSADLLG LGAAPPAAGEPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEPRQNLGRMFIFYGNETSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIBCVSD FTERPVINIQPRYGGTFQNVSVOLDITLNKFPQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLESVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVPHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIEVEES
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIRINKBLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTT*PCPGFFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBESHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAARTVFEALQ APACHENLVKVCGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPBVRPTIQDVLRSDSQLRNADVBL QGRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPBPAPASTSAVSTPSPSADLLG LGAAPPAPAGSPPSSGGSGLLVDVYSDSASVVAPLAPGGSEDNFA RFVCKNNGVLFENQLLQIGLKSBPRQNLGRMFIFYGRTSTOPI NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIBCVSD FTERPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPAMFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTTRTSKEAV SQRLCELLSAQP KRREIKETVFHHVAQAGLELSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIBVEES DEFIREDMKYKDATNKHSHLHRRDRHITIEDLWKRWKTSEVENW
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKEKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCILRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTT**PCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSESHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEWYRVIQLVINRDDVQGYAATTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKPTIQDVLRSDSQLRNADVBL QRAVBYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGRETSTOFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTERPVINIQFRYGGTFQNVSVOLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEZVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAMYRLTLRTSKEAV SQRLCELLSAQF  KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIBVEES DEFTREDMKYKDATNRHSHLHRRDKHITIBDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKEKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVHLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*PCPGFLGLSVKLLRLLQCY PPPDPAVRGRLYECLETTLINKAGEPPKSKKVQHSNAKNAVLFEA ISLIIHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSBESHEAVKTHIETVINALKTBRDVSVRQRAVDLLVAMCORSN APQIVAEMLSYLBTADYSIREBIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLLAGDPRSSELIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKPTIQDVLRSDSQLRNADVBL QQRAVBYLRLSTVASTDILATVLERMPPPPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNPA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRMPIFYGNETSTOPL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQPRYGGTPQNVSVQLPITLNKPFQPTEMASQDPFQ RWKQLSNPQQZVQNIFKAKHPMDTBVTKAKIIGFGSALLEZVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRRIKETVPHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNRHSHLHRRDKHITIBDLWKRWKTSEVHNW TLBETTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDCMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKEKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSKLIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCILRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTT**PCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSESHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEWYRVIQLVINRDDVQGYAATTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKPTIQDVLRSDSQLRNADVBL QRAVBYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGRETSTOFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTERPVINIQFRYGGTFQNVSVOLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEZVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAMYRLTLRTSKEAV SQRLCELLSAQF  KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIBVEES DEFTREDMKYKDATNRHSHLHRRDKHITIBDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTPMGLALHCIASV GSRMARAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKWPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFIGLSVKLLRLLQCY PPPDPAVRGRLYECLETTINKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQPIQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLBTADYSIREIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQPHLLHSKFHL QQRAVBYLRLSTYIKFVNLPPBVKPTIQDVLRSDSQLRNADVEL QQRAVBYLRLSTYASTDILATVLEEMPPPPERESSILAKLKKKK GPSTYTDLLEDTKRDRSVDVNGGFEPAPASTSAVSTPSFSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEPRQNLGRMFIFYGNETSTOPL NFTETILCSDDLQPNLNIQTKPVDDTVEGGAQVQVVNIECVSD PTEAPVLNIQPRYGGTPQNVSVQLPITLNKPPQPTEMSQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTBVTKAKIIGFGSALLEEVDP NPAMFVGAGIIHTKTTQIGCLLKLEPNLQAQMYRLTLRTSXEAV SQRLCELLSAQP  KRREKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKOGGIBVEES DEFIREDMKYKDATNKHSHLHRRDRHITIEDLWKRWKTSEVENW TLBDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRINMKDPILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKFKGDKAL DGYSKKKYVCKILFIFLIGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSBLIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAPAGEIPKVLVAGDTMDSVKQBAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTT*PCPGFIGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACRQOLGQFLQHRETNLRYLALSSMCTLA SSBFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLBTADYSIREBIVLKVAILABKYAVDYTW\YVD TILMLIRIAGDYVSEBWYRVIQIVINRDDVQGYAARTVFEALQ APACHENLVKVCGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVRPTIQDVLRSDSQLRNADVBL QQRAVEYLRLSTVASTDILATVLEEMPPPPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGFBPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRMFIFYGNETSTOPL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQPRYGGTPQNVSVQLPITLNKPFQPTEMASQDFFQ RWKQLSNPQQBVQNIFKAKHPMDTBVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF  KRREIKETVPHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIBVEES DEFIREDMKYKDATNKHSHLHRRDKHITIBDLWKRWKTSEVHNW TLEDTLQWLIBPVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNNMKDPILTVSI VIGYGGCWFAYTQNKTSKEHVARMMKDLESLQTAEQSLMDLQER LEKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTPMGLALHCIASV GSRMARAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKWPEBFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFIGLSVKLLRLLQCY PPPDPAVRGRLYECLETTINKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQPIQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTBRDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLBTADYSIREIVLKVAILABKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQPHLLHSKFHL QQRAVBYLRLSTYIKFVNLPPBVKPTIQDVLRSDSQLRNADVEL QQRAVBYLRLSTYASTDILATVLEEMPPPPERESSILAKLKKKK GPSTYTDLLEDTKRDRSVDVNGGFEPAPASTSAVSTPSFSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEPRQNLGRMFIFYGNETSTOPL NFTETILCSDDLQPNLNIQTKPVDDTVEGGAQVQVVNIECVSD PTEAPVLNIQPRYGGTPQNVSVQLPITLNKPPQPTEMSQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTBVTKAKIIGFGSALLEEVDP NPAMFVGAGIIHTKTTQIGCLLKLEPNLQAQMYRLTLRTSXEAV SQRLCELLSAQP  KRREKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKOGGIBVEES DEFIREDMKYKDATNKHSHLHRRDRHITIEDLWKRWKTSEVENW TLBDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRINMKDPILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER

			Control of the contro
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /~possible nucleotide deletion,
į	sequence	_	\=possible nucleotide insertion)
	<del> </del>		AHSSSLDEVDHKILEAKKALSELTTCLRERL?RWQQIEKICGFQ
1	1		IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT
1			PPIVSOFPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA
ŀ			PHAPHPSHPRHPHHPOHTPHSLPSPDPDILSVSSCPALYRNREE
Į			ERAIYFSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN
			IIS/DERYQEMRCP*RIPSGGIL
5850	3	1895	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
}			LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVFCE
		ł	SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA
1	Ĭ	1	BFFIBAVIEGLASDGGLFVPAKBFPKLSCGBWKSLVGATYVERA
1			QILLERCIHPADIPAARLGEMIETAYGENFACSKIAFVRHLSGN
l		<b>[</b>	QFILELPHGPTGSPKDLSLQLMPHIFAQCIPPSCNYMILVATSG
1	1		DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ
1		l .	RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA
l .	ŀ		KSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG
1	}	1	KILAAVYAKMMGIPIRKFICASNQNHVWTDFIKTG\HYDLRGKB
ł		<b>[</b>	N*AOTFFTVQ*IFLPNLSNLERHLHLMANKDSQLMTRLFNRLES
1			OHHFOIKKALVEKLOODFVADWCSEGECLAAINSTYNTSGYILD
l .	ŀ	<b>l</b>	PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPAIMQALKIKEI
Į.			NETSSSOLYLLGSYNALPPLHEALLERTKOQEKMEYQVCAADMN
1	1		
L		<u></u>	VLKSHVEQLVQNQFI
5851	3120	1602	RCYLOFLALLLTSTSARAAAAAAAABBPAGSPSVMTRAGDHNRQ
			RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHPAVSVFLVRLY
l .	İ	}	GNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVV
į.		1	QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
	8		ANLASTATAITIQRDWIVVVAGRDRSKLANMNATIRRIDQLTNI
+ 0		7	LAPMAVGQINTFGSPVIGCGFISGNNLVSMCVBYVLLWKVYQKT
		1	PALAVKAGLKEBETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
1	1	1	BLEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP
1		ł	LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY
			LATSKMNFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	<del> </del>	422	KTTPPSSLCPLRQLPEVRGYSGQPLTDPLTSLCRSHKCRGKGWG
1 3032	1 ~		SSSYPSLPALLRARSAPGHCTHRSCGPBWRIDS1SRLEMQGARR
1	1	1	SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGFPITSGPG/WFRQ
1			YYPFISGRH+VLPTBSDFYYVAMDFGGHGL9SHYSPGVPYYLQT
		ļ	FVSBTRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRNP
1	1	I	ESGANALAPGLPAIHGRSWES
		<del> </del>	RILGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR
5853	223	1346	
		}	PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\PPIFRP
1	1	1	LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH
i			GGVETPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP
1	Ī		HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESE
1	1	ŀ	SRWVRGNPRTGTAATLIGFSRNPTLNGSENWGSLVSIQEEGPDT
1	I	Į.	GWEREKRNPAEMGNPORWASPIHTPPLGPEILRAMPEALRAMPE
	1	i	ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP
	1		LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE
	1	1	LXHLCAMIKRVLLERLENTRKLRELTEGRTLDWPQNRITEVSAK
1		]	ROIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS
ļ		j	GAETIKDLLE/ENFPELKNELDLQMEKAHRIPLKFNEKKAASRH
	1		IRVTFL/KFORRNILQASSORKOVTYKGAKVRLTSDFSPAILNA
1			RROW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
l	1	ł	= • •
L	ļ		LGKYTNQBLSLKILLKDLLQLTENIN
5855	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP
I		I	FISLTHHVLSQSQSPLSSNCWICLSTHTQ*FTALPADLLTWTQS
	1	1	nvslhisylaipfladsflkpv/l*pgnsakhlsfklsslsmvs
1		i	GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTQTSFISPPP
			LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY
1	1		KIISTSAWQKVLCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA
1			NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN
1 '	E .	1	1

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l .	to first	amino acid	P=Proline, Q=Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	
ł	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		aedneuce	Codon, /=possible nucleotide deletion,
	ведиенсе	<u> </u>	\=possible nucleotide insertion)
Į.			FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPYWENENTLSWL
1	1	1	PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN
1	· ·		ILPPNOTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT
			GLAGITTSITSYQTLFTTLSNTVBDMHTSITSLQRQLDFLVGVI
	į		LONWRVLDLLTTEKGGTCIYLOEBCCFCVNESGIVHIAVRRLHD
1			RAAEL+HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP
1			CIFNLVSRFISORLNCFIOASMOKHIDNIFHLCHV+YOSLRGNH
1			
5055			SEAPEPRP
5856	173	1137	PWLHCLGLSAVPLFYL+/YVTFHLYGGIILLLLIFISIAGILYK
ļ	i		PQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
l			IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
1			VDYRGYGKSEGEASKEGLYLDSEAVLDYVMTSPDLDKTKIYLSG
I			RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP
1	<b>\</b>		MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ
ł	i i		LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH
1			SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADANAAPAVEPQGPALGSEPMMLGSPTSPKPG
1		303	VNAQFLPGFLMGDLPAPVTPOFRSISGPSVGVMEMRSPLLAGGS
1			PPOPVVPAHKOKSGAPPVRSIYDDISSPGIGSTPLTSRROPNIS
1	i		
1			VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ
1			GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS*
1			NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI
			DKSVMESSDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP
	L		LATAYKASTSDYQVISDRQTPKKDESLVSKANEYMFGW
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1			PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
1	-90		PSSGVPTTPPQAGGPPPPPPAAVPGPGPGPKQGPGPGGPKGGKMP
1	ľ i		GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ
1	<b>:</b>	·	GPPPGGPGGRSEBKISGPRRGFKANLSLLRRPGEKTYTQRCRFC
ł			LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR
1			ALA+NCPKPELG+YTP+GGRQLPSSLFPTHACLPLSCSV1FSPF
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	]		EVSFAVENGDSGSRYYYSDNFFDGQRERPLGDRAHEDYRYYEYN
1			HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
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į l			YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQQTERNQ
1			SLLVPANPYHTABIPDWLQVYARAPVKYDHILKWBLFQLADLDT
			YQGMLKLLFMKKLEQIVKMYBAYRQALLTKLENRKQRQQWYAQQ
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5860	2956	1270	TIRVERFPLCPGGGKAQLSSASLIGAGLLLQPPTPPPLLILLFP
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1	!		LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI
1			SWEKIHGKSSQTVAVHHPQYGFSVQGBYQGRVLPKNYSLNDATI
1			TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG
-	'		PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
			NETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI
1			QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
			QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTOK
			VHPTFQDPSLPTYPPLPALOFQWASPSTA*TSRD\LATEP*KIA
			PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF
			CYRRRTPRGDYPAKNYIPPSDMOKESOIDVLQQDBLDPYPDSV
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			KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
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1			SEGEQGIPTACAAFAQQPAG/EPRRGLAGVGEGGPQCSWVNYRC
<b>,</b> .			TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
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VFRGNPKQVQBYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFIMGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIABSQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALOFIKQYWKMHGRPLFLUVLIBEDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTBELPEFKS PBELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHBIL	r d	!		FLRDGYRTSLEDPNRCYYKPARIKLPDGIRCEFPIFFLYMMIDG
KNNPGSQKRFPSNCGRDGKLFIWGQALYIIAKLLADBLISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINBKLGLSGR PDRPIGCLGTSKTYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKNHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLLSGAVVEQLDFLRISDTBELPEFKS PBELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHBIL	1 1			
DPVQRYVPLKDQRNVSMRF9NQGPLENDLVVHVALIAESQRLQV FLMTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINBKLGLSGR PDRPIGCLGTSKTYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKHIGRPLFUVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKQYWDRLQTLISGAVVBQLDFLRISDTBKLPEFKS PRELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHBIL				1.5
FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKTYRILGKTVVCYPIIPDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLPLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTBELPEPKS PRELEPPKHSKVKRQSSTPSAPELGQQPDVNISKWKDKPTHBIL	]			
PDRPIGCLGTSKTYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLPLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTBELPEPKS PRELEPPKHSKVKRQSSTPSAPELGQQPDVNISBWKDKPTHRIL				
DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEBLPEFKS PRELEPPKHSKVKRQSSTPSAPELGQQPDVNISBWKDKPTHBIL	[		•	
LKKGI I GGVKVHVDRLQTLI SGAVVEQLDFLR I SDTBELPEFKS PRELEPPKHSKVKRQSSTPSAPELGQQPDVNI SEWKDKPTHEIL	[		4	PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID
LKKGI IGGVKVHVDRLQTLISGAVVEQLDFLRISDTBELPEPKS PRELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHBIL				DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA
PRELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHBIL				
Quint-Schroughthastmingophit tradit voluntary inn	1			
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l			
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
•	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	i	\=possible nucleotide insertion)
	<del>                                     </del>		AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAFG
l	j		HEBEVISNPLSPRVIQNIIYYKCNTHDERBAVIQOELVIHIGWI
l			
i			ISNNPELFSGTLKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP
		1	SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGFYDRVWQI
	l	į.	LERTPNGIIVAGKHLPQQPTLSDMTMYEMNFSLLVEDTLGNIDQ
			PQYRQIVVELLMVVSIVLERNPELEFQDKVDLDRLVKEAFNEFQ
ŀ		J	KDQSRLKBIEKQDDMTSFYNTPPLGKRGTCSYLTKAVMNLLLEG
	j	1	EVKPNNDDPCLIS
5872	68	665	VQGYMYRFVIKINSCYSEKTSICRHRCCPELPATQPWPTPTVFF
	[		NIAIDSESLGCI\SFKLFADKV/PKRWKKNFVLLNTGBKVLGDK
1		I	GPCFYRIIPG\LCQGGDFTHHNGTGGKSLYSKEFDDENFI/LKH
i	I	Ī	TAPGVLSTANAGPTINGSQFFICTAKTEDG*QHVVFGKVKDGMS
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5873	2240	506	RRPPEGGSGGGRTTRARMPLPWSLALPILLSWVAGGFGNAASAR
50/3	2240	1 500	
1	1	i	HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF
	Ī	l	GECVGPNKCRCPPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGS
	1	l	YKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCP
1	Ì	1	SSGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCH
l	į.	{	IGPBLQYISGRYDCIDINBCTMDSHTCSHHANCFNTQGSFKCKC
l	ì		KQGYKGNGLRCSATPENSVKEVLRAPGTIKDRIKKLLAHKNSMK
	ł	*	KKAKIKNVTPRPTRTPTPKVNLQPFNYEEIVSRGGNSHGG\KKG
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l	1		NEEKMKEGLEDEKREEKALKD*HRRERPFRG\DVFFPKVNEAGE
ł		1	FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\
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		Ì	PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSE
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E074.		2307	GLCPDSLLSVDD
5874	3	3387	GLCPDSLLSVDD ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD
5874	3	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGONNMAARRITQETFD AVIQBKAKRYHMDASGBAVSBTLOFKAQDLLRAVPRSRABMYDD
587 <b>4</b>	3	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGONNMAARRITOETFD AVIQBKAKRYHMDASGBAVSETLOFKAODLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD
5874	3	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVIQBRAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKBCGRDLBFSHSNSRDQVIGHRKLCHFRSQDWKFALRGSW
5874	3	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGONNMAARRITOETFD AVIQBKAKRYHMDASGBAVSETLOFKAODLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD
5874	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIQEKAKRYHMDASGBAVSBTLOFKAQDLLRAVPRSRABMYDD VHSDGRYSLSGSVAHSRDAGRBSLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHERLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLBKE\
5874	3	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIOBKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRABMYDD VHSDGRYSLSGSVAHSRDAGRRSLRSDVYSGPSFRSSNPSISDD SYFRKEGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\BA\DSVLRGS\SQVQA\RGRALNIVDQBGSLLG
5874	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIOBEAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKEGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI
5874	3	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIOBKAKRYHMDASGBAVSETIOFKAQDLLRAVPRSRAKMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIBKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS
5874	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVIQBKAKRYHMDASGBAVSETIQFKAQDLLRAVPRSRABMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVPSRFGIEIIKWAGFHTIKDDIKFSQLVQTLFBLET
5874	2	3387	GLCPDSLLSVDD  ACPRLARRRRVKSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHERLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRAINIVDQBGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKMAGFHTIKDDIKFSQLFQTLFBLST ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL
5874	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIGEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHERLGHFRSQDNKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKWAGFHTIKDDIKFSQLVQTLFBLST ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC
5874	3	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIOBKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRABMYDD VHSDGRYSLSGSVAHSRDAGRRSLRSDVPSGPSFRSSNPSISDD SYFRKEGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEXSFGPSAVLGDFGSSRLIBKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTIGTNPGTEDIQFPIQKIPLGLLKMLRLFRRKMS FDIIDKSDVFSRFGIBIIKMAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTMCFFBIIRPFDKYIMRLQDKLLKSVTFLLMAC NAYBLSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS
5874	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIGEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHERLGHFRSQDNKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKWAGFHTIKDDIKFSQLVQTLFBLST ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC
5874	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIOBKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRABMYDD VHSDGRYSLSGSVAHSRDAGRRSLRSDVPSGPSFRSSNPSISDD SYFRKEGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEXSFGPSAVLGDFGSSRLIBKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTIGTNPGTEDIQFPIQKIPLGLLKMLRLFRRKMS FDIIDKSDVFSRFGIBIIKMAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTMCFFBIIRPFDKYIMRLQDKLLKSVTFLLMAC NAYBLSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS
5874	3	3387	GLCPDSLLSVDD  ACPRLARRRRVKSLRRRRGWLRARWSRGQNNMAARRITGETFD  AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD  VHSDGRYSLSGSVAHSRDAGRRSLRSDVPSGPSFRSSNPSISDD  SYFRREGGRDLFVSHSNSRDQVIGHRRLGHFRSQDWKFALRGSW  EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG  KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI  QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRKMS  FDIIDRSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET  ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL  NMLIDKGAVKTKNCFFBIIRFFDKYIMRLQDKLLKSVTPLLMAC  NAYBLSVKMKTLSNPLDLALALTINSLCRKSLALLGQTFSLAS  SFRORKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML  VSSGCPLQVKKAEPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRVKSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHERLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRAINIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKMAGFHTIKDDIKFSQLIVQTLFBLST ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIRPFDKYIMRLQDKLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFKDSTLFGRBYIDHLKAMIL VSSGCPLQVKKABPEPMREBEKMIPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVLEGSLSPKERTLLKEDPAYWPLSDEN
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIGEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHERLGHFRSQDNKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLVQTLFBLST ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFRDSTLFGREYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTILQLVKRVLEGSLSPKBRTLLKEDPAYWFLSDEN SLEYKYYKLKLABMQRMSENLRGADQKPTSADCAVRAMLYSRAV
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIOBKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRABMYDD VHSDGRYSLSGSVAHSRDAGRRSLRSDVVSGPSFRSSNPSISDD SYFRKEGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\BA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTIGTNPGTEDIQFPIQKIPLDLKKLEPRKKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLVFQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKHSSALKTPRVUNEFL NMLLDKGAVKTNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC MAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFRDSTLFGRBYIDHLKAVL VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBTTLKEDPAYWFLSDEN SLBYKYYKLKLABMQRMSRNLRGADQKPTSADCAVRAMIYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTILLFLR
587 <b>4</b>	3	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIOBKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRABMYDD VHSDGRYSLSGSVAHSRDAGRRSLRSDVVSGPSFRSSNPSISDD SYFRKEGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIBKECLBKE\ SRDYDVDHSG\BA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTTLGTNPGTEDIQFPIQKIPLGLLKNLRLFRRKMS FDIIDKSDVFSRFGIBIIKMAGFHTIKDDIKFSQLVQTLFBLBT ETCARNLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTNCFFBIIRPFDKYIMRLQRRLLKSVTPLLMAC MAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFRDSTLFGRBYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIQQLVKRVIEGSLSPKBTLLKEDPAYWFLSDEN SLBYKYYKLKLABMQRMSRNLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTILLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRVKSLRRRRGWLRARWSRGQNNMAARRITGETFD  AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD  VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD  SYFRREGGRDLFFSHSNSRDQVIGHRRLGHFRSQDWKFALRGSW  EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG  KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRKMS  FDIIDRSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET  ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL  NMLLDKGAVKTKNCFFBIIRFFDKYIMRLQDKLLKSVTFLLMAC  MAYBLSVKMKTLSNPLDLALALETINSLCRKSLALLGQTFSLAS  SFRORKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML  VSSGCPLQVKKAEPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVGTLQLVKRVIEGSLSPKERTLKEDPAYWFLSDEN  SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV  RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR  APGLKHHGRQAPGLS\QARPSLPDRND\AAKO\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIOBKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRABMYDD VHSDGRYSLSGSVAHSRDAGRRSLRSDVVSGPSFRSSNPSISDD SYFRKEGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIBKECLBKE\ SRDYDVDHSG\BA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTTLGTNPGTEDIQFPIQKIPLGLLKNLRLFRRKMS FDIIDKSDVFSRFGIBIIKMAGFHTIKDDIKFSQLVQTLFBLBT ETCARNLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTNCFFBIIRPFDKYIMRLQRRLLKSVTPLLMAC MAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFRDSTLFGRBYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIQQLVKRVIEGSLSPKBTLLKEDPAYWFLSDEN SLBYKYYKLKLABMQRMSRNLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTILLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP
587 <b>4</b>	3	3387	GLCPDSLLSVDD  ACPRLARRRRVKSLRRRRGWLRARWSRGQNNMAARRITGETFD  AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD  VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD  SYFRREGGRDLFFSHSNSRDQVIGHRRLGHFRSQDWKFALRGSW  EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG  KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRKMS  FDIIDRSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET  ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL  NMLLDKGAVKTKNCFFBIIRFFDKYIMRLQDKLLKSVTFLLMAC  MAYBLSVKMKTLSNPLDLALALETINSLCRKSLALLGQTFSLAS  SFRORKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML  VSSGCPLQVKKAEPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVGTLQLVKRVIEGSLSPKERTLKEDPAYWFLSDEN  SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV  RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR  APGLKHHGRQAPGLS\QARPSLPDRND\AAKO\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHERLGHFRSQDNKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\BA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTARGGVGKLVTLRNVSTKKIPTVNRITPKTQGTTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKMAGFHTIKDDIKFSQLVQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC MAYRLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFRDSTLFGRBYIDHLKAMIL VSSGCPLQVKKARPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVLBGSLSPKBRTLLKEDPAYWFLSDEN ELEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARR\TTGTGTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLBASGPSPKPAGVDISEAPQTSSPCPSADIDMKDMGRTAR KLARFVAQVG\PRIEQF\SI\ENSTNNPDLWFL\HDQMSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGTT\GSQBSPVDLMB
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD ACPRLARRRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIOEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRRECGRDLBFSHSNSRDQVIGHERLGHFRSQDNKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVWRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKMAGFHTIKDDIKFSQLVQTLFBLST ETCAKNLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFRDSTLFGREYIDHLKAMIL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVLEGSLSPKBRTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDMGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKVYPELCSSICFTSSPHNL\HTGGGDTT\GSQBSFVDLME GEREFDEPPRRAELESPEVMPEBEDEDDEDGGBERAPA\PGRG
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIGEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVYSGPSFRSSNPSISDD SYFRREGRDLBFSHSNSRDQVIGHRRLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVYTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRPGIEIIKWAGFHTIKDDIKFSQLVQTLFBLBT ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRGEKIL*AVGLQDIAPSPAAFPWFEDSTLFGRBYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLEYKYYKLKLABMQRMSENLRGADQKPTSADCAVRAMIYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAFGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PBIEQP\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLME GRAEFEDEPPPRBAELESPEVMPEEEDEDDEGGERAPA\PGRG
587 <b>4</b>	3	3387	GLCPDSLLSVDD  ACPRLARRRRVKSLRRRRGWLRARWSRGQNNMAARRITGETFD  AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD  VHSDGRYSLSGSVAHSRDAGRRSLRSDVPSGPSFRSSNPSISDD  SYFRREGGRDLBYSHSNSRDQVIGHRRLGHFRSQDWKFALRGSW  EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQBGSLLG  KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRKMS  FDIIDRSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET  ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNBFL  MMYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS  SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGRBYIDHLKAML  VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP  QRADHRVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN  ELBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV  RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR  APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP  QDPSLBASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE  KLARFVAQVG\PBIEQF\SI\ENSTNNPDLWFI\HDQNSS\AFK  FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLMS  GRAFFEDRPPPRBELESPEWPEBEDEDDEGGBBAPA\PGRG  GPSLESSTPADGLPGBA\ABDDL/ALGAPALFTGILQVTCPFPG  RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRRVESLRRRRGWLRARWSRGQNNMAARRITGETFD AVIQEKAKRYHMDASGEAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDASGRSLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLIG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLIKNLRLPRKMS FDIIDKSDVFSRFGIBIIKMAGFHTIKDDIKFSQLFVTLFBLET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALLTPRVDNSFL NMLDKGAVKTKNCFFBIIRPFDKYIMRLQDKLLKSVTFILMAC NAYBLSVKMKTLSNPLDLALALTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGRBYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPFTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLABMQRMSENLRGADQKPTSADCAVRAMIYSRAV RNLKKKLLP\WQRRGLRAQG\LRG\WKARRA\TTGTQTTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDFSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQP\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKYFELCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLMB GRAEPEDPPPRHAELESPEVMPEEDEDDEGGEBAPA\PGRG GPSLEGSTPADGLPGBA\AEDDL/ALGAPALFTGLQVTCFPFG RGFSSKSLKVGNIPAPKRVCLIQEPKVHEPVRIAYDRPRGSPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSIGK
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRVKSLRRRRGWLRARWSRGQNNMAARRITGETFD  AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD  VHSDGRYSLSGSVAHSRDAGRRSLRSDVPSGPSFRSSNPSISDD  SYFRREGGRDLBYSHSNSRDQVIGHRRLGHFRSQDWKFALRGSW  EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQBGSLLG  KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRKMS  FDIIDRSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET  ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNBFL  MMYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS  SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGRBYIDHLKAML  VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP  QRADHRVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN  ELBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV  RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR  APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP  QDPSLBASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE  KLARFVAQVG\PBIEQF\SI\ENSTNNPDLWFI\HDQNSS\AFK  FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLMS  GRAFFEDRPPPRBELESPEWPEBEDEDDEGGBBAPA\PGRG  GPSLESSTPADGLPGBA\ABDDL/ALGAPALFTGILQVTCPFPG  RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS
587 <b>4</b>	2	3387	GLCPDSLLSVDD  ACPRLARRRRRVSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHERLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRAINIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKMAGFHTIKDDIKFSQLVFQTLFELBT ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIRPFDKYIMRLQDRLLKSVTPILMAC NAYELSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGRBYIDHLKANL VSSGCPLQVKKABPEPPMREBEKMIPFTKFBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLBYKYYKLKLABMQRMSRNLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARR\TTGTQTILLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGGTAR KLARFVAQVG\PRIEQF\SI\ENSTDNPDLWPL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGTT\GSQBSPVDLMB GPSLEGSTPADGLPGBA\AEDDL/ALGAPALFTGLLQVTCFFFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMKKEGHGLGSLGK KKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMKKEGHGLGSLGK KKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMKEGHGLGSLGK KKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGKEGHGLGSLGK
			GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIGEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRREGRDLBFSHSNSRDQVIGHERLGHFRSQDNKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTARGGVGKLVTLRNVSTKKIPTVNRITPKTQGTTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKMAGFHTIKDDIKFSQLVQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC MAYKLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFRDSTLFGRBYIDHLKANL VSSGCPLQVKKARPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN ELBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDMGRTAE KLARRVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFBLCPSICFTSSPHNL\HTGGGTT\GSQBSPVDLMB GRAEFFDEPPPRRBELESPEVMPEBEDEDDEDGGERAPA\PGRG GPSLEGSTPADGLPGBA\AEDDL/ALGAPALFTGLLQVTCFFPG GGPSEGSTPADGLPGBA\AEDDL/ALGAPALFTGLLQVTCFFPG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NIGFG\MLGKMGKBGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVP
587 <b>4</b>	296	3387	GLCPDSLLSVDD  ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD ACPRLARRRRRVRSLRRRRGWLRARWSRGQNNMAARRITGETFD AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD SYFRREGGRDLBFSHSNSRDQVIGHERLGHFRSQDNKFALRGSW EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTARGGVGKLVTLRNVSTKKIPTVWRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVFSRPGIBIIKMAGFHTIKDDIKFSQLVQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYRLSVKMKTLSNPLDLALALSTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFRDSTLFGRBYIDHLKAMIL VSSGCPLQVKKAEPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVLEGSLSPKBRTLLKEDPAYWFLSDEN ELBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLBASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PBIEQF\SI\ENSTNNPDLWFI\HDQNSS\AFK FY\RKVPELCPSICFTSSPHNL\HTGGGDTT\GSQBSPVDLMB GRAEFEDEPPPRHAELESPEVMPEBEDEDDEGGBEAPA\PGRG GPSLESSTPADGLPGEA\ARDDL\ALGAPALFTGILQVTCPPPG RGFSSKSLKVGMIPAPKRVCLLQBPKVHEPVRIAYDRPGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVP LAALGGLPLWRLSRRGVREYLLGLSAPSALGGAMRSVSYVQRVA
			GLCPDSLLSVDD  ACPRLARRRRRVSLRRRRGWLRARWSRGQNNMAARRITGETFD  AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD  VHSDGRYSLSGSVAHSRDAGRRSLRSDVPSGPSFRSSNPSISDD  SYFRREGGRDLBYSHSNSRDQVIGHRRLGHFRSQDWKFALRGSW  EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQBGSLLG  KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI  QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS  FDIIDRSDVFSRFGIEIIKMAGFHTIKDDIKFSQLFQTLFELET  ETCAKNLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNBFL  MMYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS  SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGRBYIDHLKANL  VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP  QRADHRVVGTILQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN  SLBYKYYKLKLABMQRMSBNLRGADQKPTSADCAVRAMLYSRAV  RNLKKKLLP\WQRRGLLRAQG\LRGWKARRA\TTGTQTLLFLR  APGLKHHGRQAPGLS\QAKPSLPDRND\AAKN\CPLDPV\GPSP  QDPSLBASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR  KLARFVAQVG\PEIEQF\SI\ENSTNNPDLWFL\HDQNSS\AFK  FY\RKKVFELCPSICFTSSPHNL\HTGGDTT\GSQBSPVDLMB  GRAEFFDBPPPRRAELESPEWPEEBDEDDEGGEBAPA\PGRG  GPSLEGSTPADGLPGBA\ARDDL/ALGAPALFTGLLQVTCFFFG  RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS  KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGNKBGHGLGSLGK  GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL  LFPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP
			GLCPDSLLSVDD  ACPRLARRRRVSLRRRRGWLRARWSRGQNNMAARRITGETFD  AVIQEKAKRYHNDASGEAVSETLOFKAQDLLRAVPRSRAEMYDD  VHSDGRYSLSGSVAHSRDAGRESLRSDVPSGPSFRSSNPSISDD  SYFRKEGRDLBFSHSNSRDQVIGHRRLGHFRSQDWKFALRGSW  EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRAINIVDQRGSLIG  KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS  FDIIDKSDVFSRFGIBIIKWAGFHTIKDDIKFSQLFQTLFBLET  ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALLETPRVDNBFL  NMLIDKGAVKTKNCFFBIIRFFDKYIMRLQDRLLKSVTPILIMAC  MAYBLSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS  SFRORKIL*AVGLQDIAPSPAAFPNPRDSTLFGRBYIDHLKAML  VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP  QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN  SLBYKYYKLKLABMQRMSENLRGADQKPTSADCAVRAHLYSRAV  RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR  APGLKHHGRQAFGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP  QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE  KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK  FY\RKKVFBLCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLME  GRAFFEDEPPPRBAELESPEVMPEBEDDEDGGBBAPA\PGRG  GPSLESSTPADGLPGBA\ARDDL/ALGAPALFTGILQVTCPPFG  RGFSSKSLKVGMIPAPKRVCLIQBPKVHEPVRIAYDRPRGRPMS  KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK  GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL  IFVF  LAALGGLPLWRLSRRGVREYLLGLSAPSALGGAMRSVSYVQRVA  LEFSGSLFPHATCLGDVDNDTINELVVGDTSGKVSVYKNDDSRP  WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK
			GLCPDSLLSVDD  ACPRLARRRRRVSLRRRRGWLRARWSRGQNNMAARRITGETFD  AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD  VHSDGRYSLSGSVAHSRDAGRRSLRSDVPSGPSFRSSNPSISDD  SYFRREGGRDLBYSHSNSRDQVIGHRRLGHFRSQDWKFALRGSW  EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQBGSLLG  KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI  QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS  FDIIDRSDVFSRFGIEIIKMAGFHTIKDDIKFSQLFQTLFELET  ETCAKNLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNBFL  MMYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS  SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGRBYIDHLKANL  VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP  QRADHRVVGTILQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN  SLBYKYYKLKLABMQRMSBNLRGADQKPTSADCAVRAMLYSRAV  RNLKKKLLP\WQRRGLLRAQG\LRGWKARRA\TTGTQTLLFLR  APGLKHHGRQAPGLS\QAKPSLPDRND\AAKN\CPLDPV\GPSP  QDPSLBASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR  KLARFVAQVG\PEIEQF\SI\ENSTNNPDLWFL\HDQNSS\AFK  FY\RKKVFELCPSICFTSSPHNL\HTGGDTT\GSQBSPVDLMB  GRAEFFDBPPPRRAELESPEWPEEBDEDDEGGEBAPA\PGRG  GPSLEGSTPADGLPGBA\ARDDL/ALGAPALFTGLLQVTCFFFG  RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS  KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGNKBGHGLGSLGK  GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL  LFPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP
			GLCPDSLLSVDD  ACPRLARRRRRVKSLRRRRGWLRARWSRGQNNMAARRITGETFD  AVIQEKAKRYHMDASGBAVSETLOFKAQDLLRAVPRSRAEMYDD  VHSDGRYSLSGSVAHSRDAGRRSLRSDVPSGPSFRSSNPSISDD  SYFRKEGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW  EQDFGHPVSQESSWSQBYSFGPSAVLGDFGSSRLIEKECLBKE\ SRDYDVDHSG\RA\DSVLRGS\SQVQA\RGRALNIVDQBGSLLG  KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLLKNLRLPRKMS  FDIIDKSDVFSRFGIBIIKMAGFHTIKDDIKFSQLFVTLFBLBT  ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALLTPRVDNSFL  NMAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS  SFRQBKIL*AVGLQDIADSPAAFPNFRDSTLFGRBYIDHLKANL  VSSGCPLQVKKABPEPMBEBEKMIPFTKPBIQAKAPSSLSDAVP  QRADHRVVGTIDQLVKRVLEGSLSPKBRTLLKEDPAYWFLSDEN  SLBYKYYKLKLABMQRMSRNLRGADQKPTSADCAVRAMLYSRAV  RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR  KLARFVAQVG\PBIEQP\SI\ENSTDNPDLWFL\HDQNSS\AFK  FY\RKKVFBLCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLMB  GRAEFEDBPPPRBAELESPEVMPEEDEDDEGGBRAPA\PGRG  GPSLEGSTPADGLPGBA\ABDDL/ALGAPALFTGLLQVTCFPFG  RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGSPMS  KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKBGHGLGSLGK  GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL  IFVF  LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA  LEPSGSLFPHAICLCDVDNDTLNBLVVGDTSGKVSVYKNDDSRP  WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK  VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL
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### PISOS HILLERDSLYCI SANDOGYEHTAEDPALLTKVETIMGE LGWVLRSLYKELEPKUPTPEKLINDDMMREMPEDRIGRECTI PDWSRSYHEGIVGLIMMINGYPHERAYFKURKPNYDEVOLGRWOGE KKKRYKWEWHRILISERBYLDBISKNPCROSPIDTEGHTYVAFIR MEKDDDFTIWTGLAKCHIMDLUWGHERGLWRLDSKRYNDFLUV GVDAS PYSVKKPSVYTPI PLEPPKESSAPGAPEOT  5879  3 981 RLITERABAGSGSRARGWRGSPTILLFLSFTSPRCATMASSDED GTNGGASEAGEDREAPGRRRIGGIATMUTTYDIMTAGHLUL ALAMVRYYMEKGTHERGLYKSIOKTLKFFOTPALLSI VICLIGIV PTSVIVTGVQVSSRIFMVWLITHSIKPIONERSVVLFILVAWTVT EHTRYSFYTFSLIDHLEVFI KWARTHNFFIILKPVCVAGEBLTTY AALPHVKKTGMPS IRLENKYNVSDDYYYFILLTMASYTPLFPOL YPHINLRQRRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRQRRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRQRRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRQRRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRGRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRGRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRGRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRGRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRGRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRGRKVLHEGO*LARWINFSDYYFILTTMASYTPLFPOL YPHINLRGRKVLHEGO*LARWINFSDYYFILTMASYTPLFPOL YPHINLRGRKVLHEGO*LARWINFSDYYFILTMASYTPLFPOL YPHINLRGRKVLHEGO*LARWINFSDRYFFILTMASYTPLFPOL YPHINLRGRKYLHEGO*LARWINFSCHARGT*SALTACSA **KKKRGRCSS*/MISOPOLHARKUTSRGTYBRARGT*SALTACSA **KKKRGRCSS*/MISOPOLHARKUTSRGTHARGRARAASDVL CRELANBETROLRGRKJTHACCHARKUTSRGTHARGRARAASDVL CRELANBETROLRGRKJTHACCHARKUTSRGTHARGRARAASDVL CRELANBETROLRGRAGGTHAGAGKGGULUCCPH CLCCFSDEGGEBLLKHABCCO **AGNERIABAGRARAAAARAAAAAAAAAAAAAAAAAAAAAAAAAA	Į	1	ĺ	
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PDWSRSYHEGIVGLANNONGY PHRAYFKURMTYDEVOLLRANDEL KKRAYEVEVHRILISEABVILDHSKNPCEDSFLPDTESHTYVAFIR MEKODDFTTWTQLAKCLHI WDLDVRGNERGIMREFRKNNEPLVV GVDASPYSVKKPPSVPPI PLEPPPKEGAPGAPROT  5879  3 981 RITEAAAAGSGSRAAGMAGSPPTLEPLSPSPRCAATMASSDED GTRGGASEAGEDREAPGRRRIGFLATAWLITYDIAMTAGMLVL ALAMVRYVBEKGTHRGLYKSIQKTLKFFGTFALLEIVHCLIGIV PTSVIVTGVQVSSRIFMVWLITHSIDFLORBESVVLFLVAMTVT EITRYSFYTFSLLDHLPYPIKMARTNFFILLPVGVAGELLTIY AALPHVKKTAMFSIRLPNKYNVSFDYYYFLLITMASYIPLPPQL YFHMLRQRRKVLHGG*L*KRIGKTLARPREARGFFSALTACSA NNKKKQLGCISHVVWFLKI  5880  1138  1324  SUMCLWAGGIGLGFSSONFLQRRGILARPREARGFFSALTACSA SVISKUKSSSGMWPSAASDRDSPYPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/MLSQPQHREREKEVVLLERSMAEGERARAASDVL CRSLANETRGLARTTLFATAHMCCHLAKVIDERQHAQRRVGERSF DQSEHTDGHTSVQSVIEKLQEENRLLKQXVTEVEDLANAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKISHSRLMKQLERKINDC ASVKQBLAASRTARDAALERVQMLBGQILAYKDDFMSERADRER AQSRIQRLESKVASLLHKUVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGKRFGTGSQOPERPDAGRHDAGSGGGULQCPH CLQCFSDEGGEBLLRHVARCCQ CGHPSPFTEAPRAQHLTIMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKRCASVMYSCTVSGTTLTKLSMHWVRQAPGEGLE*MSPPD LQDVETTYPQKFQGRVSMTEETSTTTQ/AYLELSSLRSEDTAV HHCATDTV  5882  2407  2216  SGCVEMIYSHSLEYNPENISVOSAVAPAQLALNSDGDL*LHSGK RTRRD*QLPSAGGPGLQRELQIGELDITSDRFILDEVOG\VDLAR HYSKQVELELQQIEQKSIRDYIQGSGAMIRLENRQAVRGKLG ELVDGLVPSALGPGLGSESIASSETTLDEVGGAMIRLENRQAVERKLG ELVDGLVPSALVTALLEAPVYTEPRFLEQLGELDAKAAAVREQB ARGTAACADVRGVLDRIVKAVTKIRFILQKIYSFRKPMINYQ TPQTALLKYRFYVQFLLGRRRATAKEIRBFILGKIYLSYIR SYLGRIMKVQYBEVARKDOLMGVEDTAKRGFFSKYSLSRINTIF TLGTRGSVISPTBLRAPILVPHTAQRGRQRYFFSALFRSQHYAL LDNSCRRYLFICHFFVVSGRAABLFHAWRTLSNTLKHLDSY				
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GTNGGASEAGEDREAPGKRRRIGFLATAWLTFYDIAMTAGWLVL ALAMVRFYMEKGTERGLYKSIQKTLKFFGTFEALLERLVHCLIGIV PTSVIVTGVQVSRIFMWLITHSIKPIQNESSVULFLVAWTT EITRYSPYTFSLLDHLPYFIKMARYNFFILLYPVGVAGELLTIY AALFHVKKTGMFSIRLPMKYNVSPDYYYFLLITMASYIPLFPQL YPFMLRQRRKVLHG\G*L*KMIK*SLQTRCFFQNNQDYLSPSF NNKKKQLCELSWIWPFKI  5880  1138  1324  SLWCLVAGGLGLGYSGNPLQRAGILARPREARGTFSALTACSA SVITSKOKSSSGNWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGCSS/WLSQPQHEREKEVVLLRSMABGEBARAASDVL CRSLANETQLRRTLTATAHMCQHLAKCLDERQHAQRNVGBRSP DQSHTTGHTSVQSVIEKLQESRRLKKQKVTEVEDLNAKKQRN ASRDBYVRGLHAQLREGLQPHEPELMKRISIRINRQLEKRINDC ASVKQBLAASRTARDAALERVQMLBQQILAYKDDFMSERADRER AQSRIQBLERKVASLLHQVSWRQDGEBPDAGRHAGSKTAKYLA ADALELMVPGGKRPGTGSQQPEPPAEGGHPGAAQRGQGDQCPH CLQCFSDEGGEBLLRHVABCQ  5881  26  441  GGHPSPTEAPRAQHLTMDCTWRLLFLVAAATGTHAQVQLLQSG SEVKKPGASVWVSCTVSGYTLTKLSMWVRQAPGKGLE*MBPPD LQDWETTYPQKPQGRVSMTERTSTETTQ/AYLELSSLRSEDTAV HHCATDTV  HCATDTV  5882  2407  2216  GGCYEMLYSHSLETNPBWISVOSAVAPAQLALNSDGDL*IHSGE RTRRD*QLPSAGSPGLQBPLQLGGLDITSDEPILDEVDG\VDLR HYSKQVKLBLQQIBQKSIRDYIQESENIASLINQITACDAVLER MEQMLGAPQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPBFLEQLGELDAKAAAVRGE ARGTAACDAVRGVLDRLRVKATYKREPTILQKLYSFRKFMTNYQ IPPOTALKKYRFYYGFLLGNBRATAKEIRDEYVETLSKIYLSYYR SYLGRIMKVQYBEVARKDDLMGVEDTAKKSFFSKYSLRSHNI IF TLGTGSSVISPTBLEAPILLVPHTAQRGPQRYPFEALFRSQHYAL LDNSCRRVLFICRFFVVSGPAAHDLFHAVMGRILSSTLKHLDSY			l	
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PTSVIVTGVQVSSRIFMVMLITHSIKDIQNERSVULFLUAWTUT BITRYSPYTESILDHLPYPIKMARYNFFILIYPVGVAGELLTIY AALPHVKKTGMFS IR LIPMKYNVSPDYYYFLLITMASYTPIFPQL YPHMLRQRRKVLHG\G*L* KRMIK*SLQTRCFFQNNQDYLSPSF NNRNKQLCEISWIVMFLKI  5880  1138  1324  SLWCLVAGGIGLGFSSQNPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSCMWPSASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAGGERARASDVL. CRSLANETHQLRRTLTATAHMCCHLAKCLDERQHAQRNVGERSF DQSKHTDGHTSVQSVIYEKLQBENRLLKGKVTFVEDULNAKNQRYN ASRDBYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEBKINDC AZVKQBLAASRTTARDAALRRVQMLBQQILAXKDDFMSERADRER AQSRIQBLEBKVASLLHNVSWRQDSREPDAGGHPGAAQRGQGDLQCPH CLQCFSDEQGEBLLRHVABCCQ  5881  26  441  GGHBFSPTEARRAQHLTMDCTTMRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCTVSCTYLTKLSMHWVRQAPGKBLE*MGPFD LQDVETITYPQKPQGRVSMTEBTSTETTQ/AYLELSSLSSEDTAV HHCATDTV  5882  2407  2216  SGCVEMIYSHSLEYNPENISVOSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPZAGGPGLQEPLQLGELDITSDBFILDBVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAPQSDLSSISSIESEIRTLQEGSGAMIRLRRNQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIRBFILQKLGKLSKYRIYIR SYLGRIMKVQYEBVARKDDLMGVEDTAKKGFSKVELSRSNTIF TLGTRGSVISPTRLBAPILVPHTAQRGEQRYPPEALFSCHYAL LDNSCRRVLFICRFFVVSGBAABDLFHAVMGRTLSMTLKHLDSY	1	1	*	
EITRYSPYTFSLLDHLPYFIKMARYMFFILLYPVGVAGELLTTY AALPHVKKTGMFSIRJBNKYMVSPDYYYFLLITMASYTPLPFQL YPHMLRQRRKVLHG\G*L*KRMIK*SLQTRCPFQNNQDYLSPSF NNKKNQLCEISMIVWFLKI  5880  1138  1324  SLWCLVAGGLGLGPSSQNPLQRAGILARPREARGTFSALTACSA SVITSKGXSSSGW#PSAASDRSPVELRPPGPVQLPSGTGWVLSD *KKKRGRCSS/MLSQPQHEREKEVVLLRRSMABGERARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGBRSP DQSEHTDGHTSVQSVIEKLQBERRLLKQXVTHVEDLNAKWQRIN ASRDRYVRGLHAQLRCLQIPHEPELMRKEISRLNKQLEKKINDV ASRDRYVRGLHAQLRCLQIPHEPELMRKEISRLNKQLEKKINDV AASVQRLABASRTARDAALERVQMLBQQILAYKDDFMSERADRER AQSRIQBLEEKVASLLHQVSWRQDSKEPDAGRIHAGSKTAKYLA ADALELMVPGGRRPGTGSQQPBPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGBELLRHVABCCQ  SGVKKPGASVMYSCYVGSYTLTKLSMHWVRQAPGKGLE*MOPFD LQDVETIYPQKFQGRVSMTEBTSTETTQ/AYLELSSLRSEDTAV HHCATDTV  LQDVETIYPQKFQGRVSMTEBTSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVOSAVAPAQLALNSDGDL*LHSGK RTRRD*QLPSAGSPGLQEPLQLGELDITSDBFILDBVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAPGSDLSSISSEIRTLQEGGAMMIRLENRQAVRGKLG ELVDGLVVPSALVTAILEAPVYTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIRBFILQKITSFRKPMTNYQ IPQTALLKYRFFYQFILGNBRATAKEIRDEYVETLSKIYLSYYR SYLGRIMKVQYEBVARKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCRRYLFICEFFVVSGPAAHDLFHAVMGRILSMTLKHLDSY	l	1	1	
AALPHVKKTGMFSIRLPNKYNVSPDYYYFLLITMASYIPLPPQL YFHMLRQRRKVLHG\G*L* KRMIK*SLQTRCFFQNNQDYLSPSF NNKNKQLCEISWIVWFLKI  5880 1138 1324 SLWCLVAGGLGLGSSQNPLQRAGILARFRARGTFSALTACSA SVTSKGKSSSGWMPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHREKEVVLLRRSMARGERARAASDVL CRELANETHQLRRTILTATAHMCQHLAKCLDERQHAQRNVGBRSP DQSKHTDGHTSVQSVIEKLQBERKLLKQKVTHVEDLMAKNQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLBQQILAYKDDFMSERADRER AQSRIQRLEEKVASLLHQVSWRQDSREPDAGRHAGSKTAKYLA ADALELMVPGGWRPGTGQQPBPPAEGGHPGAAQRGQGDLQCPH CLQCFSDRGGBELLRHVABCCQ  5881 26 441 GGHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCTVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFPGGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882 2407 2216 SGCVEMLYSHSLEYNPBWISVQSAVAPAQLALNSDGDL*IHSGE RTRRD*QLPSAGGPGLQBPLQLGELDITSDEFILDEVDG\VDLR HYSKQVBLBLQQTRQKSIRDYIQSSENTASLENQITACDAVLER MEQMLGAPQSDLSSISSEITRLQEQSGAMNIRLNRQAVRGKLG BLVDGLVVPSALVYAILERAPVTBPRFLEQLQELDAKAAAVREQE BLVGGLVVPSALVYAILERAPVTBPRFLEQLQELDAKAAAVREQE BLVGGLVVPSALVYAILERAPVTBPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREPILQKIYSFRKPMTNYQ 1PQTALLKYRFFYQFLLGMBRATAKEIRDSYVETLSKIYLSYYR SYLGRIMKVQYBRVARKDDLMGVEDDTAKKGFFSKYSLKSRNTIF TLGTRGSVISPTBLEAP ILVPHTAQRGEQRYPPRALFRSQHYAL LDNSCRRYLFICRFFVVSGPAAHDLFHAVMGRTLSMTLKHLDSY	l .	Į.		PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT
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C 055	15		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	1		PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV
i		ĺ	SINQTIPNERTMQLLGQLQVEVRNFVLRVAABFSSRKEQLVPLI
1	Ì	ļ	NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEFIEELLS
	1	]	PPFGGLVAFVKEAEALIERGQAERLRGEEARVTQLIRGFGSSWK
1		ļ	SSVESLSQDVMRSFTNFRNGTSI1QGALTQL1Q\LYHRFHRV\L
			SOPOLRALPARAELINIHHLMVKLKKHKPNF
5883	2	1374	BPPGRRFRAVMEAGAGAGAGAGWSCPGPGPTVTTLGSYRASEG
1			CERKKGQRWGSLERRGMQAMEGEVLLPALYEEREEBEBEBEBEVB
1	1		EEEEQVQKGGSVGSLSVNKHRGLSLTETELEBLRAQVLQLVABL
1	1		BETRELAGOHEDDSLELQGLLEDERLASAQQAEVFTKQIQQLQG
			BLRSLREEISLLEHEKESELKEIEQELHLAQAEIQSLRQAAEDS
1			ATBHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRARME
1			MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNEKYRALQESNS
			SLTGQLADLESERTQRATERWLQSQTLSMTSAESQTSEMDFLEP
1			DPEMQLLRQQLRDAEEQMHGMKNKCQELCCELERLQHHRQVSBE
1	•		EQRRLQRELKCAQNEVLRFOTSHS\SPSHPLPPIPPSSPCLL+A
			LVVISALLWCWWAETSS
5884	4261	2522	GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR
1		•	SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVPVV
İ			FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLQF
1 .			SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVROM
1			HLLXSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAKLCE
1			IPSTSDTKSDTATGGESAGHATSSQRPSGCSDQRPARDLNIRVE
			RLTKKI BERREEKRKBEEQREIKKEIERRKTGKEMLDYKRKOEB
1			BLTKRMLBERNREKAEDRAARERIKQQIALDRAERAARFAKTKE
			EVEAAKAAALLAKQABMEVKRESYARERSTVARIQFRLPDGSSF
1			TNOPPSDAPLEBAROPAAQTVGNTYGNFSLATMFPRREFTKEDY
1 1			KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSSGDIW
1 1	-		TLLGTVLYPFLAIWRLISNFLFSNPPPTOTSVRVTSSEPPNPAS
			SSKSEKREPVRKRVLEKRGDDFKKRGKIYRLRTQDDGRDENNTW
			NGNSTQQM
5885	900	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDRFLDV
			IYWFRQIIAVVLGVIWGVLPLRGFLGIAGPCLINAGVLYLYFSN
1 (			YLQIDEBEYGGTWELTKEGFMTSFA/IVHGHLDHLLHCHPL*LM
!			VYSSQVLPIQSKGPS
5886	86	1341	PFRGRALITLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS
1 1			GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFRLKTSKLPPLKNG
			BVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVBSKNVAL
}			PKGTIVLASPGWTTHSISDGKDLRKLLTEWPDTIPLSLALGTVG
1 1			MPGLTAYPGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC
	ļ	ļ	KVVGAVGSDEKVAYLQKLGPDVVFNYKTVESLBETLKKASPDGY
			DCYFDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP
	ľ		PPBIGIYQELRMEAFVYYRWQGDARQKALKDLLKWVLELPYFVI
	ļ		D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE
			NMPAAFMGMLKGDNLGKTIVKA
5887	1937	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLEE
	i		RPDRCHPGGDDRGPQLHRGSPG/SPSBLSRRPGPPGLPGLQGPP
1 1			PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS
j J	į		ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI
	1	į	PCIHITN\*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNARSY
	ł		VSFTTKLDIPTAAKYRYGVPLQTSDSFLRPPSSLTSSLCTDNNP
ļ j	Í		
	1	1	AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK
	j	Ì	KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV
	}	ţ	LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ
	i	1	BNTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI
	ŀ	1	LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ
		ļ	KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHPITQSFNRK
	ľ	1	DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPEAN
	ł	Ì	SGNERTILISTAVTPVDVSAPARAGFRAPPAINARLPFNFFFPF
			V

SEQ	Predicted	1 n 37 3 and	I have a self-search control of the search o
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	1	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG
1 2000	1 3.3	2002	LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLP
1	1		CLDESRFENLGVSSLGERKKLLSY1ORLVOIHVDTMKVINDPIH
1	Ì		
1	ł	ì	CHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
1	J	1	SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
İ	1	ì	PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
i	} .		QYGLIPKEDICFIKEQIVGPLESPVEDSLWPYKGRPKNKSFLYE
Į.	ì		IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
i	1		DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT
1		]	DAFLKADDYIBITGAGGKKYRISTAIDDMBAYTKLTDNIFLBIL
1		ł	YSTDPKLKDAREILKQIKYRNLFKYVGETQPTGQIKIKREDYES
Į.	1		LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQBKNPIDHVS
1	1	<u> </u>	FYCETAPNRAIRITKNOVSOLLP\BKFAEO\LIRVYCKKVDRKS
1	1		LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
	1		NDSTFSPKIPTRLPRRLPKSRV\OLFKDDPM
		·	
5889	1831	731	LPAACGRPVTARPRQAPEGRSGRPRDL>PYPPQVFPPRPDRVAI
1		ł	VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
i .	1	•	LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
i	1		FGIPIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR
]	ł.	İ	KTRDGFBEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
i	į.		SATHYVAKLNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
1	İ	ļ	AABGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
1	<b>\$</b>	1	DEGANTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ
			LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
			GRPDPRPASAAGGHAGERMSORDTLVHLFAGGCGGTVGAILTCP
1	1	,	LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
i			ILBKEGPRSLFRGLGPNLVGVAPSRATYFAAYSNCKEKLNDVFD
l	ł		PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
		Į.	1
1	i		RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
1	1		KQKLLEYKTASTMENDEESVKRASDFVGMMLAAATSK\LVATTI
	1	·	AYPHEVVRTRLREGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
			LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
ì		1	GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
ł		İ	LEVVKTRLQSSSVTLYISEVQLNIMAGASVNRVVSPGPLHCLKV
		1	ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
1	1	)	PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
		1	RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
1	1	}	KOKILEYKTASIMENDEESVKBASDFVGMMLAAATSK\LVATTI
1	I	1	AYPHEVVRTRLREEGTKYRSFFOTLSLLVQEEGYGSLYRGLTTH
1	1	1	LVROIP\NTAIMMATYELVVYLLNG
5892	1764	320	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGPA
2032	1/04	379	
1	1	1	DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
}	i		TPDKLLSAVMTAVLKDVNLRPBQLGDICVGNVLQPGAGAIMARI
}	l		AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
1			CGVESMSLADRONPGNITSRLMEKEKARDCLIPMGITSENVAKR
	1	1	FGISREKQDTFALASQQKAARAQSKGCFQABIVFVTTTVHDDKG
1	l .	ĺ	TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS
1	Ī		DGAAATLLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
ł	1		AIPVALQKAGLTVSDVDIFBINE\AFASQAAYCVEKLRLPP*EG
Ì	i	1	*TPLGGASGP*GHPLGLHWGHVOVITLAO*S*SARGKRAYRSGC
1	1		
L	<del></del>		PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT
ļ	İ		CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
1	l	· ·	MPEDFFNFLHNSKLLEYFRIFAKKFDLLKYIQFQYTTVLSVRKCP
l	i	Ì	DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
1	İ		GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
1	ſ		NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
		1	-
i	]	l	TAVKNMTROOMNRWPNHENYCLRPONKYIMKEPVINDDVPSRII.
İ			TAVKNMIEQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLL COALKVKSTVKELTETSAIPEDGTVEENIDVIIFATGYSFSFPF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
1	nucleotide	location	Glutamic Acid, F=Phenylalarine, G=Glycine,
NO:	1 .	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location		
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	<del> </del>		LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQPLGSIFPT
ļ	Į.		ABLOARWYTRYFKGLCSLPSERTMMMDIIKRNEKRIDLFGESOS
ļ	1		QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAVRLYFGPCN
	1		SY*YRLVGPGOWEGARNAIPTOKORILKPLKTRALKDSSNFSVS
ł	1	ŀ	PLLKIIGLLAVVVAFF\COLOWS
		1673	
5894	174	1673	RYSPKKVLONKESSLKLGMATALVSAHSLAPLNLKKEGLRVVRE
			DHYSTWEQGFKLQGNSKGLGQEPLCKQFRQLRYEETTGPREALS
ŀ	1	•	RERRECOOMEDPETHTKEHILELEVEROPLITEPKREOARVORH
			HPESREDVVVVLEDLQLDLGETGQQVDPDQPKKQKILVEEMAPL
			KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIVVTDSCGRVES
ĺ	ĺ	1	SGKISEPMEAHNEGSNLERHQAKPKEKIEYKCSEREQRFIQHLD
1	ŀ		LIEHASTHTGKKLCBSDVCQSSSLTGHKKVLS*ERKVIQC\HGV
1	1	1	LGKAFORSSHLVRHOKTHLGEKPYQCNECGKVFSQNAGLLEHLR
l	Į.	Į.	IHTGERPYLCIHCGRNFRRSSHLNRHORIHSQEEPCECKECGKT
i		1	FSQALLTHHQRIHSHSKSHQCNECGKAFSLTSDLIRHHRIHTG
<b>!</b>	]		BKPFKCNICQKAFRLNSHLAQHVRIHNEBKPYQCSECGEAFRQR
ł	1		SGLFOHORYHHKDKLA
COOF	2967	86	HPSLLGAIPPYPPPSSPWPPPLYLPWNSHRKSRHFINQRGIHGE
5895	2967	86	MRLFVSDGVPGCLFVLAAAGRARGRAEVLISTVGPEDCVVPFLT
	•	1	RPKVPVLQLDSGNYLPSTSAICRYFF\LLSGWEQDDLTNQWLEW
]			
	1		EATELOPTLSAALYYL\VVQGKKG\RDVLGSVRRTLTHIDHSLS
			RQ\NCPFLAGETRSLADIVLWGALYPLLQDPAYLPEBLSALHSW
	i		FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1			EGKGLSPIEPEEEELATLSEREIAMAVTAWEKGLESLPPLRPQQ
			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
i	Į.		RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
•	i		TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI
١.	ļ		NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
1			PGSDWTPNAQFITPFFGFRENPSKPRWQ*TRDLK\WGNPGTP*E
			GFRDK\VFYVWFDATIGYLSITANYTDQWBRWW\KNPBQVDLYQ
ļ	}		FM\AKDNVPFHSLVFPSSALGARDNYTL\VSHLIATEYLNYEDG
i			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
1		1	FEWTDLLLKNINS\ELLINILGNFINRA\GMPVSKFFGG\YVPEMV
l			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
Ì			
	i		GNQYI\QVNBPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
	l	Į.	QPYMPTVSATIQAQLQLPPPACSILLTMPLCTLPAGHQIGTVSP
	1	1	LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
1	]	Í	IMDEVTKQGNIVRELKAQKADKNEVAASVAKLLDLKKQLAVAEG
L			KPPBAPKGKKKK
5896	2967	86	HPSLLGATPFYPPPSSPWPPPLYLPWNSHRKSRHFINQRGIHGE
		1	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
1		1	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWRQDDLTNQWLEW
		]	EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
		Į.	RQ\NCPFLAGRTESLADIVLWGALYPLLQDPAYLPEKLSALHSW
1	1		FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1	1		BGKGLSPIBPEKEKLATLSEBBIAMAVTAWEKGLESLPPLRPQQ
(	1		NPVLPVAGERNYLITSALPYVNNVPHLGNIIGCVLSADVFARYS
	4		RLROWNTLYLCGTDEYGTATETKAL\EBGLTPQBICDKYHIIHA
1	1		DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
ł			TVEQLRCEHCARP\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
1			NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLEEWLGRTL
l	Ì		PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\NGNPGTP*E
ſ	1		GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
1	1	1	FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLIATEYLNYRDG
		1	K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
	J		FSWTDLLLKNNS\BLLNNLGNFINRA\GMFVSKFFGG\YVPEMV
		ł	LTPDDORLLA\HVTLELOHYHO\LLEKVRIRDALRSILTIS\RH
	1	1	GNOYI \QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
1		į.	
			QPYMPTVSATIQAQLQLPPPACSILLTMFLCTLPAGHQIGTVSP
L		<u></u>	LFQKLENDQIBSLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA

SSO predicted mucleotide location mucleotide location corresponding to first maino acid sequence corresponding to first maino acid sequence corresponding to first maino acid sequence				
mucleotide   corresponding to first maino acid residue of maino acid residue of maino acid residue of maino acid sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide deletion,	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
mucleotide   corresponding to first maino acid residue of maino acid residue of maino acid residue of maino acid sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide sequence   mucleotide deletion,	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Location   Corresponding		micleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
LeLeucine, M-Methionine, N-Asparagine,   brirth   amino acid   residue of   residue of   residue of   amino acid   sequence   sequence   sequence   sequence   Sequ	MO.			
to first amino acid am	1			
amino acid		corresponding	to first	
amino acid		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
menian of antino acid sequence (Codon, #possible mucleotide deletion, #=5cop				
amino acid sequence  Codon, /=possible nucleotide insertion)  Lypossible nucleotide insertion  Lypossible nucleotide insertion  Lypossible nucleotide insertion  Lypospockskok  Rypospockskok  HESPAROKKOKA  HESPAROKKOKA  HESPAROKOKOKA  HESPAROKOKOKA  HESPAROKOKOKA  HESPAROKOKOKA  HESPAROKOKOKA  HESPAROKOKOKA  HESPAROKOKOKA  HESPAROKOKOKA  RATSIQPTISABATYILVAWORKOKEDDULSSVERTITHINGRISIS  RATSIQPTISABATYILVAWORKOKEDDULSSVERTITHINGRISIS  RATSIQPTISABATYILVAWORKOKEDDULSSVERTITHINGRISIS  RATSIQPTISABATYILVAWORKOKEDDULSSVERTITHINGRISIS  RATSIQPTISABATYILVAWORKOKEDDULSSVERTITHINGRISIS  RATSIQPTISABATYILVAWORKOKEDDULSSVERTITHINGRISIS  RATSIQPTISABATYILVAWORKOKEDDULSSVERTITHINGRISIS  RATSIQPTISABATYILVAWORKOKEDDULSSVERTITHINGRISIS  RATSIQPTISABATYILVAWORKOKEDDULSSVERTITHINGRISIS  REGENTIVALORIUS PROPERTITE RANDAVANEGE SELPPERIORISTIC  REGENTIVALORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTIVALORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTIVALORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTIVALIS SELDANGEN TITROLAK REGENTORIUS  REGENTIVALIS SELDANGEN TITROLAK REGENTORIUS  REGENTIVALIS SELDANGEN TITROLAK REGENTORIUS  REGENTIVALIS SELDANGEN TITROLAK REGENTORIUS  REGENTIVALIS SELDANGEN TITROLAK REGENTORIUS  REGENTIVALIS SELDANGEN TITROLAK REGENTORIUS  REGENTIVAL SELDANGEN TITROLAK REGENTORIUS  REGENTIVAL SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS  REGENTARIORIUS SELDANGEN TITROLAK REGENTORIUS SELDAN				
\possible nucleotide insertion		residue of	amino acia	w=Trypcopnan, i=Tyrosine, k=Onknown, =Scop
\possible nucleotide insertion		amino acid	sequence	Codon, /=possible nucleotide deletion,
LIDBYTTQGINTVELKADKRADKRIEWAREWEKLIDIKKQLAVEE   KPRENPEKKKK   KPRENPEKKKK   KPRENPEKKKK   KPRENPEKKKK   KPRENPEKKKE   KPRENPEKKKE   KPRENPEKKKE   KPRENPEKKKE   KPRENPEKKE		camiance	-	
SPS7   86		sequence		A POST A PART A
1967  1967  1968  1967  1968				
HILLEVISION/PCCLPVIANARRARGRAVILISTYCEEDCVVPPIL   RYVIVALORISMYLY INSTAILCRY PLISANARYTI NYMOGRAG EDVISSYRRTI-HTHRISL   RO   Norphilagetes individually plicolopalines is selected in the property of the pr				KPPEAPKGKKKK
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ΙĎ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ			
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
<del></del>	204		QKAPEEFELLSKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG
1	1	}	/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
ì	1	1	
		1	NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL
}	1		NTARLLGLQA
5901	1	2121	VAIBQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
3301	1 -	}	KTHLDTVLPKLTCPQCNKBPPNQESLLKHVTIHFMITSTYYICE
	i	1	SCDKQFTSVDDLQKHLLDMHTFVFFRCTLCQKVFDSKVSIQLHL
	ţ		SCURQF15VDDLQARDDAH1FVFFRC1BCQBVFB3RV31QBBB
İ			\AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK
	l		CIFCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL
ł	1	ł .	REKHCVPETKTPNCGTNGASEQVQKEBVKLQTLLTNSQESHNSH
l	1	[	DGSERDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES
l	1	İ	AIVKKKAELIKGNYKCNVCSRTPFSENGLREHMQTHLGPVKHYM
l	1	1	
I	1	<b> </b>	CPICGERPPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEBFL
I		İ	EHCQMEPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMQKTGN
Ì	1	1	GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
l	1	!	CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVCGL
j		İ	KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP
1	1	İ	OVSPMPRISPSOSDEKKTYOCIKCOMVFYNENDIQVHVANHMID
l	ł	l	EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV
j		•	PVQANKLQQHIPSAHGQEDKIYDCTQCPQKFFFQTBLQNHTMTQ
ŀ			HSS
5902	712	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*R8F
3302	1 /**	""	IPLXPRQ*ED*MFQSWLHAWGDTLEEAPEQCAMAMFGYMTDTGT
	ì		TAPIVAKA PD. MEGAMINAMOD I DERE ARECYDEDALD CACE
İ			VEPLQTVRVETQGDDLQSLLPHFLDEWLYKFSADEFFIP\GWGE
			BPSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT
	1	1	PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA
		[	GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP
		i	LPEAVLALYNSTRDRVAGESABPEPEPEADYYAKEVTRVLMVET
	-	1	HNEIYDKFKQSTHSIYMFFNTSBLRBAVPEPVLLSRABLRLLRL
1	1	l .	
ļ	į.		KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
l '	ŀ	1	RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL
	(	1	ATIHGMNRPFLILMATPLERAQHLQS\SRHRQAL\DTNY\CFSF
			HGGRNCLRC/VHC*HLIFRKDL\GW\KWI\HE\PKGYHANFC\L
1		1	LCCCPVTWSLOTOVSKVLALVNO\HKPG\ASAAP\CCVPOALEP\
			GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\
		·	LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS MMEEIRNAINTFKEEQRLIYEELIKEEKTTNMELSAISRKIDIW
5904	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMREIENAINTFKEKQRLIYEELIKEEKTTNNELSAISRKIDIW ALGNSETEKAPRAISSKYPVDKVTPSTLPBEVLDFEKFLQQTGG
5904	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMREIENAINTFKEKQRLIYEELIKEEKTTNNELSAISRKIDIW ALGNSETEKAPRAISSKYPVDKVTPSTLPBEVLDFEKFLQQTGG
5904	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMREIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDIW ALGNSETEKAPRAISSKYPVDKVTPSTLPBEVLDFEKFLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ
5904	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMREIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDIW ALGNSETEKAPRAISSKYPVDKVTPSTLPBEVLDFEKFLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP
5904	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIENAINTFKEEQELIYEELIKEEKTTNMELSAISRKIDTW ALGNSETEKAFRAISSKVPVDKVTPSTLPBEVLLPEKPLQQTGG RQGAWDDYDHQNFVKVPNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHHKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL
5904	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRNAINTFKEBGRLIYEELIKEEKTTNMELSAISRKIDTW ALGNSTTEKAPRAISSKVPVDKVTPSTLPBEVLDPEKPLQQTGG RQAWDDYDNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HBKWYQKFLALEERKKESIQIWKTKKQQKRBEIPKLKEKADNTP VLFHMKQEDNQKQKEBQRKKQKLAVRAWKKQKSIEMSMKCASQL KEEEEKKKHQKRRQRQFKLKLLLESYTQQKKEQEBFLRLEKEI
5904	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRAINTFKESQRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSBTEKAPRAISSKVPVDKVTPSTLPBEVLDPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKPLALEERKKESIQIWKTKKQQKREBIPKLKEKADNTP VLFHNKQEDNQKQKEBQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEEBKEKKHQKRRQRQFKIKLILLESTTQQKKEGEEFLRLEKEI REKAEKAEKRNAADEISRFQERDLHKLELKILDRQAKBDEKSQ
\$ <b>904</b>	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRNAINTFKEBGRLIYEELIKEEKTTNMELSAISRKIDTW ALGNSTTEKAPRAISSKVPVDKVTPSTLPBEVLDPEKPLQQTGG RQAWDDYDNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HBKWYQKFLALEERKKESIQIWKTKKQQKRBEIPKLKEKADNTP VLFHMKQEDNQKQKEBQRKKQKLAVRAWKKQKSIEMSMKCASQL KEEEEKKKHQKRRQRQFKLKLLLESYTQQKKEQEBFLRLEKEI
5904	3	1126	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRAINTFKESQRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSBTEKAPRAISSKVPVDKVTPSTLPBEVLDPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKPLALEERKKESIQIWKTKKQQKREBIPKLKEKADNTP VLFHNKQEDNQKQKEBQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEEBKEKKHQKRRQRQFKIKLILLESTTQQKKEGEEFLRLEKEI REKAEKAEKRNAADEISRFQERDLHKLELKILDRQAKBDEKSQ
			LPIVYY\VGRRPKVEQLSNMIVRSCKCS  MMBEIRNAINTFKERGRLIYEELIKEEKTINNELSAISRKIDTW ALGNSBTEKAFRAISSKVPVDKVTPSTLPEVILDPEKPLQQTGG RQGAWDDYDHQNFVKVRNKIKGKPTFMEBVLEHLPGKTODEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREBIPKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEBEKEKKHQKRRQRQFKIKILLESTTQQKKEQBEFLRLEKEI REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRIGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR
5904 5905	287	1126 2912	LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRMAINTFKERGRLIYEELIKEEKTINNELSAISRKIDTW ALGNSETEKAFRAISSKYPVDKVTPSTLPEVILDPEKPLQQTGG RQGAWDDYDHQNPVKVRNKKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEEEKSKKHQKRRQRQFKLKLILESTTQQKKEQREFIRLEKEI REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTKKSMR
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIENAINTFKEEQRLIYEELIKEEKTTNMELSAISRKIDTW ALGNSTTEKAFRAISSKVPVDKVTPSTLPBEVLLPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHHKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEREKEKKHQKRRQRQPKLKLLLESYTQQKKEQBEFLRLEKEI REKAEKAEKKNAADEISKFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKETVRLTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIENAINTFKEEGRLIYBELIKEEKTTNNELSAISRKIDTW ALGNSTTEKAFRAISSKVPVDKVTPSTLPBEVLDPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VIFHNKQEDNQKQKEEQRKKQKLAVERWKKQKSIEMSMKCASQL KEEEEKEKKHQKRRQRQPKLKLLLESYTQQKKEQEEFLRLEKEI REKAEKAEKRNAADBISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRNAINTFKEBGRLIYBELIKEEKTTNNELSAISRKIDTW ALGNSTTEKAFRAISSKVPVDKVTPSTLPBEVLDPEKPLQQTGG RQAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HBKWYQKFLALEERKKESIQIWKTKKQQKRBEIFKLKKADNTP VLFHNKQBDNQKCEBQRKKQKLAVRAWKKQKSIEMSMKCASQL KEEBEKEKKHQKRRQRQFKLKLLLESYTQQKKEQEBFLRLEKEI RBKAEKABKRNAADBISRFQERDLHKLELKILDRQAKEDEKSQ KORRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTYGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRNAINTFKEBGRLIYBELIKEEKTTNNELSAISRKIDTW ALGNSTTEKAFRAISSKVPVDKVTPSTLPBEVLDPEKPLQQTGG RQAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HBKWYQKFLALEERKKESIQIWKTKKQQKRBEIFKLKKADNTP VLFHNKQBDNQKCEBQRKKQKLAVRAWKKQKSIEMSMKCASQL KEEBEKEKKHQKRRQRQFKLKLLLESYTQQKKEQEBFLRLEKEI RBKAEKABKRNAADBISRFQERDLHKLELKILDRQAKEDEKSQ KORRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTYGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRNAINTFKEBGRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSTTEKAPRAISSKVPVDKVTPSTLPBEVLDPEKPLQQTGE RQAWDDYDKVPNKHKKGKPTFMEEVLEHLPGKTQDEVQQ HBKWYQKFLALEERKKESIQIWKTKKQQKRBEIPKLKEKADNTP VLFHNKQEDNQKQKEBQRKKQKLAVRAWKKQKSIEMSMKCASQL KEEBEKKKHQKRRQRQFKLKLLLESYTQQKKEQBEFLRLEKEI REKAEKAEKRNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTKKSMR MASFPPRVNEKEIVRLRTYGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNLEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWV\
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRMAINTFKERGRLIYEELIKEEKTINNELSAISRKIDTW ALGNSETEKAFRAISKVPVDKVTPSTLPEVLLDFEVLQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTODEVQQ HEKWYQKPLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEEBEKKHQKRRQRQFKIKILLESTTQQKKEQEEFLRLEKEI REKAEKAEKRKNAADEISRFOERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTKKSMR  MASFPPRVNEKEIVRLETTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPERQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLINLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMVVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRMAINTFKERGRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSETEKAFRAISSKYPVDKVTPSTLPBEVLDPEKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEREKEKKHQKERQRQFKLKLLLESYTQQKKEQREFIRLEKEI REKAEKAEKRKNAADEISKFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTKKSMR MASFPPRVNEKEIVRLRTKGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPERQSRCVNIEMH RFFFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSILLVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHISHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSTTEKAFRAISSKYPVDKVTPSTLPBEVLDPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEEEKEKKHQKRRQRQPKLKLLLESYTQQKKEQBEFLRLEKEI REKAEKAEKKRNAADEISKFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKETVRLTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH RFRFGQDQLLLATGINSGRIKIWDVYTGKLLIMUVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MKVLRGHQNWV\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVURCWSMSTFCF SFFLFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI
			LPIVYY\VGRRPRVEQLSNMIVRSCKCS  MMEEIENAINTFKEEGRLIYBELIKEEKTTNNELSAISRKIDTW ALGNSTTEKAFRAISSKVPVDKVTPSTLPBEVLDPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVERWKKQKSIEMSMKCASQL KEEEEKEKKHQKRRQRQPKLKLLLESYTQQKKEQEEFLRLEKEI REKAEKAEKRNAADBISRFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIENH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDGN\MMKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHECWSMSTFCF SFFLFFFFKVISFTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDLLRL*FNLKFVLIFF*K*CIVSVQK
			LPIVYY\VGRRPRVEQLSNMIVRSCKCS  MMEEIENAINTFKEEGRLIYBELIKEEKTTNNELSAISRKIDTW ALGNSTTEKAFRAISSKVPVDKVTPSTLPBEVLDPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVERWKKQKSIEMSMKCASQL KEEEEKEKKHQKRRQRQPKLKLLLESYTQQKKEQEEFLRLEKEI REKAEKAEKRNAADBISRFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIENH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDGN\MMKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHECWSMSTFCF SFFLFFFFKVISFTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDLLRL*FNLKFVLIFF*K*CIVSVQK
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIENAINTFKEEGRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSTTEKAFRAISSKVPVDKVTPSTLPBEVLDPRKPLQQTGG RQAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVRAWKKQKSIEMSMKCASQL KEEEBKEKKHQKRRQRQFKLKLLLESYTQQKKEQEBFLRLEKEI RBKAEKAEKRNAADBISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATNVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFYLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS*
			LPIVYY\VGRRPRVEQLSNMIVRSCKCS  MMEETRAINTFREGGRLTYEELIKEEKTTNBELSAISRKIDTW ALGNSETEKAFRAISKVPVDKVTPSTLPEVILDPEVLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTODEVQQ HEKWYQKPLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEBEKEKKHQKRRQRQFKIKILLESTTQQKKEQBEFLRLEKEI REKAEKAEKRKNAADEISRFOERDLHKLLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTKKSMR  MASFPPRVNEKEIVRLÄTKGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIDCGDIVWSLAFGSSVPEKQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLINLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVURCWSMSTFCF SFFLFFFFKVISFTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPKEIALLQERRLS*DRPPSSHLL*TTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKWVKF*FIEM
			LPIVYY\VGRRPKVEQLSNMIVRSCKCS  MMEEIRMAINTFKERGRLIYEELIKEEKTINBELSAISRKIDTW ALGNSETEKAFRAISSKYPVDKVTPSTLPBEVLDPEKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEULEHLPGKTQDEVQQ HEKWYQKPLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEEEKSKKHQKRRQRQFKLKLLLESTTQQKKEQREFIRLEKEI REKAEKABKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTKKSMR  MASFPPRVNEKEIVRLRTYGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH RFFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MKVLKGHONWY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKWVKF*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRMAINTFKEGGRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSETEKAFRAISSKYPVDKVTPSTLPBEVLDPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKPLALEERKKESIQIWKTKKQQKREEIFKLKKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEREKEKKHQKRRQRQPKLKLLLESYTQQKKEQEEFIRLEKEI RKKAEKAEKKRNAADEISKFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTKKSMR MASFPPRVNEKEIVRLRTXGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBRQSRCVNIEWH RFFFGQDQLLLATGLNSGRIKIWDVYTGKLLLNUVDHTGVVRDL TFAPDGSILLVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHISHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILGDSRDILRL*PNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKWVKP*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFRCSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK
			LPIVYY\VGRRPRVEQLSNMIVRSCKCS  MMEEIENAINTFKEEGRLIYEELIKEERTTNNELSAISRKIDTW ALGNSTTEKAFRAISSKYPVDKVTPSTLPBEVLDPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKPLALEERKKES TQIWKTKKQQKREEIFKLKEKADNTP VLFHHKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEEEKEKKHQKRRQRQPKLKLLLESYTQQKKEQBEFLRLEKEI REKAEKAEKKRNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKETVRLRTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH RPFFGQDQLLLATGINSGRIKIWDVYTGKLLLNUVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MKVLKGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPKEIALLQEERLS*DKPPSSHLI*QFTVNIKILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKWVKF*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCOWSNNILTIRFLSVYFFKNLVVSGKK REGGL*YLITLFISVYFS*LVFGINGFQYSFVKKHCLYFMFRLI
			LPIVYY\VGRRPKVEQLSNMIVRSCKCS  MMBEIRNAINTFKERGRLIYEELIKEEKTINBELSAISRKIDTW ALGNSETEKAFRAISKVPVDKVTPSTLPBEVLDPEKPLQQTGG RQGAWDDYDHQNPVKVRNKIKGKPTFMEBULEHLPGKTODEVQQ HEKWYQKPLALEERKKESIQIWKTKKQQKRBEIPKLKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEBEKEKKHQKRRQRQFKIKI.LLESTTQQKKEGBEFLRLEKEI REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR  MASFPPRVNEKEIVRLETTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGSVPEKGGRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSILLVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLPWLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFP*K*CIVSVQK KKKPKRIALLQERRLS*DRPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPPYIQMTYDRG*FGKNKWVKF*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFRCSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLLVSGKK REGL*YLTLFISVYFS*LVFGINGFQYSFVVKLHCLYFMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIXNA*
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS  MMEEIRMAINTFKEGGRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSETEKAFRAISSKYPVDKVTPSTLPBEVLDPRKPLQQTGG RQGAWDDYDHQNPVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKPLALEERKKESIQIWKTKKQQKREEIFKLKKEKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL KEEREKEKKHQKRRQRQPKLKLLLESYTQQKKEQEEFIRLEKEI RKKAEKAEKKRNAADEISKFQERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTKKSMR MASFPPRVNEKEIVRLRTXGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBRQSRCVNIEWH RFFFGQDQLLLATGLNSGRIKIWDVYTGKLLLNUVDHTGVVRDL TFAPDGSILLVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHISHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILGDSRDILRL*PNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKWVKP*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFRCSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK